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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 54.6792 Seconds
(without alignments)
2460.550 Million cell updates/sec

Perfect score: 1657
Sequence: 1 MARCFSLVLLLTSIWTTRLL.....NPEESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
3	1657	100.0	322	3	US-09-905-291A-201	Sequence 201, App
93	1657	100.0	322	4	US-10-223-085-32	Sequence 32, Appl
94	1657	100.0	322	4	US-10-223-084-32	Sequence 32, Appl
95	1657	100.0	322	4	US-10-223-088-32	Sequence 32, Appl
96	1657	100.0	322	4	US-10-223-090-32	Sequence 32, Appl
98	1657	100.0	322	4	US-10-223-087-32	Sequence 32, Appl
101	1657	100.0	322	4	US-10-223-083-32	Sequence 32, Appl
102	1657	100.0	322	4	US-10-079-111-1	Sequence 1, Appli
103	1657	100.0	322	4	US-10-223-089-32	Sequence 32, Appl
108	1657	100.0	322	4	US-10-299-976-201	Sequence 201, App
136	1657	100.0	322	4	US-10-063-742-6	Sequence 6, Appli
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230	1657	100.0	322	4	US-10-298-993-201	Sequence 201, App
231	1657	100.0	322	4	US-10-305-654-32	Sequence 32, Appl
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233	1657	100.0	322	4	US-10-449-656-201	Sequence 201, App
234	1657	100.0	322	4	US-10-448-713-201	Sequence 201, App
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1165	111	6.7	2409	4	US-10-177-293-90	Sequence 90, Appl
1166	111	6.7	2409	5	US-10-741-600-1175	Sequence 1175, Ap
1167	111	6.7	2409	5	US-10-741-600-1177	Sequence 1177, Ap
1168	111	6.7	2409	5	US-10-482-029-194	Sequence 194, App
1169	111	6.7	2409	5	US-10-852-335A-184	Sequence 184, App
1170	110	6.6	341	3	US-09-948-820-48	Sequence 48, Appl
1171	110	6.6	341	5	US-10-613-076-48	Sequence 48, Appl
1172	109	6.6	353	5	US-10-960-275-11	Sequence 11, Appl
1173	109	6.6	1321	4	US-10-241-220-82	Sequence 82, Appl
1174	109	6.6	1321	4	US-10-295-027-262	Sequence 262, App
1175	109	6.6	1321	4	US-10-408-765A-1421	Sequence 1421, Ap
1176	109	6.6	1321	4	US-10-698-190-18	Sequence 18, Appl
1177	109	6.6	1321	5	US-10-872-972-82	Sequence 82, Appl
1178	109	6.6	1321	5	US-10-872-991-82	Sequence 82, Appl
1179	108	6.5	322	4	US-10-120-907A-32	Sequence 32, Appl
1180	108	6.5	322	4	US-10-120-907A-33	Sequence 33, Appl
1181	108	6.5	354	4	US-10-120-907A-3	Sequence 3, Appli
1182	108	6.5	354	4	US-10-120-907A-7	Sequence 7, Appli
1183	108	6.5	354	4	US-10-120-907A-9	Sequence 9, Appli
1184	108	6.5	354	4	US-10-120-907A-11	Sequence 11, Appl
1185	108	6.5	354	4	US-10-120-907A-13	Sequence 13, Appl
1186	108	6.5	354	4	US-10-120-907A-15	Sequence 15, Appl
1187	108	6.5	354	4	US-10-120-907A-17	Sequence 17, Appl
1188	108	6.5	354	4	US-10-120-907A-19	Sequence 19, Appl
1189	108	6.5	354	4	US-10-120-907A-21	Sequence 21, Appl
1190	108	6.5	354	4	US-10-120-907A-23	Sequence 23, Appl
1191	108	6.5	354	4	US-10-120-907A-24	Sequence 24, Appl
1192	108	6.5	354	4	US-10-120-907A-28	Sequence 28, Appl
1193	108	6.5	354	4	US-10-120-907A-29	Sequence 29, Appl
1194	108	6.5	354	4	US-10-120-907A-30	Sequence 30, Appl
1195	108	6.5	354	4	US-10-120-907A-36	Sequence 36, Appl
1196	108	6.5	354	4	US-10-120-907A-38	Sequence 38, Appl
1197	108	6.5	354	4	US-10-120-907A-42	Sequence 42, Appl
1198	108	6.5	354	4	US-10-120-907A-64	Sequence 64, Appl
1199	108	6.5	354	4	US-10-120-907A-66	Sequence 66, Appl
1200	108	6.5	354	5	US-10-754-473-19	Sequence 19, Appl
1201	108	6.5	354	5	US-10-754-473-22	Sequence 22, Appl
1202	108	6.5	721	4	US-10-120-907A-5	Sequence 5, Appli
1203	108	6.5	721	4	US-10-120-907A-25	Sequence 25, Appl
1204	108	6.5	721	4	US-10-120-907A-43	Sequence 43, Appl
1205	108	6.5	721	4	US-10-120-907A-65	Sequence 65, Appl
1206	108	6.5	721	4	US-10-120-907A-67	Sequence 67, Appl
1207	107	6.5	93	4	US-10-133-172-5	Sequence 5, Appli
1208	107	6.5	315	4	US-10-667-723-4	Sequence 4, Appli
1209	107	6.5	339	5	US-10-754-473-21	Sequence 21, Appl
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1211	107	6.5	355	4	US-10-120-907A-31	Sequence 31, Appl
1212	107	6.5	355	5	US-10-754-473-20	Sequence 20, Appl
1213	107	6.5	355	5	US-10-960-275-9	Sequence 9, Appli
1214	107	6.5	1268	4	US-10-698-190-24	Sequence 24, Appl
1215	107	6.5	1795	6	US-11-097-143-36210	Sequence 36210, A
1216	107	6.5	2420	4	US-10-028-248A-4	Sequence 4, Appli
1217	107	6.5	2420	4	US-10-107-782-4	Sequence 4, Appli
1218	105	6.3	354	4	US-10-120-907A-37	Sequence 37, Appl
1219	105	6.3	354	5	US-10-754-473-18	Sequence 18, Appl
1220	104	6.3	98	3	US-09-799-118-4	Sequence 4, Appli
1221	104	6.3	139	4	US-10-741-601-342	Sequence 342, App
1222	104	6.3	139	5	US-10-473-127-2037	Sequence 2037, Ap
1223	104	6.3	139	5	US-10-473-127-2040	Sequence 2040, Ap
1224	104	6.3	139	5	US-10-741-600-1050	Sequence 1050, Ap
1225	104	6.3	1712	6	US-11-097-143-8400	Sequence 8400, Ap
1226	102.5	6.2	183	6	US-11-097-143-24753	Sequence 24753, A
1227	102	6.2	309	4	US-10-425-114-41494	Sequence 41494, A
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1229	101.5	6.1	590	3	US-09-957-187-12	Sequence 12, Appl
1230	101.5	6.1	590	6	US-11-058-709-12	Sequence 12, Appl
1231	100.5	6.1	402	4	US-10-343-953-2	Sequence 2, Appli
1232	100.5	6.1	402	4	US-10-257-174-47	Sequence 47, Appl
1233	100.5	6.1	1379	6	US-11-097-143-33612	Sequence 33612, A
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1235	99	6.0	201	4	US-10-120-907A-40	Sequence 40, Appl
1236	99	6.0	201	4	US-10-120-907A-41	Sequence 41, Appl
1237	99	6.0	260	4	US-10-460-512-3	Sequence 3, Appli
1238	99	6.0	260	5	US-10-897-911-3	Sequence 3, Appli
1239	99	6.0	260	5	US-10-898-615-3	Sequence 3, Appli
1240	99	6.0	1428	6	US-11-097-143-37923	Sequence 37923, A
1241	99	6.0	5376	4	US-10-028-248A-74	Sequence 74, Appl
1242	99	6.0	5376	4	US-10-107-782-74	Sequence 74, Appl
1243	98.5	5.9	1126	6	US-11-097-143-35952	Sequence 35952, A
1244	98	5.9	2112	6	US-11-097-143-8001	Sequence 8001, Ap
1245	95.5	5.8	376	3	US-09-801-368-206	Sequence 206, App
1246	95.5	5.8	585	5	US-10-868-381-58	Sequence 58, Appl
1247	95.5	5.8	1217	4	US-10-437-963-183891	Sequence 183891,
1248	95.5	5.8	5374	4	US-10-028-248A-75	Sequence 75, Appl
1249	95.5	5.8	5374	4	US-10-107-782-75	Sequence 75, Appl
1250	93.5	5.6	258	3	US-09-764-853-840	Sequence 840, App
1251	93.5	5.6	258	4	US-10-091-438-205	Sequence 205, App
1252	93.5	5.6	261	3	US-09-764-853-669	Sequence 669, App
1253	93.5	5.6	261	4	US-10-091-438-144	Sequence 144, App
1254	93.5	5.6	320	5	US-10-450-763-31869	Sequence 31869, A
1255	93.5	5.6	339	5	US-10-391-939A-2	Sequence 2, Appli
1256	93.5	5.6	339	5	US-10-391-939A-28	Sequence 28, Appl
1257	93.5	5.6	359	4	US-10-188-012-17	Sequence 17, Appl
1258	93.5	5.6	359	4	US-10-188-012-19	Sequence 19, Appl
1259	93.5	5.6	359	4	US-10-188-012-23	Sequence 23, Appl
1260	93.5	5.6	359	4	US-10-295-027-302	Sequence 302, App
1261	93.5	5.6	359	4	US-10-188-832-64	Sequence 64, Appl
1262	93.5	5.6	359	5	US-10-391-939A-4	Sequence 4, Appli
1263	93.5	5.6	359	5	US-10-663-497-17	Sequence 17, Appl
1264	93.5	5.6	359	5	US-10-663-497-19	Sequence 19, Appl
1265	93.5	5.6	359	5	US-10-663-497-23	Sequence 23, Appl
1266	93.5	5.6	359	5	US-10-718-321-8	Sequence 8, Appli
1267	93.5	5.6	359	5	US-10-847-918-25	Sequence 25, Appl
1268	93.5	5.6	366	5	US-10-450-763-38282	Sequence 38282, A
1269	93.5	5.6	1595	5	US-10-484-218-20	Sequence 20, Appl
1270	92.5	5.6	40	5	US-10-487-620-26	Sequence 26, Appl
1271	92.5	5.6	300	3	US-09-953-499-10	Sequence 10, Appl
1272	92.5	5.6	300	4	US-10-265-542-10	Sequence 10, Appl
1273	92.5	5.6	300	4	US-10-633-008-10	Sequence 10, Appl
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1275	92.5	5.6	300	4	US-10-785-221-10	Sequence 10, Appl
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1277	92.5	5.6	300	4	US-10-767-904-10	Sequence 10, Appl
1278	92.5	5.6	300	5	US-10-767-374-10	Sequence 10, Appl
1279	92.5	5.6	300	5	US-10-785-607-10	Sequence 10, Appl
1280	92.5	5.6	300	5	US-10-785-351-12	Sequence 12, Appl
1281	92.5	5.6	365	4	US-10-188-012-21	Sequence 21, Appl
1282	92.5	5.6	365	5	US-10-663-497-21	Sequence 21, Appl
1283	92.5	5.6	569	4	US-10-282-122A-60442	Sequence 60442, A
1284	92.5	5.6	994	4	US-10-369-493-1516	Sequence 1516, Ap
1285	92	5.6	364	4	US-10-188-012-25	Sequence 25, Appl
1286	92	5.6	364	5	US-10-663-497-25	Sequence 25, Appl
1287	92	5.6	966	3	US-09-801-368-372	Sequence 372, App
1288	92	5.6	966	4	US-10-451-467A-52	Sequence 52, Appl
1289	91.5	5.5	166	3	US-09-764-853-777	Sequence 777, App
1290	91.5	5.5	166	4	US-10-091-438-181	Sequence 181, App
1291	91.5	5.5	350	4	US-10-239-431A-6	Sequence 6, Appli
1292	91.5	5.5	376	4	US-10-239-431A-4	Sequence 4, Appli
1293	91.5	5.5	610	4	US-10-239-431A-2	Sequence 2, Appli
1294	91.5	5.5	639	3	US-09-825-144-9	Sequence 9, Appli
1295	91.5	5.5	639	3	US-09-823-240-5	Sequence 5, Appli
1296	91.5	5.5	681	4	US-10-353-856-23	Sequence 23, Appl
1297	91.5	5.5	1103	4	US-10-369-493-3228	Sequence 3228, Ap
1298	91	5.5	246	4	US-10-032-201B-188	Sequence 188, App
1299	91	5.5	2207	4	US-10-437-963-189767	Sequence 189767,
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1301	91	5.5	4493	5	US-10-704-781-3	Sequence 3, Appli
1302	90.5	5.5	463	4	US-10-425-114-66913	Sequence 66913, A
1303	90.5	5.5	463	4	US-10-425-115-322413	Sequence 322413,
1304	90.5	5.5	505	4	US-10-442-017-17	Sequence 17, Appl
1305	90.5	5.5	1714	6	US-11-097-143-7350	Sequence 7350, Ap
1306	90.5	5.5	1976	6	US-11-097-143-35049	Sequence 35049, A

1307	90	5.4	364	4	US-10-188-012-27	Sequence 27, Appl
1308	90	5.4	364	5	US-10-663-497-27	Sequence 27, Appl
1309	90	5.4	629	6	US-11-097-143-5313	Sequence 5313, Ap
1310	90	5.4	957	3	US-09-840-746-19	Sequence 19, Appl
1311	90	5.4	1130	4	US-10-425-115-339478	Sequence 339478,
1312	90	5.4	1217	4	US-10-734-564-122	Sequence 122, App
1313	90	5.4	1367	3	US-09-801-368-108	Sequence 108, App
1314	89.5	5.4	195	4	US-10-074-978A-350	Sequence 350, App
1315	89.5	5.4	305	4	US-10-188-012-5	Sequence 5, Appli
1316	89.5	5.4	305	4	US-10-188-012-7	Sequence 7, Appli
1317	89.5	5.4	305	5	US-10-663-497-5	Sequence 5, Appli
1318	89.5	5.4	305	5	US-10-663-497-7	Sequence 7, Appli
1319	89.5	5.4	1368	5	US-10-732-923-13518	Sequence 13518, A
1320	89.5	5.4	1369	5	US-10-732-923-13517	Sequence 13517, A
1321	89	5.4	307	6	US-11-097-143-24429	Sequence 24429, A
1322	89	5.4	416	4	US-10-371-525-26	Sequence 26, Appl
1323	89	5.4	416	4	US-10-371-069-26	Sequence 26, Appl
1324	89	5.4	416	4	US-10-371-645-26	Sequence 26, Appl
1325	89	5.4	416	4	US-10-371-260-26	Sequence 26, Appl
1326	89	5.4	416	5	US-10-684-422-68	Sequence 68, Appl
1327	89	5.4	416	5	US-10-287-436A-533	Sequence 533, App
1328	89	5.4	416	5	US-10-287-436A-1224	Sequence 1224, Ap
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1332	89	5.4	2588	4	US-10-437-963-138279	Sequence 138279,
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1334	88.5	5.3	358	5	US-10-450-763-45673	Sequence 45673, A
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1336	88.5	5.3	615	4	US-10-239-818-14	Sequence 14, Appl
1337	88	5.3	125	4	US-10-424-599-221671	Sequence 221671,
1338	88	5.3	995	3	US-09-984-130-48	Sequence 48, Appl
1339	88	5.3	995	3	US-09-836-353A-48	Sequence 48, Appl
1340	88	5.3	3507	4	US-10-369-493-5784	Sequence 5784, Ap
1341	87.5	5.3	536	4	US-10-218-743-21	Sequence 21, Appl
1342	87.5	5.3	555	4	US-10-218-743-15	Sequence 15, Appl
1343	87.5	5.3	555	4	US-10-218-743-18	Sequence 18, Appl
1344	87.5	5.3	649	4	US-10-425-115-295178	Sequence 295178,
1345	87.5	5.3	717	4	US-10-104-047-3100	Sequence 3100, Ap
1346	87.5	5.3	1085	4	US-10-159-339-10	Sequence 10, Appl
1347	87.5	5.3	1085	4	US-10-041-615-108	Sequence 108, App
1348	87.5	5.3	1085	4	US-10-436-715-21	Sequence 21, Appl
1349	87.5	5.3	1085	4	US-10-436-715-75	Sequence 75, Appl
1350	87.5	5.3	1322	4	US-10-369-493-13040	Sequence 13040, A
1351	87	5.3	288	3	US-09-216-393-341	Sequence 341, App
1352	87	5.3	288	3	US-09-216-393-344	Sequence 344, App
1353	87	5.3	288	4	US-10-321-856-341	Sequence 341, App
1354	87	5.3	288	4	US-10-321-856-344	Sequence 344, App
1355	87	5.3	363	5	US-10-926-543-87	Sequence 87, Appl
1356	87	5.3	363	5	US-10-631-467-1565	Sequence 1565, Ap
1357	87	5.3	611	4	US-10-425-114-54378	Sequence 54378, A
1358	87	5.3	631	3	US-09-841-132-325	Sequence 325, App
1359	87	5.3	631	5	US-10-872-155-325	Sequence 325, App
1360	87	5.3	650	4	US-10-425-115-353793	Sequence 353793,
1361	87	5.3	664	5	US-10-197-220-168	Sequence 168, App
1362	87	5.3	664	6	US-11-109-468-168	Sequence 168, App
1363	87	5.3	1016	3	US-09-841-260-95	Sequence 95, Appl
1364	87	5.3	1016	4	US-10-007-693-95	Sequence 95, Appl
1365	87	5.3	1016	4	US-10-467-534-41	Sequence 41, Appl
1366	87	5.3	1016	4	US-10-762-058-95	Sequence 95, Appl
1367	87	5.3	1016	5	US-10-197-220-95	Sequence 95, Appl
1368	87	5.3	1016	5	US-10-498-327-95	Sequence 95, Appl
1369	87	5.3	1016	6	US-11-109-468-95	Sequence 95, Appl
1370	87	5.3	1537	3	US-09-801-368-104	Sequence 104, App
1371	87	5.3	1537	4	US-10-369-493-1398	Sequence 1398, Ap
1372	87	5.3	1537	5	US-10-324-035-17	Sequence 17, Appl
1373	87	5.3	1575	6	US-11-097-143-28878	Sequence 28878, A
1374	86.5	5.2	162	4	US-10-437-963-145598	Sequence 145598,
1375	86.5	5.2	175	4	US-10-424-599-183022	Sequence 183022,
1376	86.5	5.2	245	4	US-10-425-115-334180	Sequence 334180,
1377	86.5	5.2	503	3	US-09-801-368-424	Sequence 424, App
1378	86.5	5.2	503	4	US-10-369-493-1943	Sequence 1943, Ap
1379	86.5	5.2	687	4	US-10-282-122A-53666	Sequence 53666, A
1380	86.5	5.2	714	5	US-10-450-763-45506	Sequence 45506, A
1381	86.5	5.2	714	5	US-10-450-763-46006	Sequence 46006, A
1382	86.5	5.2	1579	5	US-10-504-582-158	Sequence 158, App
1383	86.5	5.2	2781	4	US-10-263-929-122	Sequence 122, App
1384	86.5	5.2	2781	4	US-10-754-342-10	Sequence 10, Appl
1385	86.5	5.2	2781	5	US-10-723-860-1472	Sequence 1472, Ap
1386	86.5	5.2	2907	4	US-10-754-342-1	Sequence 1, Appli
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1388	86	5.2	857	4	US-10-425-114-45539	Sequence 45539, A
1389	86	5.2	1080	4	US-10-205-219-62	Sequence 62, Appl
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1391	86	5.2	1190	5	US-10-450-763-36034	Sequence 36034, A
1392	85.5	5.2	346	4	US-10-416-328-6	Sequence 6, Appli
1393	85.5	5.2	346	4	US-10-432-290-11	Sequence 11, Appl
1394	85.5	5.2	346	5	US-10-498-778-6	Sequence 6, Appli
1395	85.5	5.2	652	4	US-10-467-490-5	Sequence 5, Appli
1396	85.5	5.2	662	4	US-10-425-115-230245	Sequence 230245,
1397	85.5	5.2	686	4	US-10-282-122A-43763	Sequence 43763, A
1398	85.5	5.2	781	4	US-10-074-978A-286	Sequence 286, App
1399	85.5	5.2	781	4	US-10-664-456-16	Sequence 16, Appl
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1405	85.5	5.2	1794	3	US-09-965-738-299	Sequence 299, App
1406	85.5	5.2	1799	3	US-09-965-738-149	Sequence 149, App
1407	85.5	5.2	1821	3	US-09-965-738-82	Sequence 82, Appl
1408	85.5	5.2	2055	4	US-10-193-874-20	Sequence 20, Appl
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1410	85.5	5.2	2586	3	US-09-729-485A-14	Sequence 14, Appl
1411	85.5	5.2	2586	3	US-09-802-318-11	Sequence 11, Appl
1412	85.5	5.2	2586	3	US-09-802-318-14	Sequence 14, Appl
1413	85.5	5.2	2586	3	US-09-905-129-11	Sequence 11, Appl
1414	85.5	5.2	2586	3	US-09-905-129-14	Sequence 14, Appl
1415	85.5	5.2	2586	3	US-09-991-630-11	Sequence 11, Appl
1416	85.5	5.2	2586	3	US-09-991-630-14	Sequence 14, Appl
1417	85.5	5.2	2586	4	US-10-454-351-11	Sequence 11, Appl
1418	85.5	5.2	2586	4	US-10-454-351-14	Sequence 14, Appl
1419	85.5	5.2	2587	3	US-09-729-485A-16	Sequence 16, Appl
1420	85.5	5.2	2587	3	US-09-802-318-16	Sequence 16, Appl
1421	85.5	5.2	2587	3	US-09-905-129-16	Sequence 16, Appl
1422	85.5	5.2	2587	3	US-09-991-630-16	Sequence 16, Appl
1423	85.5	5.2	2587	4	US-10-454-351-16	Sequence 16, Appl
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1425	85.5	5.2	2589	4	US-10-454-351-24	Sequence 24, Appl
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173	76.5	4.6	773	7	US-11-010-239-63	Sequence 63, Appl
174	76.5	4.6	1249	7	US-11-126-022-25	Sequence 25, Appl
175	76.5	4.6	1307	7	US-11-072-512-2438	Sequence 2438, Ap
176	76	4.6	336	7	US-11-096-568A-34180	Sequence 34180, A
177	76	4.6	367	7	US-11-096-568A-34179	Sequence 34179, A
178	76	4.6	393	7	US-11-096-568A-34178	Sequence 34178, A
179	76	4.6	400	7	US-11-087-099-8803	Sequence 8803, Ap
180	76	4.6	499	7	US-11-096-568A-32028	Sequence 32028, A
181	76	4.6	509	7	US-11-124-327-2	Sequence 2, Appli
182	76	4.6	536	6	US-10-453-372-30	Sequence 30, Appl
183	76	4.6	542	6	US-10-453-372-10	Sequence 10, Appl
184	76	4.6	552	6	US-10-453-372-14	Sequence 14, Appl
185	76	4.6	560	7	US-11-080-991-62	Sequence 62, Appl
186	76	4.6	572	6	US-10-453-372-16	Sequence 16, Appl
187	76	4.6	588	6	US-10-453-372-8	Sequence 8, Appli
188	76	4.6	588	6	US-10-453-372-12	Sequence 12, Appl
189	76	4.6	758	7	US-11-043-693-1	Sequence 1, Appli
190	76	4.6	1014	7	US-11-204-187-20	Sequence 20, Appl
191	76	4.6	1338	6	US-10-821-234-1622	Sequence 1622, Ap
192	76	4.6	1338	7	US-11-109-156-23	Sequence 23, Appl
193	76	4.6	1338	7	US-11-075-047A-2	Sequence 2, Appli
194	75.5	4.6	484	7	US-11-096-568A-6203	Sequence 6203, Ap
195	75.5	4.6	488	7	US-11-096-568A-6202	Sequence 6202, Ap
196	75.5	4.6	499	7	US-11-096-568A-6201	Sequence 6201, Ap
197	75.5	4.6	2343	6	US-10-330-773-904	Sequence 904, App
198	75	4.5	335	7	US-11-096-568A-21687	Sequence 21687, A
199	75	4.5	336	7	US-11-096-568A-21686	Sequence 21686, A
200	75	4.5	941	7	US-11-169-232-14	Sequence 14, Appl
201	75	4.5	1022	7	US-11-169-232-84	Sequence 84, Appl
202	75	4.5	1038	7	US-11-169-232-74	Sequence 74, Appl
203	75	4.5	1049	7	US-11-169-232-58	Sequence 58, Appl
204	75	4.5	1140	7	US-11-169-232-104	Sequence 104, App
205	75	4.5	1270	7	US-11-169-232-44	Sequence 44, Appl
206	75	4.5	1311	7	US-11-169-232-42	Sequence 42, Appl
207	75	4.5	1313	7	US-11-169-232-142	Sequence 142, App
208	75	4.5	1314	7	US-11-169-232-50	Sequence 50, Appl
209	75	4.5	1320	7	US-11-169-232-46	Sequence 46, Appl
210	75	4.5	1320	7	US-11-169-232-60	Sequence 60, Appl
211	75	4.5	1354	7	US-11-169-232-48	Sequence 48, Appl
212	75	4.5	1361	7	US-11-169-232-40	Sequence 40, Appl
213	75	4.5	1363	7	US-11-169-232-52	Sequence 52, Appl
214	75	4.5	1404	7	US-11-169-232-2	Sequence 2, Appli
215	75	4.5	1404	7	US-11-169-232-62	Sequence 62, Appl
216	75	4.5	1874	6	US-10-821-234-1182	Sequence 1182, Ap
217	74.5	4.5	249	7	US-11-128-059-56	Sequence 56, Appl
218	74.5	4.5	441	7	US-11-096-568A-30300	Sequence 30300, A
219	74.5	4.5	671	7	US-11-087-099-8628	Sequence 8628, Ap
220	74.5	4.5	681	7	US-11-096-568A-2501	Sequence 2501, Ap
221	74.5	4.5	733	7	US-11-096-568A-24028	Sequence 24028, A
222	74.5	4.5	759	7	US-11-096-568A-24027	Sequence 24027, A
223	74.5	4.5	764	7	US-11-096-568A-24026	Sequence 24026, A
224	74.5	4.5	998	6	US-10-510-524-1	Sequence 1, Appli
225	74.5	4.5	998	7	US-11-203-251A-88	Sequence 88, Appl
226	74.5	4.5	2801	6	US-10-330-773-630	Sequence 630, App
227	74	4.5	124	7	US-11-128-059-64	Sequence 64, Appl
228	74	4.5	339	6	US-10-498-026-35	Sequence 35, Appl
229	74	4.5	339	6	US-10-498-026-36	Sequence 36, Appl
230	74	4.5	397	7	US-11-096-568A-20883	Sequence 20883, A
231	74	4.5	717	7	US-11-096-568A-28799	Sequence 28799, A
232	74	4.5	860	7	US-11-022-562-217	Sequence 217, App
233	74	4.5	1158	6	US-10-467-657-3112	Sequence 3112, Ap
234	74	4.5	1164	7	US-11-087-099-2278	Sequence 2278, Ap
235	74	4.5	1164	7	US-11-087-099-9070	Sequence 9070, Ap
236	74	4.5	1694	7	US-11-052-554A-83	Sequence 83, Appl
237	73.5	4.4	232	6	US-10-527-500-37	Sequence 37, Appl
238	73.5	4.4	541	7	US-11-201-916-4	Sequence 4, Appli
239	73.5	4.4	713	7	US-11-256-548-2	Sequence 2, Appli
240	73.5	4.4	826	6	US-10-873-528-194	Sequence 194, App
241	73	4.4	304	7	US-11-087-177-4	Sequence 4, Appli
242	73	4.4	311	7	US-11-096-568A-11193	Sequence 11193, A
243	73	4.4	329	6	US-10-995-561-694	Sequence 694, App
244	73	4.4	353	7	US-11-096-568A-11192	Sequence 11192, A
245	73	4.4	488	7	US-11-202-330-5	Sequence 5, Appli
246	73	4.4	512	7	US-11-108-172-1093	Sequence 1093, Ap
247	73	4.4	558	7	US-11-052-554A-20	Sequence 20, Appl
248	73	4.4	558	7	US-11-134-563-12	Sequence 12, Appl
249	73	4.4	646	6	US-10-995-561-695	Sequence 695, App

250	73	4.4	708	6	US-10-636-320-2	Sequence 2, Appli
251	73	4.4	750	7	US-11-124-368A-244	Sequence 244, App
252	73	4.4	750	7	US-11-124-368A-249	Sequence 249, App
253	73	4.4	918	6	US-10-995-561-696	Sequence 696, App
254	73	4.4	948	6	US-10-523-503-68	Sequence 68, Appl
255	73	4.4	1166	6	US-10-501-035-205	Sequence 205, App
256	73	4.4	1207	6	US-10-821-234-1109	Sequence 1109, Ap
257	72.5	4.4	281	7	US-11-087-177-3	Sequence 3, Appli
258	72.5	4.4	302	7	US-11-096-568A-15531	Sequence 15531, A
259	72.5	4.4	389	7	US-11-096-568A-6654	Sequence 6654, Ap
260	72.5	4.4	445	6	US-10-793-626-1294	Sequence 1294, Ap
261	72.5	4.4	498	6	US-10-510-947-9	Sequence 9, Appli
262	72.5	4.4	582	7	US-11-096-568A-24623	Sequence 24623, A
263	72.5	4.4	605	7	US-11-096-568A-24622	Sequence 24622, A
264	72.5	4.4	673	7	US-11-096-568A-24621	Sequence 24621, A
266	72.5	4.4	678	7	US-11-102-240-34	Sequence 34, Appl
267	72.5	4.4	678	7	US-11-103-195-34	Sequence 34, Appl
268	72.5	4.4	743	7	US-11-072-512-2340	Sequence 2340, Ap
269	72.5	4.4	1152	6	US-10-501-035-222	Sequence 222, App
270	72.5	4.4	2244	7	US-11-131-263-41	Sequence 41, Appl
271	72.5	4.4	2314	7	US-11-097-728-2	Sequence 2, Appli
272	72.5	4.4	2353	7	US-11-097-728-6	Sequence 6, Appli
273	72.5	4.4	2801	7	US-11-124-368A-305	Sequence 305, App
274	72.5	4.4	2801	7	US-11-124-367A-433	Sequence 433, App
275	72.5	4.4	2896	7	US-11-124-368A-306	Sequence 306, App
276	72.5	4.4	2896	7	US-11-124-367A-434	Sequence 434, App
277	72.5	4.4	2910	6	US-10-330-773-39	Sequence 39, Appl
278	72.5	4.4	3256	7	US-11-124-368A-304	Sequence 304, App
279	72.5	4.4	3256	7	US-11-124-367A-432	Sequence 432, App
280	72	4.3	245	7	US-11-087-099-299	Sequence 299, App
281	72	4.3	245	7	US-11-096-568A-33799	Sequence 33799, A
282	72	4.3	255	7	US-11-096-568A-7533	Sequence 7533, Ap
283	72	4.3	308	7	US-11-072-512-3898	Sequence 3898, Ap
284	72	4.3	458	6	US-10-540-091-24	Sequence 24, Appl
285	72	4.3	545	7	US-11-201-916-8	Sequence 8, Appli
286	72	4.3	747	7	US-11-182-592-2	Sequence 2, Appli
287	72	4.3	784	6	US-10-467-657-5968	Sequence 5968, Ap
288	72	4.3	1009	6	US-10-514-531-11	Sequence 11, Appl
289	71.5	4.3	232	6	US-10-884-730-366	Sequence 366, App
290	71.5	4.3	308	7	US-11-096-568A-20980	Sequence 20980, A
291	71.5	4.3	330	7	US-11-098-686-10903	Sequence 10903, A
292	71.5	4.3	348	7	US-11-096-568A-20979	Sequence 20979, A
293	71.5	4.3	353	7	US-11-096-568A-12810	Sequence 12810, A
294	71.5	4.3	368	7	US-11-096-568A-20978	Sequence 20978, A
295	71.5	4.3	447	6	US-10-641-678-58	Sequence 58, Appl
296	71.5	4.3	1340	7	US-11-098-686-11135	Sequence 11135, A
297	71	4.3	250	7	US-11-128-059-62	Sequence 62, Appl
298	71	4.3	343	7	US-11-080-091-4	Sequence 4, Appli
299	71	4.3	345	7	US-11-087-177-19	Sequence 19, Appl
300	71	4.3	354	7	US-11-189-817-2	Sequence 2, Appli
301	71	4.3	554	5	US-09-978-360A-410	Sequence 410, App
302	71	4.3	578	7	US-11-087-099-542	Sequence 542, App
303	71	4.3	579	7	US-11-087-099-6979	Sequence 6979, Ap
304	71	4.3	579	7	US-11-087-099-7852	Sequence 7852, Ap
305	71	4.3	581	7	US-11-087-099-2154	Sequence 2154, Ap
306	71	4.3	581	7	US-11-087-099-2375	Sequence 2375, Ap
307	71	4.3	581	7	US-11-087-099-3070	Sequence 3070, Ap
308	71	4.3	581	7	US-11-087-099-3227	Sequence 3227, Ap
309	71	4.3	581	7	US-11-087-099-3736	Sequence 3736, Ap
310	71	4.3	581	7	US-11-087-099-5261	Sequence 5261, Ap
311	71	4.3	581	7	US-11-087-099-7613	Sequence 7613, Ap
312	71	4.3	581	7	US-11-087-099-8783	Sequence 8783, Ap
313	71	4.3	581	7	US-11-087-099-9181	Sequence 9181, Ap
314	71	4.3	581	7	US-11-087-099-10957	Sequence 10957, A
315	71	4.3	581	7	US-11-087-099-11208	Sequence 11208, A
316	71	4.3	581	7	US-11-087-099-11354	Sequence 11354, A
317	71	4.3	581	7	US-11-087-099-12146	Sequence 12146, A
318	71	4.3	582	7	US-11-087-099-4567	Sequence 4567, Ap
319	71	4.3	626	7	US-11-010-748A-1	Sequence 1, Appli
320	71	4.3	1118	7	US-11-113-751-42	Sequence 42, Appl
321	71	4.3	1153	7	US-11-113-751-44	Sequence 44, Appl
322	70.5	4.3	163	7	US-11-096-568A-4288	Sequence 4288, Ap
323	70.5	4.3	231	7	US-11-096-568A-1421	Sequence 1421, Ap
324	70.5	4.3	232	6	US-10-884-730-363	Sequence 363, App
325	70.5	4.3	232	6	US-10-884-730-364	Sequence 364, App
326	70.5	4.3	232	6	US-10-884-730-365	Sequence 365, App
327	70.5	4.3	292	7	US-11-073-226-6	Sequence 6, Appli
328	70.5	4.3	497	7	US-11-072-512-3603	Sequence 3603, Ap
329	70.5	4.3	512	6	US-10-821-234-1032	Sequence 1032, Ap
330	70.5	4.3	750	7	US-11-096-568A-30499	Sequence 30499, A
331	70.5	4.3	885	7	US-11-096-568A-30498	Sequence 30498, A
332	70.5	4.3	911	7	US-11-096-568A-30497	Sequence 30497, A
333	70.5	4.3	989	6	US-10-821-234-975	Sequence 975, App
334	70.5	4.3	1980	7	US-11-179-624-3	Sequence 3, Appli
335	70	4.2	221	7	US-11-096-568A-28866	Sequence 28866, A
336	70	4.2	224	7	US-11-096-568A-7141	Sequence 7141, Ap
337	70	4.2	256	7	US-11-096-568A-7140	Sequence 7140, Ap
338	70	4.2	289	7	US-11-096-568A-28865	Sequence 28865, A
339	70	4.2	323	7	US-11-096-568A-21688	Sequence 21688, A
340	70	4.2	393	5	US-09-930-864-1	Sequence 1, Appli
341	70	4.2	427	7	US-11-096-568A-28864	Sequence 28864, A
342	70	4.2	467	7	US-11-087-099-2054	Sequence 2054, Ap
343	70	4.2	485	6	US-10-501-035-349	Sequence 349, App
344	70	4.2	531	7	US-11-096-568A-19343	Sequence 19343, A
345	70	4.2	578	6	US-10-821-234-1039	Sequence 1039, Ap
346	70	4.2	609	7	US-11-110-082-40	Sequence 40, Appl
347	70	4.2	733	7	US-11-096-568A-29646	Sequence 29646, A
348	70	4.2	735	7	US-11-096-568A-29645	Sequence 29645, A
349	70	4.2	735	7	US-11-096-568A-31569	Sequence 31569, A
350	70	4.2	768	7	US-11-096-568A-29644	Sequence 29644, A
351	70	4.2	768	7	US-11-096-568A-31568	Sequence 31568, A
352	70	4.2	770	7	US-11-096-568A-31567	Sequence 31567, A
353	70	4.2	1256	6	US-10-517-696-111	Sequence 111, App
354	70	4.2	1416	7	US-11-128-059-60	Sequence 60, Appl
355	70	4.2	2011	7	US-11-080-991-56	Sequence 56, Appl
356	69.5	4.2	106	7	US-11-096-568A-19298	Sequence 19298, A
357	69.5	4.2	162	7	US-11-096-568A-641	Sequence 641, App
358	69.5	4.2	173	7	US-11-096-568A-452	Sequence 452, App
359	69.5	4.2	173	7	US-11-096-568A-453	Sequence 453, App
360	69.5	4.2	175	7	US-11-087-099-6466	Sequence 6466, Ap
361	69.5	4.2	215	6	US-10-467-657-476	Sequence 476, App
363	69.5	4.2	312	6	US-10-973-115B-336	Sequence 336, App
364	69.5	4.2	349	7	US-11-096-568A-10641	Sequence 10641, A
365	69.5	4.2	453	7	US-11-052-554A-224	Sequence 224, App
366	69.5	4.2	461	7	US-11-096-568A-10640	Sequence 10640, A
367	69.5	4.2	497	7	US-11-072-512-3773	Sequence 3773, Ap
368	69.5	4.2	519	7	US-11-087-099-9352	Sequence 9352, Ap
369	69.5	4.2	533	6	US-10-330-773-666	Sequence 666, App
370	69.5	4.2	567	7	US-11-016-503-2	Sequence 2, Appli
371	69.5	4.2	618	7	US-11-087-099-9161	Sequence 9161, Ap
372	69.5	4.2	626	7	US-11-072-512-2827	Sequence 2827, Ap
373	69.5	4.2	646	7	US-11-087-099-6754	Sequence 6754, Ap
374	69.5	4.2	713	6	US-10-330-773-668	Sequence 668, App
375	69.5	4.2	862	7	US-11-051-720-1443	Sequence 1443, Ap
376	69.5	4.2	1007	7	US-11-051-720-1445	Sequence 1445, Ap
377	69.5	4.2	1120	7	US-11-051-720-1733	Sequence 1733, Ap
378	69.5	4.2	1305	7	US-11-051-720-1370	Sequence 1370, Ap
379	69.5	4.2	16990	7	US-11-175-689-7	Sequence 7, Appli
380	69	4.2	143	7	US-11-096-568A-8463	Sequence 8463, Ap
381	69	4.2	180	7	US-11-096-568A-12758	Sequence 12758, A
382	69	4.2	443	7	US-11-087-099-7683	Sequence 7683, Ap
383	69	4.2	476	7	US-11-055-822-540	Sequence 540, App
384	69	4.2	476	7	US-11-055-822-542	Sequence 542, App
385	69	4.2	476	7	US-11-055-822-1122	Sequence 1122, Ap
386	69	4.2	476	7	US-11-055-822-1124	Sequence 1124, Ap
387	69	4.2	654	6	US-10-528-031-1	Sequence 1, Appli
388	69	4.2	694	7	US-11-096-568A-29818	Sequence 29818, A
389	69	4.2	696	7	US-11-256-548-23	Sequence 23, Appl
390	69	4.2	705	7	US-11-087-099-10564	Sequence 10564, A
391	69	4.2	720	7	US-11-256-548-6	Sequence 6, Appli
392	69	4.2	761	6	US-10-485-517-252	Sequence 252, App
393	69	4.2	802	7	US-11-087-099-4882	Sequence 4882, Ap
394	69	4.2	820	7	US-11-087-099-12246	Sequence 12246, A
395	69	4.2	910	7	US-11-206-587-17	Sequence 17, Appl
396	69	4.2	1158	7	US-11-075-646-6	Sequence 6, Appli
397	68.5	4.1	245	7	US-11-096-568A-21710	Sequence 21710, A

398	68.5	4.1	339	7	US-11-096-568A-21709	Sequence 21709, A
399	68.5	4.1	341	7	US-11-096-568A-21708	Sequence 21708, A
400	68.5	4.1	411	7	US-11-096-568A-7197	Sequence 7197, Ap
401	68.5	4.1	436	7	US-11-124-368A-236	Sequence 236, App
402	68.5	4.1	451	7	US-11-096-568A-7196	Sequence 7196, Ap
403	68.5	4.1	455	7	US-11-087-099-10931	Sequence 10931, A
404	68.5	4.1	464	7	US-11-096-568A-7530	Sequence 7530, Ap
405	68.5	4.1	467	7	US-11-096-568A-7195	Sequence 7195, Ap
406	68.5	4.1	467	7	US-11-096-568A-7529	Sequence 7529, Ap
407	68.5	4.1	509	7	US-11-096-568A-7528	Sequence 7528, Ap
408	68.5	4.1	529	7	US-11-210-316-28	Sequence 28, Appl
409	68.5	4.1	557	7	US-11-016-503-4	Sequence 4, Appli
410	68.5	4.1	567	7	US-11-016-503-10	Sequence 10, Appl
411	68.5	4.1	589	7	US-11-096-568A-9189	Sequence 9189, Ap
412	68.5	4.1	589	7	US-11-096-568A-9191	Sequence 9191, Ap
413	68.5	4.1	605	7	US-11-096-568A-9188	Sequence 9188, Ap
414	68.5	4.1	696	7	US-11-052-554A-100	Sequence 100, App
415	68.5	4.1	696	7	US-11-052-554A-101	Sequence 101, App
416	68.5	4.1	709	7	US-11-072-512-2349	Sequence 2349, Ap
417	68.5	4.1	748	6	US-10-330-773-394	Sequence 394, App
418	68.5	4.1	798	6	US-10-770-726-64	Sequence 64, Appl
419	68.5	4.1	825	7	US-11-087-099-1341	Sequence 1341, Ap
420	68.5	4.1	886	7	US-11-087-099-11456	Sequence 11456, A
421	68.5	4.1	897	7	US-11-137-465-35	Sequence 35, Appl
422	68.5	4.1	1070	7	US-11-087-099-5657	Sequence 5657, Ap
423	68.5	4.1	1344	7	US-11-072-512-2452	Sequence 2452, Ap
424	68.5	4.1	1669	6	US-10-330-773-392	Sequence 392, App
425	68	4.1	246	7	US-11-052-554A-50	Sequence 50, Appl
426	68	4.1	263	7	US-11-096-568A-9712	Sequence 9712, Ap
427	68	4.1	269	6	US-10-839-799-109	Sequence 109, App
428	68	4.1	312	6	US-10-986-501-124	Sequence 124, App
429	68	4.1	347	7	US-11-096-568A-16579	Sequence 16579, A
430	68	4.1	406	7	US-11-096-568A-15346	Sequence 15346, A
431	68	4.1	415	7	US-11-096-568A-15345	Sequence 15345, A
432	68	4.1	422	7	US-11-169-041-224	Sequence 224, App
433	68	4.1	472	7	US-11-165-211-4	Sequence 4, Appli
434	68	4.1	472	7	US-11-165-226-4	Sequence 4, Appli
435	68	4.1	550	7	US-11-087-099-5463	Sequence 5463, Ap
436	68	4.1	648	7	US-11-096-568A-27576	Sequence 27576, A
437	68	4.1	693	6	US-10-714-995-24	Sequence 24, Appl
438	68	4.1	1078	7	US-11-096-568A-30451	Sequence 30451, A
439	68	4.1	1116	7	US-11-096-568A-30450	Sequence 30450, A
440	68	4.1	1123	7	US-11-096-568A-30449	Sequence 30449, A
441	68	4.1	1323	6	US-10-517-939-312	Sequence 312, App
442	68	4.1	2053	7	US-11-013-759-9	Sequence 9, Appli
443	68	4.1	2426	7	US-11-203-806A-11	Sequence 11, Appl
444	68	4.1	3712	7	US-11-019-711-48	Sequence 48, Appl
445	68	4.1	3712	7	US-11-019-711-51	Sequence 51, Appl
446	67.5	4.1	96	7	US-11-096-568A-6177	Sequence 6177, Ap
447	67.5	4.1	163	7	US-11-096-568A-9622	Sequence 9622, Ap
448	67.5	4.1	173	7	US-11-096-568A-9621	Sequence 9621, Ap
449	67.5	4.1	176	7	US-11-096-568A-9620	Sequence 9620, Ap
450	67.5	4.1	238	7	US-11-096-568A-26721	Sequence 26721, A
451	67.5	4.1	400	7	US-11-096-568A-3236	Sequence 3236, Ap
452	67.5	4.1	403	7	US-11-169-041-185	Sequence 185, App
453	67.5	4.1	411	7	US-11-024-959-330	Sequence 330, App
454	67.5	4.1	413	7	US-11-096-568A-20771	Sequence 20771, A
455	67.5	4.1	418	7	US-11-096-568A-3235	Sequence 3235, Ap
456	67.5	4.1	423	7	US-11-098-686-10135	Sequence 10135, A
457	67.5	4.1	436	7	US-11-096-568A-3234	Sequence 3234, Ap
458	67.5	4.1	532	7	US-11-087-099-8860	Sequence 8860, Ap
459	67.5	4.1	577	7	US-11-201-916-31	Sequence 31, Appl
460	67.5	4.1	600	7	US-11-072-512-3397	Sequence 3397, Ap
461	67.5	4.1	608	6	US-10-763-712A-16	Sequence 16, Appl
462	67.5	4.1	608	6	US-10-763-712A-90	Sequence 90, Appl
463	67.5	4.1	618	7	US-11-087-099-6625	Sequence 6625, Ap
464	67.5	4.1	623	7	US-11-096-568A-26597	Sequence 26597, A
465	67.5	4.1	630	7	US-11-236-198-5	Sequence 5, Appli
466	67.5	4.1	637	7	US-11-096-568A-27876	Sequence 27876, A
467	67.5	4.1	649	7	US-11-236-198-3	Sequence 3, Appli
468	67.5	4.1	704	7	US-11-096-568A-27875	Sequence 27875, A
469	67.5	4.1	725	7	US-11-096-568A-26596	Sequence 26596, A
470	67.5	4.1	732	7	US-11-096-568A-27874	Sequence 27874, A
471	67.5	4.1	758	7	US-11-096-568A-26595	Sequence 26595, A
472	67.5	4.1	961	7	US-11-113-424-35	Sequence 35, Appl
473	67.5	4.1	1026	7	US-11-169-041-205	Sequence 205, App
474	67.5	4.1	1122	7	US-11-191-374-3	Sequence 3, Appli
475	67.5	4.1	1122	7	US-11-191-375-3	Sequence 3, Appli
476	67.5	4.1	1122	7	US-11-191-588-3	Sequence 3, Appli
477	67.5	4.1	1267	7	US-11-096-568A-28960	Sequence 28960, A
478	67.5	4.1	1274	7	US-11-096-568A-28959	Sequence 28959, A
479	67.5	4.1	1480	7	US-11-096-568A-28958	Sequence 28958, A
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481	67.5	4.1	1678	7	US-11-124-367A-340	Sequence 340, App
482	67.5	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
483	67.5	4.1	1978	7	US-11-212-443-60	Sequence 60, Appl
484	67.5	4.1	4374	7	US-11-128-572-2	Sequence 2, Appli
485	67	4.0	137	7	US-11-072-512-2849	Sequence 2849, Ap
486	67	4.0	149	7	US-11-096-568A-12138	Sequence 12138, A
487	67	4.0	208	7	US-11-072-512-2188	Sequence 2188, Ap
488	67	4.0	209	7	US-11-096-568A-3341	Sequence 3341, Ap
489	67	4.0	246	7	US-11-073-226-1	Sequence 1, Appli
490	67	4.0	273	6	US-10-353-783-54	Sequence 54, Appl
491	67	4.0	304	7	US-11-080-091-10	Sequence 10, Appl
492	67	4.0	309	6	US-10-873-528-156	Sequence 156, App
493	67	4.0	317	7	US-11-087-099-9345	Sequence 9345, Ap
494	67	4.0	332	7	US-11-096-568A-14684	Sequence 14684, A
495	67	4.0	336	7	US-11-087-099-4886	Sequence 4886, Ap
496	67	4.0	336	7	US-11-096-568A-5652	Sequence 5652, Ap
497	67	4.0	343	7	US-11-016-564-17	Sequence 17, Appl
498	67	4.0	344	7	US-11-174-816-47	Sequence 47, Appl
499	67	4.0	344	7	US-11-174-819-32	Sequence 32, Appl
500	67	4.0	345	7	US-11-087-177-21	Sequence 21, Appl
501	67	4.0	362	7	US-11-080-091-12	Sequence 12, Appl
502	67	4.0	389	7	US-11-188-743-23	Sequence 23, Appl
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506	67	4.0	472	7	US-11-165-211-2	Sequence 2, Appli
507	67	4.0	472	7	US-11-165-211-3	Sequence 3, Appli
508	67	4.0	472	7	US-11-165-211-5	Sequence 5, Appli
509	67	4.0	472	7	US-11-165-226-1	Sequence 1, Appli
510	67	4.0	472	7	US-11-165-226-2	Sequence 2, Appli
511	67	4.0	472	7	US-11-165-226-3	Sequence 3, Appli
512	67	4.0	472	7	US-11-165-226-5	Sequence 5, Appli
513	67	4.0	514	7	US-11-195-739-1	Sequence 1, Appli
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515	67	4.0	536	7	US-11-018-868-42	Sequence 42, Appl
516	67	4.0	543	7	US-11-096-568A-31276	Sequence 31276, A
517	67	4.0	552	7	US-11-087-099-10983	Sequence 10983, A
518	67	4.0	581	7	US-11-096-568A-31275	Sequence 31275, A
519	67	4.0	619	6	US-10-517-939-352	Sequence 352, App
520	67	4.0	645	7	US-11-072-512-3227	Sequence 3227, Ap
521	67	4.0	681	7	US-11-067-121-9	Sequence 9, Appli
522	67	4.0	765	7	US-11-087-099-905	Sequence 905, App
523	67	4.0	823	7	US-11-087-099-1971	Sequence 1971, Ap
524	67	4.0	976	6	US-10-966-483-2	Sequence 2, Appli
525	67	4.0	976	6	US-10-511-273-1	Sequence 1, Appli
526	67	4.0	976	7	US-11-233-796-2	Sequence 2, Appli
527	67	4.0	976	7	US-11-072-175-138	Sequence 138, App
528	67	4.0	976	7	US-11-203-251A-77	Sequence 77, Appl
529	67	4.0	1075	7	US-11-098-686-10295	Sequence 10295, A
530	67	4.0	1218	7	US-11-052-554A-123	Sequence 123, App
531	67	4.0	1279	6	US-10-793-626-3188	Sequence 3188, Ap
532	67	4.0	4384	6	US-10-821-234-1120	Sequence 1120, Ap
533	66.5	4.0	160	7	US-11-087-099-4973	Sequence 4973, Ap
534	66.5	4.0	180	7	US-11-096-568A-3993	Sequence 3993, Ap
535	66.5	4.0	191	7	US-11-096-568A-3992	Sequence 3992, Ap
536	66.5	4.0	221	6	US-10-714-887-144	Sequence 144, App
537	66.5	4.0	235	5	US-09-978-360A-782	Sequence 782, App
538	66.5	4.0	261	7	US-11-087-099-3530	Sequence 3530, Ap
539	66.5	4.0	278	7	US-11-072-512-3938	Sequence 3938, Ap
540	66.5	4.0	298	7	US-11-080-091-9	Sequence 9, Appli
541	66.5	4.0	303	7	US-11-096-568A-27931	Sequence 27931, A
543	66.5	4.0	310	6	US-10-973-115B-152	Sequence 152, App
544	66.5	4.0	310	7	US-11-043-806-394	Sequence 394, App

545	66.5	4.0	310	7	US-11-043-806-395	Sequence 395, App
546	66.5	4.0	310	7	US-11-043-806-397	Sequence 397, App
547	66.5	4.0	314	7	US-11-096-568A-3237	Sequence 3237, Ap
548	66.5	4.0	319	7	US-11-096-568A-24347	Sequence 24347, A
549	66.5	4.0	362	7	US-11-256-548-3	Sequence 3, Appli
550	66.5	4.0	380	7	US-11-087-099-1300	Sequence 1300, Ap
551	66.5	4.0	388	7	US-11-096-568A-27930	Sequence 27930, A
552	66.5	4.0	389	7	US-11-096-568A-27929	Sequence 27929, A
553	66.5	4.0	502	7	US-11-098-686-10593	Sequence 10593, A
554	66.5	4.0	648	6	US-10-917-905-6	Sequence 6, Appli
555	66.5	4.0	673	6	US-10-330-773-674	Sequence 674, App
556	66.5	4.0	786	6	US-10-467-962B-103	Sequence 103, App
557	66.5	4.0	812	7	US-11-120-308-126	Sequence 126, App
558	66.5	4.0	897	7	US-11-087-099-11042	Sequence 11042, A
559	66.5	4.0	1267	7	US-11-109-156-35	Sequence 35, Appl
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561	66.5	4.0	3100	7	US-11-235-732-7	Sequence 7, Appli
562	66	4.0	149	7	US-11-087-099-7791	Sequence 7791, Ap
563	66	4.0	212	7	US-11-025-834A-16	Sequence 16, Appl
564	66	4.0	235	7	US-11-159-597-2	Sequence 2, Appli
565	66	4.0	235	7	US-11-219-359-5	Sequence 5, Appli
566	66	4.0	253	7	US-11-096-568A-21716	Sequence 21716, A
567	66	4.0	270	7	US-11-096-568A-16865	Sequence 16865, A
568	66	4.0	292	7	US-11-129-143-96	Sequence 96, Appl
569	66	4.0	300	7	US-11-096-568A-27037	Sequence 27037, A
570	66	4.0	333	7	US-11-096-568A-21892	Sequence 21892, A
571	66	4.0	334	7	US-11-096-568A-21891	Sequence 21891, A
572	66	4.0	337	7	US-11-087-099-3435	Sequence 3435, Ap
573	66	4.0	340	6	US-10-501-035-354	Sequence 354, App
574	66	4.0	344	7	US-11-174-816-46	Sequence 46, Appl
575	66	4.0	344	7	US-11-174-819-30	Sequence 30, Appl
576	66	4.0	367	7	US-11-072-512-2763	Sequence 2763, Ap
577	66	4.0	380	7	US-11-087-099-6673	Sequence 6673, Ap
578	66	4.0	434	7	US-11-096-568A-21798	Sequence 21798, A
579	66	4.0	462	7	US-11-177-648-27	Sequence 27, Appl
580	66	4.0	462	7	US-11-177-648-92	Sequence 92, Appl
581	66	4.0	462	7	US-11-177-648-93	Sequence 93, Appl
582	66	4.0	462	7	US-11-177-648-94	Sequence 94, Appl
583	66	4.0	462	7	US-11-177-648-95	Sequence 95, Appl
584	66	4.0	464	7	US-11-096-568A-21797	Sequence 21797, A
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587	66	4.0	508	7	US-11-087-099-10016	Sequence 10016, A
588	66	4.0	525	7	US-11-074-176-146	Sequence 146, App
590	66	4.0	607	6	US-10-973-115B-344	Sequence 344, App
591	66	4.0	607	7	US-11-176-863-2	Sequence 2, Appli
592	66	4.0	648	7	US-11-098-686-10873	Sequence 10873, A
593	66	4.0	690	6	US-10-613-744-19	Sequence 19, Appl
594	66	4.0	690	6	US-10-511-657-2	Sequence 2, Appli
595	66	4.0	738	6	US-10-880-881-23	Sequence 23, Appl
596	66	4.0	780	7	US-11-087-099-251	Sequence 251, App
597	66	4.0	793	7	US-11-060-914-2	Sequence 2, Appli
598	66	4.0	799	6	US-10-493-909-8	Sequence 8, Appli
599	66	4.0	822	6	US-10-493-909-48	Sequence 48, Appl
600	66	4.0	823	7	US-11-087-099-11109	Sequence 11109, A
601	66	4.0	874	6	US-10-510-386-28	Sequence 28, Appl
602	66	4.0	928	7	US-11-130-594-8	Sequence 8, Appli
603	66	4.0	928	7	US-11-201-801-8	Sequence 8, Appli
604	66	4.0	931	7	US-11-230-145-2	Sequence 2, Appli
605	66	4.0	1035	6	US-10-966-483-20	Sequence 20, Appl
606	66	4.0	1035	7	US-11-021-441-4	Sequence 4, Appli
607	66	4.0	1047	6	US-10-510-386-200	Sequence 200, App
608	66	4.0	1161	7	US-11-075-646-8	Sequence 8, Appli
609	66	4.0	1551	7	US-11-087-099-10366	Sequence 10366, A
610	66	4.0	1647	7	US-11-052-554A-260	Sequence 260, App
611	66	4.0	2059	7	US-11-087-100-4	Sequence 4, Appli
612	66	4.0	2059	7	US-11-087-084-4	Sequence 4, Appli
613	66	4.0	2059	7	US-11-087-085-4	Sequence 4, Appli
614	66	4.0	3567	6	US-10-453-372-1112	Sequence 1112, Ap
615	65.5	4.0	145	6	US-10-793-626-1504	Sequence 1504, Ap
616	65.5	4.0	165	6	US-10-821-234-1539	Sequence 1539, Ap
617	65.5	4.0	192	7	US-11-096-568A-3893	Sequence 3893, Ap
618	65.5	4.0	205	7	US-11-096-568A-3892	Sequence 3892, Ap
619	65.5	4.0	257	7	US-11-096-568A-25250	Sequence 25250, A
620	65.5	4.0	436	7	US-11-024-959-394	Sequence 394, App
621	65.5	4.0	445	6	US-10-467-657-5092	Sequence 5092, Ap
622	65.5	4.0	470	6	US-10-878-556A-101	Sequence 101, App
623	65.5	4.0	485	7	US-11-096-568A-26552	Sequence 26552, A
624	65.5	4.0	539	7	US-11-096-568A-13358	Sequence 13358, A
625	65.5	4.0	541	7	US-11-201-916-17	Sequence 17, Appl
626	65.5	4.0	560	7	US-11-018-868-40	Sequence 40, Appl
627	65.5	4.0	567	6	US-10-485-517-216	Sequence 216, App
628	65.5	4.0	612	6	US-10-467-657-3988	Sequence 3988, Ap
629	65.5	4.0	652	6	US-10-821-234-1016	Sequence 1016, Ap
630	65.5	4.0	683	7	US-11-124-368A-243	Sequence 243, App
631	65.5	4.0	707	7	US-11-072-512-3162	Sequence 3162, Ap
632	65.5	4.0	777	7	US-11-124-368A-238	Sequence 238, App
633	65.5	4.0	778	7	US-11-124-368A-240	Sequence 240, App
634	65.5	4.0	791	7	US-11-124-368A-245	Sequence 245, App
635	65.5	4.0	836	7	US-11-124-368A-246	Sequence 246, App
636	65.5	4.0	877	6	US-10-485-517-200	Sequence 200, App
637	65.5	4.0	925	6	US-10-453-372-1124	Sequence 1124, Ap
638	65.5	4.0	966	6	US-10-877-346-32	Sequence 32, Appl
639	65.5	4.0	972	6	US-10-453-372-1128	Sequence 1128, Ap
640	65.5	4.0	997	7	US-11-080-991-50	Sequence 50, Appl
641	65.5	4.0	999	7	US-11-113-424-36	Sequence 36, Appl
642	65.5	4.0	2432	6	US-10-821-234-899	Sequence 899, App
643	65.5	4.0	2551	7	US-11-052-554A-368	Sequence 368, App
644	65.5	4.0	3095	7	US-11-235-732-4	Sequence 4, Appli
645	65.5	4.0	14130	7	US-11-175-689-9	Sequence 9, Appli
646	65	3.9	160	6	US-10-533-811-13	Sequence 13, Appl
647	65	3.9	162	6	US-10-467-657-9046	Sequence 9046, Ap
648	65	3.9	181	6	US-10-746-959C-10	Sequence 10, Appl
649	65	3.9	196	7	US-11-096-568A-24825	Sequence 24825, A
650	65	3.9	204	7	US-11-052-554A-377	Sequence 377, App
651	65	3.9	211	7	US-11-096-568A-24824	Sequence 24824, A
652	65	3.9	234	7	US-11-096-568A-21717	Sequence 21717, A
653	65	3.9	244	7	US-11-052-554A-60	Sequence 60, Appl
654	65	3.9	244	7	US-11-096-568A-9713	Sequence 9713, Ap
655	65	3.9	248	7	US-11-096-568A-13135	Sequence 13135, A
656	65	3.9	305	6	US-10-055-877-126	Sequence 126, App
657	65	3.9	305	6	US-10-055-877-264	Sequence 264, App
658	65	3.9	305	7	US-11-080-091-2	Sequence 2, Appli
659	65	3.9	305	7	US-11-087-177-7	Sequence 7, Appli
660	65	3.9	309	7	US-11-037-243-118	Sequence 118, App
661	65	3.9	370	7	US-11-096-568A-6444	Sequence 6444, Ap
662	65	3.9	379	7	US-11-087-099-10889	Sequence 10889, A
663	65	3.9	380	7	US-11-087-099-4525	Sequence 4525, Ap
664	65	3.9	380	7	US-11-087-099-4810	Sequence 4810, Ap
665	65	3.9	431	7	US-11-096-568A-6443	Sequence 6443, Ap
666	65	3.9	432	7	US-11-055-822-1096	Sequence 1096, Ap
667	65	3.9	445	7	US-11-072-512-2209	Sequence 2209, Ap
669	65	3.9	449	6	US-10-973-115B-224	Sequence 224, App
670	65	3.9	462	7	US-11-177-648-96	Sequence 96, Appl
671	65	3.9	468	7	US-11-096-568A-6442	Sequence 6442, Ap
672	65	3.9	509	7	US-11-008-727-16	Sequence 16, Appl
673	65	3.9	555	7	US-11-072-512-2530	Sequence 2530, Ap
674	65	3.9	619	7	US-11-136-244-3	Sequence 3, Appli
675	65	3.9	625	7	US-11-072-512-3210	Sequence 3210, Ap
676	65	3.9	628	7	US-11-037-243-86	Sequence 86, Appl
677	65	3.9	640	7	US-11-136-244-4	Sequence 4, Appli
678	65	3.9	653	6	US-10-501-035-358	Sequence 358, App
679	65	3.9	718	7	US-11-024-959-273	Sequence 273, App
680	65	3.9	764	7	US-11-072-512-2379	Sequence 2379, Ap
681	65	3.9	814	7	US-11-124-368A-186	Sequence 186, App
682	65	3.9	922	7	US-11-072-512-2694	Sequence 2694, Ap
683	65	3.9	1036	7	US-11-096-568A-28315	Sequence 28315, A
684	65	3.9	1070	7	US-11-096-568A-28314	Sequence 28314, A
685	65	3.9	1131	7	US-11-072-512-2866	Sequence 2866, Ap
686	65	3.9	1198	6	US-10-451-375-4	Sequence 4, Appli
687	65	3.9	1276	7	US-11-096-568A-28313	Sequence 28313, A
688	65	3.9	1981	6	US-10-374-954-23	Sequence 23, Appl
689	65	3.9	1992	7	US-11-013-759-3	Sequence 3, Appli
690	65	3.9	1992	7	US-11-013-759-13	Sequence 13, Appl
691	65	3.9	1998	6	US-10-374-954-21	Sequence 21, Appl
692	65	3.9	2009	6	US-10-374-954-2	Sequence 2, Appli
693	65	3.9	2047	7	US-11-013-759-4	Sequence 4, Appli

694	65	3.9	2047	7	US-11-013-759-7	Sequence 7, Appli
695	64.5	3.9	223	7	US-11-087-099-7197	Sequence 7197, Ap
696	64.5	3.9	250	7	US-11-096-568A-3195	Sequence 3195, Ap
697	64.5	3.9	264	7	US-11-096-568A-5205	Sequence 5205, Ap
698	64.5	3.9	282	6	US-10-055-877-127	Sequence 127, App
699	64.5	3.9	282	7	US-11-087-177-9	Sequence 9, Appli
700	64.5	3.9	315	7	US-11-072-512-2198	Sequence 2198, Ap
701	64.5	3.9	370	7	US-11-096-568A-3216	Sequence 3216, Ap
702	64.5	3.9	370	7	US-11-096-568A-3217	Sequence 3217, Ap
703	64.5	3.9	371	6	US-10-467-657-1926	Sequence 1926, Ap
704	64.5	3.9	378	7	US-11-087-099-8872	Sequence 8872, Ap
705	64.5	3.9	378	7	US-11-087-099-11183	Sequence 11183, A
706	64.5	3.9	380	7	US-11-087-099-5374	Sequence 5374, Ap
707	64.5	3.9	381	7	US-11-087-099-12159	Sequence 12159, A
708	64.5	3.9	388	7	US-11-087-099-4330	Sequence 4330, Ap
709	64.5	3.9	393	7	US-11-096-568A-3215	Sequence 3215, Ap
710	64.5	3.9	407	7	US-11-096-568A-5204	Sequence 5204, Ap
711	64.5	3.9	433	7	US-11-096-568A-5203	Sequence 5203, Ap
712	64.5	3.9	482	6	US-10-821-234-972	Sequence 972, App
713	64.5	3.9	519	7	US-11-087-099-5406	Sequence 5406, Ap
714	64.5	3.9	579	7	US-11-072-512-2360	Sequence 2360, Ap
715	64.5	3.9	645	7	US-11-072-512-3418	Sequence 3418, Ap
717	64.5	3.9	649	7	US-11-102-240-132	Sequence 132, App
718	64.5	3.9	649	7	US-11-103-195-132	Sequence 132, App
719	64.5	3.9	651	7	US-11-198-819-22	Sequence 22, Appl
720	64.5	3.9	729	7	US-11-096-568A-19858	Sequence 19858, A
721	64.5	3.9	754	6	US-10-467-962B-63	Sequence 63, Appl
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723	64.5	3.9	848	7	US-11-096-568A-19856	Sequence 19856, A
724	64.5	3.9	863	7	US-11-077-550-34	Sequence 34, Appl
725	64.5	3.9	1124	7	US-11-087-099-4425	Sequence 4425, Ap
726	64.5	3.9	1127	7	US-11-077-550-58	Sequence 58, Appl
727	64.5	3.9	1129	7	US-11-077-550-56	Sequence 56, Appl
728	64.5	3.9	2244	7	US-11-131-263-9	Sequence 9, Appli
729	64.5	3.9	2244	7	US-11-131-263-18	Sequence 18, Appl
730	64.5	3.9	2244	7	US-11-131-263-30	Sequence 30, Appl
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732	64.5	3.9	2910	7	US-11-087-084-2	Sequence 2, Appli
733	64.5	3.9	2910	7	US-11-087-085-2	Sequence 2, Appli
734	64	3.9	122	7	US-11-087-099-6151	Sequence 6151, Ap
735	64	3.9	131	7	US-11-096-568A-12238	Sequence 12238, A
736	64	3.9	145	7	US-11-152-601-43	Sequence 43, Appl
737	64	3.9	187	7	US-11-096-568A-11277	Sequence 11277, A
738	64	3.9	198	7	US-11-087-099-11173	Sequence 11173, A
739	64	3.9	203	7	US-11-050-857-488	Sequence 488, App
740	64	3.9	203	7	US-11-043-806-370	Sequence 370, App
741	64	3.9	262	7	US-11-096-568A-11276	Sequence 11276, A
742	64	3.9	266	7	US-11-096-568A-11275	Sequence 11275, A
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746	64	3.9	319	6	US-10-793-626-2008	Sequence 2008, Ap
747	64	3.9	324	7	US-11-087-099-4966	Sequence 4966, Ap
748	64	3.9	335	6	US-10-873-528-4	Sequence 4, Appli
749	64	3.9	338	7	US-11-096-568A-30980	Sequence 30980, A
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751	64	3.9	342	7	US-11-174-816-18	Sequence 18, Appl
752	64	3.9	342	7	US-11-174-819-71	Sequence 71, Appl
753	64	3.9	346	7	US-11-096-568A-30979	Sequence 30979, A
755	64	3.9	349	6	US-10-973-115B-424	Sequence 424, App
756	64	3.9	373	6	US-10-498-026-113	Sequence 113, App
757	64	3.9	379	7	US-11-087-099-8341	Sequence 8341, Ap
758	64	3.9	381	7	US-11-096-568A-17861	Sequence 17861, A
759	64	3.9	382	7	US-11-096-568A-17860	Sequence 17860, A
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762	64	3.9	387	7	US-11-129-741-611	Sequence 611, App
763	64	3.9	387	7	US-11-096-568A-13773	Sequence 13773, A
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772	64	3.9	537	7	US-11-087-099-4695	Sequence 4695, Ap
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774	64	3.9	613	7	US-11-096-568A-12981	Sequence 12981, A
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776	64	3.9	640	6	US-10-999-886-4	Sequence 4, Appli
777	64	3.9	756	6	US-10-055-877-188	Sequence 188, App
778	64	3.9	769	7	US-11-188-743-15	Sequence 15, Appl
779	64	3.9	860	7	US-11-087-099-6246	Sequence 6246, Ap
780	64	3.9	972	7	US-11-177-894-17	Sequence 17, Appl
781	64	3.9	976	7	US-11-148-770-31	Sequence 31, Appl
782	64	3.9	976	7	US-11-177-894-15	Sequence 15, Appl
783	64	3.9	976	7	US-11-177-894-16	Sequence 16, Appl
784	64	3.9	976	7	US-11-177-894-18	Sequence 18, Appl
785	64	3.9	976	7	US-11-177-894-19	Sequence 19, Appl
786	64	3.9	976	7	US-11-177-894-20	Sequence 20, Appl
787	64	3.9	976	7	US-11-177-894-21	Sequence 21, Appl
788	64	3.9	1123	7	US-11-037-243-77	Sequence 77, Appl
789	64	3.9	1613	6	US-10-055-877-145	Sequence 145, App
790	64	3.9	1637	6	US-10-055-877-144	Sequence 144, App
791	64	3.9	4868	7	US-11-044-111-24	Sequence 24, Appl
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794	63.5	3.8	249	6	US-10-821-234-1125	Sequence 1125, Ap
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798	63.5	3.8	311	7	US-11-096-568A-5368	Sequence 5368, Ap
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800	63.5	3.8	319	7	US-11-087-099-9069	Sequence 9069, Ap
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802	63.5	3.8	335	7	US-11-087-099-4668	Sequence 4668, Ap
803	63.5	3.8	336	6	US-10-517-696-153	Sequence 153, App
804	63.5	3.8	336	7	US-11-096-568A-5367	Sequence 5367, Ap
805	63.5	3.8	350	6	US-10-517-696-125	Sequence 125, App
806	63.5	3.8	358	7	US-11-096-568A-21943	Sequence 21943, A
807	63.5	3.8	372	6	US-10-517-696-129	Sequence 129, App
808	63.5	3.8	372	7	US-11-096-568A-5366	Sequence 5366, Ap
809	63.5	3.8	375	7	US-11-096-568A-21942	Sequence 21942, A
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813	63.5	3.8	393	7	US-11-052-554A-254	Sequence 254, App
814	63.5	3.8	396	6	US-10-517-696-147	Sequence 147, App
815	63.5	3.8	396	7	US-11-096-568A-33507	Sequence 33507, A
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818	63.5	3.8	409	6	US-10-517-696-149	Sequence 149, App
819	63.5	3.8	420	6	US-10-517-696-141	Sequence 141, App
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823	63.5	3.8	475	6	US-10-501-035-309	Sequence 309, App
824	63.5	3.8	475	6	US-10-517-696-117	Sequence 117, App
825	63.5	3.8	483	6	US-10-517-696-132	Sequence 132, App
826	63.5	3.8	484	6	US-10-517-696-120	Sequence 120, App
827	63.5	3.8	485	6	US-10-517-696-142	Sequence 142, App
828	63.5	3.8	492	6	US-10-517-696-131	Sequence 131, App
829	63.5	3.8	492	7	US-11-098-686-11360	Sequence 11360, A
830	63.5	3.8	517	6	US-10-517-696-144	Sequence 144, App
831	63.5	3.8	524	6	US-10-517-696-122	Sequence 122, App
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834	63.5	3.8	541	7	US-11-201-916-14	Sequence 14, Appl
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840	63.5	3.8	654	6	US-10-510-947-6	Sequence 6, Appli
841	63.5	3.8	693	6	US-10-995-561-632	Sequence 632, App

842	63.5	3.8	736	7	US-11-085-185-4	Sequence 4, Appli
843	63.5	3.8	778	6	US-10-821-234-1276	Sequence 1276, Ap
844	63.5	3.8	830	6	US-10-055-877-32	Sequence 32, Appl
845	63.5	3.8	871	7	US-11-077-550-2	Sequence 2, Appli
846	63.5	3.8	871	7	US-11-077-550-8	Sequence 8, Appli
847	63.5	3.8	871	7	US-11-077-550-26	Sequence 26, Appl
848	63.5	3.8	871	7	US-11-077-550-153	Sequence 153, App
849	63.5	3.8	873	7	US-11-077-550-6	Sequence 6, Appli
850	63.5	3.8	873	7	US-11-077-550-149	Sequence 149, App
851	63.5	3.8	873	7	US-11-077-550-151	Sequence 151, App
852	63.5	3.8	879	7	US-11-077-550-159	Sequence 159, App
853	63.5	3.8	894	7	US-11-077-550-4	Sequence 4, Appli
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857	63.5	3.8	1127	7	US-11-077-550-40	Sequence 40, Appl
858	63.5	3.8	1129	7	US-11-077-550-42	Sequence 42, Appl
859	63.5	3.8	1178	7	US-11-087-099-10105	Sequence 10105, A
860	63.5	3.8	1230	7	US-11-087-099-1702	Sequence 1702, Ap
861	63.5	3.8	1230	7	US-11-087-099-8922	Sequence 8922, Ap
862	63.5	3.8	1255	7	US-11-050-857-487	Sequence 487, App
863	63.5	3.8	1255	7	US-11-043-806-398	Sequence 398, App
864	63.5	3.8	1315	6	US-10-995-561-630	Sequence 630, App
865	63.5	3.8	1607	7	US-11-098-686-10178	Sequence 10178, A
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867	63.5	3.8	2000	7	US-11-069-834-56	Sequence 56, Appl
868	63.5	3.8	2015	7	US-11-052-554A-374	Sequence 374, App
869	63.5	3.8	2145	7	US-11-087-099-10331	Sequence 10331, A
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871	63.5	3.8	2176	7	US-11-193-771-25	Sequence 25, Appl
872	63.5	3.8	2176	7	US-11-193-789-25	Sequence 25, Appl
873	63.5	3.8	2176	7	US-11-193-806-25	Sequence 25, Appl
874	63.5	3.8	2176	7	US-11-193-857-25	Sequence 25, Appl
875	63.5	3.8	2296	6	US-10-995-561-633	Sequence 633, App
876	63.5	3.8	2296	7	US-11-193-561-23	Sequence 23, Appl
877	63.5	3.8	2296	7	US-11-193-771-23	Sequence 23, Appl
878	63.5	3.8	2296	7	US-11-193-789-23	Sequence 23, Appl
879	63.5	3.8	2296	7	US-11-193-806-23	Sequence 23, Appl
880	63.5	3.8	2296	7	US-11-193-857-23	Sequence 23, Appl
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882	63.5	3.8	3487	7	US-11-087-099-10423	Sequence 10423, A
883	63	3.8	148	7	US-11-052-554A-359	Sequence 359, App
884	63	3.8	192	7	US-11-072-512-3585	Sequence 3585, Ap
885	63	3.8	193	7	US-11-096-568A-24769	Sequence 24769, A
886	63	3.8	246	6	US-10-467-657-2424	Sequence 2424, Ap
887	63	3.8	257	7	US-11-067-121-18	Sequence 18, Appl
888	63	3.8	290	7	US-11-087-099-4115	Sequence 4115, Ap
889	63	3.8	307	6	US-10-498-026-111	Sequence 111, App
890	63	3.8	316	7	US-11-096-568A-28013	Sequence 28013, A
891	63	3.8	327	6	US-10-055-877-183	Sequence 183, App
892	63	3.8	331	7	US-11-096-568A-16226	Sequence 16226, A
893	63	3.8	336	7	US-11-087-099-11933	Sequence 11933, A
894	63	3.8	344	7	US-11-174-816-45	Sequence 45, Appl
895	63	3.8	344	7	US-11-174-819-28	Sequence 28, Appl
896	63	3.8	352	7	US-11-087-099-5875	Sequence 5875, Ap
897	63	3.8	359	7	US-11-087-099-7177	Sequence 7177, Ap
898	63	3.8	362	7	US-11-087-099-7379	Sequence 7379, Ap
899	63	3.8	363	7	US-11-087-099-9842	Sequence 9842, Ap
900	63	3.8	371	7	US-11-096-568A-31340	Sequence 31340, A
901	63	3.8	386	7	US-11-055-822-586	Sequence 586, App
902	63	3.8	408	7	US-11-096-568A-31339	Sequence 31339, A
903	63	3.8	471	7	US-11-087-099-8817	Sequence 8817, Ap
904	63	3.8	472	7	US-11-165-226-10	Sequence 10, Appl
905	63	3.8	472	7	US-11-165-226-11	Sequence 11, Appl
906	63	3.8	472	7	US-11-165-226-12	Sequence 12, Appl
907	63	3.8	472	7	US-11-165-226-13	Sequence 13, Appl
908	63	3.8	475	7	US-11-087-099-4508	Sequence 4508, Ap
909	63	3.8	476	7	US-11-139-499-12	Sequence 12, Appl
910	63	3.8	485	7	US-11-043-889-52	Sequence 52, Appl
911	63	3.8	488	7	US-11-072-512-2639	Sequence 2639, Ap
912	63	3.8	497	6	US-10-501-035-337	Sequence 337, App
913	63	3.8	501	6	US-10-485-517-381	Sequence 381, App
914	63	3.8	513	6	US-10-641-678-66	Sequence 66, Appl
915	63	3.8	514	6	US-10-641-678-67	Sequence 67, Appl
916	63	3.8	546	7	US-11-072-512-2051	Sequence 2051, Ap
917	63	3.8	548	7	US-11-096-568A-402	Sequence 402, App
918	63	3.8	581	7	US-11-236-198-7	Sequence 7, Appli
919	63	3.8	615	7	US-11-096-568A-401	Sequence 401, App
920	63	3.8	615	7	US-11-096-568A-403	Sequence 403, App
921	63	3.8	629	7	US-11-096-568A-29173	Sequence 29173, A
922	63	3.8	643	7	US-11-096-568A-400	Sequence 400, App
923	63	3.8	645	6	US-10-485-517-244	Sequence 244, App
924	63	3.8	678	7	US-11-096-568A-29172	Sequence 29172, A
925	63	3.8	706	7	US-11-087-099-4237	Sequence 4237, Ap
926	63	3.8	719	7	US-11-096-568A-29171	Sequence 29171, A
927	63	3.8	726	7	US-11-096-568A-28626	Sequence 28626, A
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929	63	3.8	756	7	US-11-096-568A-28625	Sequence 28625, A
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932	63	3.8	798	7	US-11-096-568A-28221	Sequence 28221, A
933	63	3.8	801	7	US-11-096-568A-28220	Sequence 28220, A
934	63	3.8	808	7	US-11-087-099-7073	Sequence 7073, Ap
935	63	3.8	808	7	US-11-096-568A-28624	Sequence 28624, A
936	63	3.8	871	7	US-11-087-099-6053	Sequence 6053, Ap
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938	63	3.8	1083	7	US-11-113-751-40	Sequence 40, Appl
939	63	3.8	1121	7	US-11-024-959-459	Sequence 459, App
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941	63	3.8	1637	6	US-10-821-234-1204	Sequence 1204, Ap
942	63	3.8	1645	7	US-11-043-806-364	Sequence 364, App
943	63	3.8	1928	6	US-10-480-330-30	Sequence 30, Appl
944	63	3.8	1965	6	US-10-480-330-4	Sequence 4, Appli
945	63	3.8	1966	6	US-10-480-330-2	Sequence 2, Appli
946	63	3.8	1966	6	US-10-480-330-6	Sequence 6, Appli
947	63	3.8	1966	6	US-10-480-330-8	Sequence 8, Appli
948	63	3.8	1966	6	US-10-480-330-10	Sequence 10, Appl
949	63	3.8	1966	6	US-10-480-330-12	Sequence 12, Appl
950	63	3.8	1966	6	US-10-480-330-14	Sequence 14, Appl
951	63	3.8	1966	6	US-10-480-330-16	Sequence 16, Appl
952	63	3.8	1966	6	US-10-480-330-18	Sequence 18, Appl
953	63	3.8	1966	6	US-10-480-330-20	Sequence 20, Appl
954	63	3.8	1966	6	US-10-480-330-22	Sequence 22, Appl
955	63	3.8	1966	6	US-10-480-330-24	Sequence 24, Appl
956	63	3.8	1966	6	US-10-480-330-26	Sequence 26, Appl
957	63	3.8	1966	6	US-10-480-330-28	Sequence 28, Appl
958	63	3.8	2074	7	US-11-043-806-365	Sequence 365, App
959	63	3.8	2105	7	US-11-052-554A-173	Sequence 173, App
960	63	3.8	2221	7	US-11-126-313-30	Sequence 30, Appl
961	63	3.8	2224	7	US-11-043-806-392	Sequence 392, App
962	63	3.8	2224	7	US-11-043-806-393	Sequence 393, App
963	62.5	3.8	146	6	US-10-467-657-5594	Sequence 5594, Ap
964	62.5	3.8	158	7	US-11-096-568A-7142	Sequence 7142, Ap
965	62.5	3.8	180	7	US-11-096-568A-3506	Sequence 3506, Ap
966	62.5	3.8	232	5	US-09-978-360A-642	Sequence 642, App
967	62.5	3.8	246	7	US-11-096-568A-26953	Sequence 26953, A
968	62.5	3.8	271	6	US-10-353-783-52	Sequence 52, Appl
969	62.5	3.8	277	7	US-11-096-568A-26952	Sequence 26952, A
971	62.5	3.8	299	6	US-10-973-115B-366	Sequence 366, App
972	62.5	3.8	299	7	US-11-000-463-275	Sequence 275, App
973	62.5	3.8	299	7	US-11-000-463-747	Sequence 747, App
974	62.5	3.8	299	7	US-11-000-463-748	Sequence 748, App
975	62.5	3.8	299	7	US-11-173-037-7	Sequence 7, Appli
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979	62.5	3.8	404	7	US-11-096-568A-28877	Sequence 28877, A
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981	62.5	3.8	440	7	US-11-087-099-8456	Sequence 8456, Ap
982	62.5	3.8	442	7	US-11-102-621-126	Sequence 126, App
983	62.5	3.8	446	7	US-11-096-568A-28876	Sequence 28876, A
984	62.5	3.8	457	7	US-11-096-568A-32234	Sequence 32234, A
985	62.5	3.8	464	7	US-11-087-099-7754	Sequence 7754, Ap
986	62.5	3.8	467	7	US-11-096-568A-7912	Sequence 7912, Ap
987	62.5	3.8	489	7	US-11-096-568A-32213	Sequence 32213, A
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991	62.5	3.8	524	6	US-10-517-696-113	Sequence 113, App
992	62.5	3.8	539	7	US-11-096-568A-32212	Sequence 32212, A
993	62.5	3.8	542	7	US-11-074-176-30	Sequence 30, Appl
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997	62.5	3.8	575	7	US-11-096-568A-27577	Sequence 27577, A
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999	62.5	3.8	585	7	US-11-108-172-1067	Sequence 1067, Ap
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1004	62.5	3.8	756	6	US-10-055-877-189	Sequence 189, App
1005	62.5	3.8	867	7	US-11-077-550-179	Sequence 179, App
1006	62.5	3.8	871	7	US-11-077-550-155	Sequence 155, App
1007	62.5	3.8	873	7	US-11-077-550-163	Sequence 163, App
1008	62.5	3.8	873	7	US-11-077-550-165	Sequence 165, App
1009	62.5	3.8	880	7	US-11-087-099-950	Sequence 950, App
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1014	62.5	3.8	1162	6	US-10-451-375-3	Sequence 3, Appli
1015	62.5	3.8	1680	6	US-10-517-939-362	Sequence 362, App
1016	62.5	3.8	2304	6	US-10-330-773-310	Sequence 310, App
1017	62.5	3.8	2367	7	US-11-051-453-42	Sequence 42, Appl
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1043	62	3.7	341	7	US-11-240-769-72	Sequence 72, Appl
1044	62	3.7	341	7	US-11-096-568A-23537	Sequence 23537, A
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1049	62	3.7	346	6	US-10-973-115B-432	Sequence 432, App
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1082	62	3.7	1075	7	US-11-100-640-12	Sequence 12, Appl
1083	62	3.7	1130	7	US-11-077-550-139	Sequence 139, App
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1091	62	3.7	1532	7	US-11-124-367A-403	Sequence 403, App
1092	62	3.7	1532	7	US-11-124-367A-404	Sequence 404, App
1093	62	3.7	1532	7	US-11-124-367A-405	Sequence 405, App
1094	62	3.7	1532	7	US-11-124-367A-407	Sequence 407, App
1095	62	3.7	1535	7	US-11-124-367A-408	Sequence 408, App
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1097	62	3.7	1571	7	US-11-134-587B-13	Sequence 13, Appl
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1103	61.5	3.7	189	6	US-10-055-877-209	Sequence 209, App
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1109	61.5	3.7	235	7	US-11-126-126-16	Sequence 16, Appl
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1133	61.5	3.7	396	7	US-11-087-099-7395	Sequence 7395, Ap
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1148	61.5	3.7	540	7	US-11-212-443-168	Sequence 168, App
1149	61.5	3.7	541	7	US-11-169-041-136	Sequence 136, App
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1159	61.5	3.7	684	7	US-11-096-568A-26673	Sequence 26673, A
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1162	61.5	3.7	731	7	US-11-098-686-10415	Sequence 10415, A
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1166	61.5	3.7	877	7	US-11-077-550-157	Sequence 157, App
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1173	61.5	3.7	1129	7	US-11-077-550-48	Sequence 48, Appl
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1175	61.5	3.7	1171	7	US-11-087-099-3806	Sequence 3806, Ap
1176	61.5	3.7	1171	7	US-11-087-099-7445	Sequence 7445, Ap
1177	61.5	3.7	1171	7	US-11-087-099-9917	Sequence 9917, Ap
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1179	61.5	3.7	1308	7	US-11-113-202-16	Sequence 16, Appl
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1181	61.5	3.7	3623	6	US-10-995-561-593	Sequence 593, App
1182	61	3.7	139	6	US-10-467-657-2748	Sequence 2748, Ap
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1186	61	3.7	273	6	US-10-995-561-917	Sequence 917, App
1187	61	3.7	273	7	US-11-087-099-2253	Sequence 2253, Ap
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1203	61	3.7	338	7	US-11-055-822-622	Sequence 622, App
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1211	61	3.7	380	7	US-11-087-099-8656	Sequence 8656, Ap
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1229	61	3.7	545	7	US-11-065-943-73	Sequence 73, Appl
1230	61	3.7	545	7	US-11-087-099-951	Sequence 951, App
1231	61	3.7	547	7	US-11-087-099-3034	Sequence 3034, Ap
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1235	61	3.7	597	7	US-11-051-720-1354	Sequence 1354, Ap
1236	61	3.7	610	7	US-11-096-568A-31381	Sequence 31381, A
1237	61	3.7	665	7	US-11-124-368A-289	Sequence 289, App
1238	61	3.7	685	7	US-11-072-512-2916	Sequence 2916, Ap
1239	61	3.7	718	7	US-11-074-176-306	Sequence 306, App
1240	61	3.7	723	7	US-11-074-176-18	Sequence 18, Appl
1241	61	3.7	745	6	US-10-793-626-1742	Sequence 1742, Ap
1242	61	3.7	797	6	US-10-330-773-663	Sequence 663, App
1243	61	3.7	810	6	US-10-453-372-1116	Sequence 1116, Ap
1244	61	3.7	843	7	US-11-129-104-89	Sequence 89, Appl
1245	61	3.7	852	7	US-11-087-099-4834	Sequence 4834, Ap
1246	61	3.7	873	7	US-11-087-099-7920	Sequence 7920, Ap
1247	61	3.7	899	7	US-11-124-368A-290	Sequence 290, App
1248	61	3.7	980	6	US-10-330-773-507	Sequence 507, App
1249	61	3.7	1064	7	US-11-087-099-10112	Sequence 10112, A
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1251	61	3.7	1075	6	US-10-821-234-1202	Sequence 1202, Ap
1252	61	3.7	1139	7	US-11-096-568A-27582	Sequence 27582, A
1253	61	3.7	1224	7	US-11-096-568A-27581	Sequence 27581, A
1254	61	3.7	1240	7	US-11-096-568A-27580	Sequence 27580, A
1255	61	3.7	1439	7	US-11-124-368A-291	Sequence 291, App
1256	61	3.7	1493	7	US-11-183-136-26	Sequence 26, Appl
1257	61	3.7	1579	6	US-10-330-773-939	Sequence 939, App
1258	61	3.7	1613	7	US-11-108-528-84	Sequence 84, Appl
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1261	61	3.7	2214	7	US-11-080-991-94	Sequence 94, Appl
1262	61	3.7	2723	6	US-10-895-064-388	Sequence 388, App
1263	61	3.7	2723	7	US-11-129-741-388	Sequence 388, App
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1273	60.5	3.7	237	6	US-10-884-730-336	Sequence 336, App
1274	60.5	3.7	245	7	US-11-186-284-167	Sequence 167, App
1275	60.5	3.7	248	7	US-11-176-830-528	Sequence 528, App
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1279	60.5	3.7	272	7	US-11-087-099-8109	Sequence 8109, Ap
1280	60.5	3.7	272	7	US-11-087-099-9485	Sequence 9485, Ap
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1282	60.5	3.7	277	6	US-10-972-587-20	Sequence 20, Appl
1283	60.5	3.7	278	6	US-10-861-934-16	Sequence 16, Appl

1284	60.5	3.7	278	6	US-10-861-934-26	Sequence 26, Appl
1285	60.5	3.7	279	6	US-10-861-934-24	Sequence 24, Appl
1286	60.5	3.7	279	6	US-10-861-934-32	Sequence 32, Appl
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1296	60.5	3.7	333	7	US-11-096-568A-1901	Sequence 1901, Ap
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1305	60.5	3.7	380	7	US-11-052-554A-369	Sequence 369, App
1306	60.5	3.7	383	7	US-11-031-206-199	Sequence 199, App
1307	60.5	3.7	417	6	US-10-793-626-950	Sequence 950, App
1308	60.5	3.7	422	6	US-10-517-939-238	Sequence 238, App
1309	60.5	3.7	444	7	US-11-004-590-232	Sequence 232, App
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1314	60.5	3.7	472	6	US-10-467-657-6774	Sequence 6774, Ap
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1316	60.5	3.7	476	7	US-11-024-959-385	Sequence 385, App
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1319	60.5	3.7	511	7	US-11-096-568A-146	Sequence 146, App
1320	60.5	3.7	521	7	US-11-096-568A-29256	Sequence 29256, A
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1322	60.5	3.7	545	7	US-11-201-916-34	Sequence 34, Appl
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1324	60.5	3.7	585	7	US-11-241-347-15	Sequence 15, Appl
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1326	60.5	3.7	608	7	US-11-241-347-9	Sequence 9, Appli
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1335	60.5	3.7	761	7	US-11-212-443-22	Sequence 22, Appl
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1337	60.5	3.7	803	6	US-10-821-234-1643	Sequence 1643, Ap
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1345	60.5	3.7	965	7	US-11-147-047-51	Sequence 51, Appl
1346	60.5	3.7	1137	7	US-11-012-762-70	Sequence 70, Appl
1347	60.5	3.7	1178	6	US-10-995-561-851	Sequence 851, App
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1354	60.5	3.7	2314	7	US-11-013-759-11	Sequence 11, Appl
1355	60.5	3.7	2766	6	US-10-877-346-62	Sequence 62, Appl
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1358	60	3.6	112	7	US-11-096-568A-7599	Sequence 7599, Ap
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1360	60	3.6	142	7	US-11-186-284-105	Sequence 105, App
1361	60	3.6	150	6	US-10-467-657-2040	Sequence 2040, Ap
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1364	60	3.6	214	7	US-11-096-568A-30021	Sequence 30021, A
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1368	60	3.6	262	7	US-11-096-568A-21488	Sequence 21488, A
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1377	60	3.6	312	6	US-10-498-026-56	Sequence 56, Appl
1378	60	3.6	324	7	US-11-087-099-8018	Sequence 8018, Ap
1379	60	3.6	324	7	US-11-087-099-9180	Sequence 9180, Ap
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1381	60	3.6	330	7	US-11-087-099-10594	Sequence 10594, A
1382	60	3.6	331	7	US-11-087-099-9629	Sequence 9629, Ap
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1385	60	3.6	339	7	US-11-087-099-6189	Sequence 6189, Ap
1386	60	3.6	342	7	US-11-087-099-10231	Sequence 10231, A
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1388	60	3.6	344	7	US-11-016-564-16	Sequence 16, Appl
1389	60	3.6	348	7	US-11-087-099-7041	Sequence 7041, Ap
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1395	60	3.6	362	7	US-11-052-554A-204	Sequence 204, App
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1409	60	3.6	438	7	US-11-074-176-152	Sequence 152, App
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1413	60	3.6	456	7	US-11-000-463-923	Sequence 923, App
1414	60	3.6	468	7	US-11-087-099-11555	Sequence 11555, A
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1416	60	3.6	479	7	US-11-096-568A-19818	Sequence 19818, A
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1419	60	3.6	496	7	US-11-072-512-3006	Sequence 3006, Ap
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1427	60	3.6	550	7	US-11-087-099-11870	Sequence 11870, A
1428	60	3.6	554	7	US-11-096-568A-10891	Sequence 10891, A
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1433	60	3.6	663	7	US-11-216-245-1	Sequence 1, Appli
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1436	60	3.6	690	6	US-10-973-115B-306	Sequence 306, App
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1445	60	3.6	839	7	US-11-076-431-6	Sequence 6, Appli
1446	60	3.6	839	7	US-11-076-431-8	Sequence 8, Appli
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1457	60	3.6	1129	6	US-10-995-561-706	Sequence 706, App
1458	60	3.6	1145	7	US-11-096-568A-27584	Sequence 27584, A
1459	60	3.6	1570	6	US-10-330-773-936	Sequence 936, App
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1461	59.5	3.6	106	5	US-09-978-360A-551	Sequence 551, App
1462	59.5	3.6	106	5	US-09-978-360A-701	Sequence 701, App
1463	59.5	3.6	148	7	US-11-087-099-539	Sequence 539, App
1464	59.5	3.6	148	7	US-11-096-568A-20684	Sequence 20684, A
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1466	59.5	3.6	162	7	US-11-096-568A-7425	Sequence 7425, Ap
1467	59.5	3.6	175	7	US-11-096-568A-3912	Sequence 3912, Ap
1468	59.5	3.6	180	7	US-11-096-568A-7424	Sequence 7424, Ap
1469	59.5	3.6	188	7	US-11-087-099-9413	Sequence 9413, Ap
1470	59.5	3.6	198	7	US-11-087-099-2043	Sequence 2043, Ap
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1475	59.5	3.6	236	7	US-11-096-568A-22845	Sequence 22845, A
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1482	59.5	3.6	266	7	US-11-087-099-6865	Sequence 6865, Ap
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1485	59.5	3.6	298	7	US-11-096-568A-25290	Sequence 25290, A
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1487	59.5	3.6	312	7	US-11-096-568A-34393	Sequence 34393, A
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1489	59.5	3.6	313	6	US-10-485-517-293	Sequence 293, App
1490	59.5	3.6	316	7	US-11-152-811-4	Sequence 4, Appli
1491	59.5	3.6	316	7	US-11-072-512-2455	Sequence 2455, Ap
1492	59.5	3.6	317	7	US-11-096-568A-12521	Sequence 12521, A
1493	59.5	3.6	320	7	US-11-096-568A-5457	Sequence 5457, Ap
1494	59.5	3.6	321	7	US-11-096-568A-5456	Sequence 5456, Ap
1495	59.5	3.6	325	7	US-11-096-568A-5455	Sequence 5455, Ap
1496	59.5	3.6	331	7	US-11-096-568A-3911	Sequence 3911, Ap
1497	59.5	3.6	335	7	US-11-087-099-1878	Sequence 1878, Ap
1498	59.5	3.6	342	6	US-10-467-657-4232	Sequence 4232, Ap
1499	59.5	3.6	347	6	US-10-821-234-1379	Sequence 1379, Ap
1500	59.5	3.6	353	7	US-11-207-626A-42	Sequence 42, Appl

Search completed: March 20, 2006, 14:17:16
Job time : 17.7335 secs

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OM protein - protein search, using sw model
Run on:          March 20, 2006, 14:17:31 ; Search time 64.5519 Seconds
                                           (without alignments)
                                           2191.725 Million cell updates/sec
Title:           US-10-063-510-6
Perfect score:   1657
Sequence:        1 MARCFSLVLLLTSIWTTRLL.....NPEESKSPSKTTVRCLEAEV 322
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:      2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       A_Geneseq_21:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                SUMMARIES
  No.   Score  Match Length DB  ID                          Description
RESULT 1
ID   AAY13379 standard; protein; 322 AA.
DE   Amino acid sequence of protein PRO263.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 2
ID   AAY87287 standard; protein; 322 AA.
DE   Human signal peptide containing protein HSPP-64 SEQ ID NO:64.
PN   WO200000610-A2.
PD   06-JAN-2000.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             100.0%;  Score 1657;  DB 3;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 3
ID   ADC78521 standard; protein; 322 AA.
DE   Human PRO263 protein.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 3;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 4
ID   AAB80247 standard; protein; 322 AA.
DE   Human PRO263 protein.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 5
ID   AAB87528 standard; protein; 322 AA.
DE   Human PRO263.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 6
ID   AAB88391 standard; protein; 322 AA.
DE   Human membrane or secretory protein clone PSEC0135.
PN   EP1067182-A2.
PD   10-JAN-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             100.0%;  Score 1657;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 7
ID   ABG95853 standard; protein; 322 AA.
DE   Human secreted/transmembrane protein PRO263.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 8
ID   ABB84832 standard; protein; 322 AA.
DE   Human PRO263 protein sequence SEQ ID NO:32.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 9
ID   ABB95438 standard; protein; 322 AA.
DE   Human angiogenesis related protein PRO263 SEQ ID NO: 32.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 1657;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 10
ID   ABU71625 standard; protein; 322 AA.
DE   Human PRO polypeptide #36.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 6;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 11
ID   ABU71480 standard; protein; 322 AA.
DE   Human PRO polypeptide #36.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 6;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 12
ID   ABU71926 standard; protein; 322 AA.
DE   Human secreted/transmembrane protein PRO263.
PN   US2003003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1657;  DB 6;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 1e-147;
RESULT 13
ID   ABO01809 standard; protein; 322 AA.
DE   Novel human secreted and transmembrane protein PRO263.
PN   US2002197671-A1.
PD   26-DEC-2002.
```

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 14
ID ABU90878 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 15
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 16
ID ABU71954 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 17
ID ABU54382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 18
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 19
ID ABU71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 20
ID ABU72289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 21
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 22
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 23
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 24
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 25
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 26
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 27
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 28
ID ABO53263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 29
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 30
ID ABU89270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 31
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;

Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 32
ID ABU69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 33
ID ABU96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 34
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 35
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 36
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 37
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 38
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 39
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 40
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 41
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 42
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 43
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 44
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 45
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 46
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 47
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 48
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 49
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 50

ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 51
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 52
ID ADA41958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 53
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 54
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 55
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 56
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 57
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 58
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 59
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 60
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 61
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 62
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 63
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 64
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 65
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 66
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 67
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 68
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 69
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 70
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 71
ID ADC06962 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 72
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 73
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 74
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 75
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 76
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 77
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 78
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 79
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 80
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 81
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 82
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 83
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 84
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 85
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 86
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 87
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 88
ID ADF95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 89
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 90
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 91
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 92
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 93
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 94
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 95
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 96
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 97
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 98
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 99
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 100
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 101
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 102
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 103
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 104
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;

Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 105
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 106
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 107
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 108
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 109
ID ADH53653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 110
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 111
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 112
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 113
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 114
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 115
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 116
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 117
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 118
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 119
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 120
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 121
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 122
ID ADI11563 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 123

ID ADH98208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 124
ID ADH98548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 125
ID ADH98038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 126
ID ADI05026 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 127
ID ADI03376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 128
ID ADI04771 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 129
ID ADH78225 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 130
ID ADI19569 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 131
ID ADH90317 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 132
ID ADI03036 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 133
ID ADH77885 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 134
ID ADH97868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 135
ID ADI01253 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 136
ID ADI01948 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 137
ID ADI03206 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 138
ID ADI11393 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 139
ID ADI02295 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 140
ID ADI11733 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 141
ID ADI05370 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 142
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 143
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 144
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 145
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 146
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 147
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 148
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 149
ID ADH79782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 150
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 151
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 152
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 153
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 154
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 155
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 156
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 157
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 158
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 159
ID ADL93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 160
ID ADC52144 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 161
ID ADE79279 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 162
ID ADE79703 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 163
ID ADE73379 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 164
ID ADE41282 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 165
ID ADE71444 standard; protein; 322 AA.
DE Human PDEBC Incyte 3044710CD1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 166
ID ADE73914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 167
ID ADE99468 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 168
ID ADE98587 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 169
ID ADE99014 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 170
ID ADG40484 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 171
ID ADF73878 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 172
ID ADF73454 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 173
ID ADH06576 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 174
ID ADH06406 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 175
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 176
ID ADH27717 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;

RESULT 177
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 178
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 179
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 180
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 181
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 182
ID ADG69337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 183
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 184
ID ADG92724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 185
ID ADG83898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 186
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 187
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 188
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 189
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 190
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 191
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 192
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 193
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 194
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 195
ID ADH33860 standard; protein; 322 AA.

DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 196
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 197
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 198
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 199
ID ADG69167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 200
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 201
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 202
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 203
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 204
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 205
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 206
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 207
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 208
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 209
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 210
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 211
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 212
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 213
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.

PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 214
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 215
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 216
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 217
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 218
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 219
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 220
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 221
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 222
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 223
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 224
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 225
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 226
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 227
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 228
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 229
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 230
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 231
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 232
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 233
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 234
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 235
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 236
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 237
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 238
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 239
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 240
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 241
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 242
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 243
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 244
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 245
ID ADR11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 246
ID ADR17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 247
ID ADS74636 standard; protein; 322 AA.
DE Human secreted/transmembrane protein #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 248
ID ADT03673 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 249
ID ADY77701 standard; protein; 322 AA.
DE Neoplastic disease detection protein PRO263.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 250
ID ADY63147 standard; protein; 322 AA.
DE Human clone PSEC0135 protein, SEQ ID 150.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1657; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 251
ID AEA37911 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-147;
RESULT 252
ID ADR41495 standard; protein; 344 AA.
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1657; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
RESULT 253
ID ABB11979 standard; peptide; 344 AA.
DE Human PRO263 homologue, SEQ ID NO:2349.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 1654; DB 4; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.1e-147;
RESULT 254
ID AAW56249 standard; protein; 322 AA.
DE Amino acid sequence of a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.6%; Score 1651; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 3.7e-147;
RESULT 255
ID ABB90289 standard; protein; 322 AA.
DE Human polypeptide SEQ ID NO 2665.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.6%; Score 1651; DB 5; Length 322;
Best Local Similarity 99.7%; Pred. No. 3.7e-147;
RESULT 256
ID ADN05866 standard; protein; 322 AA.
DE Antipsoriatic protein sequence #1096.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.9%; Score 1638; DB 8; Length 322;
Best Local Similarity 99.1%; Pred. No. 6.3e-146;
RESULT 257
ID ADQ21089 standard; protein; 322 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 98.9%; Score 1638; DB 8; Length 322;
Best Local Similarity 99.1%; Pred. No. 6.3e-146;
RESULT 258
ID ABU69126 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 91.2%; Score 1511.5; DB 6; Length 297;
Best Local Similarity 92.2%; Pred. No. 5.1e-134;
RESULT 259
ID ADO08255 standard; protein; 297 AA.

DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 90.6%; Score 1500.5; DB 8; Length 297;
Best Local Similarity 91.9%; Pred. No. 5.6e-133;
RESULT 260
ID AAB34702 standard; protein; 250 AA.
DE Human secreted protein encoded by DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 73.5%; Score 1218.5; DB 3; Length 250;
Best Local Similarity 92.0%; Pred. No. 2e-106;
RESULT 261
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 66.6%; Score 1103; DB 4; Length 318;
Best Local Similarity 69.7%; Pred. No. 2.3e-95;
RESULT 262
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 49.5%; Score 821; DB 5; Length 255;
Best Local Similarity 65.0%; Pred. No. 7.9e-69;
RESULT 263
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 35.7%; Score 592; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
RESULT 264
ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 16.7%; Score 277; DB 2; Length 58;
Best Local Similarity 98.3%; Pred. No. 2.8e-18;
RESULT 265
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 15.8%; Score 261; DB 2; Length 69;
Best Local Similarity 96.4%; Pred. No. 1.2e-16;
RESULT 266
ID ADW24431 standard; protein; 364 AA.
DE Rat CD44.
PN WO200024869-A2.
PD 04-MAY-2000.
PA (UYYA) UNIV YALE.
PA (VIGN/) VIGNERY A.
Query Match 13.8%; Score 229; DB 3; Length 364;
Best Local Similarity 24.3%; Pred. No. 1.2e-12;
RESULT 267
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 13.8%; Score 229; DB 5; Length 364;
Best Local Similarity 24.3%; Pred. No. 1.2e-12;
RESULT 268
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 13.4%; Score 222.5; DB 2; Length 362;
Best Local Similarity 25.5%; Pred. No. 4.9e-12;
RESULT 269
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 13.4%; Score 222.5; DB 6; Length 365;
Best Local Similarity 24.5%; Pred. No. 5e-12;
RESULT 270
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 13.4%; Score 222.5; DB 7; Length 365;
Best Local Similarity 24.5%; Pred. No. 5e-12;
RESULT 271
ID AEA03024 standard; protein; 365 AA.
DE CD14 receptor amino acid sequence SEQ ID NO:50.
PN US2005112141-A1.
PD 26-MAY-2005.
PA (TERM/) TERMAN D S.
Query Match 13.4%; Score 222.5; DB 9; Length 365;
Best Local Similarity 24.5%; Pred. No. 5e-12;
RESULT 272
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 13.4%; Score 222; DB 2; Length 503;
Best Local Similarity 25.7%; Pred. No. 8.7e-12;
RESULT 273
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.

PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.4%; Score 222; DB 7; Length 503;
Best Local Similarity 25.7%; Pred. No. 8.7e-12;
RESULT 274
ID ADZ51063 standard; protein; 778 AA.
DE Amino acid sequence of murine CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 12.7%; Score 210; DB 9; Length 778;
Best Local Similarity 32.3%; Pred. No. 2.1e-10;
RESULT 275
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.6%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.4e-10;
RESULT 276
ID ADQ39384 standard; protein; 668 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.6%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.4e-10;
RESULT 277
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 278
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 279
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 280
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 281
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 282
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 4; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 283
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 284
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 285
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 286
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 287
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 288
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 289
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 290
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.

PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.5%; Score 207; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
RESULT 291
ID AAY99851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 12.4%; Score 205; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 292
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 293
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 294
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 295
ID ADV70207 standard; protein; 361 AA.
DE Tumor-associated antigenic target polypeptide TAT449.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 296
ID ADY19504 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 5310.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 297
ID AEA63870 standard; protein; 361 AA.
DE Protein of human anti-CD44 antibody.
PN JP2005154389-A.
PD 16-JUN-2005.
PA (UYTY) UNIV TOKYO.
PA (FUJY) FUJI PHARM IND CO LTD.
Query Match 12.4%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 298
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.8e-10;
RESULT 299
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.8e-10;
RESULT 300
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 204; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.8e-10;
RESULT 301
ID ADY16699 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 2505.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.3%; Score 204; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.8e-10;
RESULT 302
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 6; Length 608;
Best Local Similarity 21.8%; Pred. No. 6.3e-10;
RESULT 303
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 12.3%; Score 203.5; DB 4; Length 700;
Best Local Similarity 21.8%; Pred. No. 7.7e-10;
RESULT 304
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203.5; DB 6; Length 700;
Best Local Similarity 21.8%; Pred. No. 7.7e-10;
RESULT 305
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 7; Length 700;
Best Local Similarity 21.8%; Pred. No. 7.7e-10;
RESULT 306
ID ADW43568 standard; protein; 700 AA.
DE CD44vRA.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 9; Length 700;
Best Local Similarity 21.8%; Pred. No. 7.7e-10;
RESULT 307
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203; DB 7; Length 361;
Best Local Similarity 24.4%; Pred. No. 3.4e-10;
RESULT 308
ID ADW43572 standard; protein; 361 AA.
DE CD44s.

PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 3.4e-10;
RESULT 309
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/tmFAScyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.3%; Score 203; DB 4; Length 436;
Best Local Similarity 25.4%; Pred. No. 4.5e-10;
RESULT 310
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 436;
Best Local Similarity 25.4%; Pred. No. 4.5e-10;
RESULT 311
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 312
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 313
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.3%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 314
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 315
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 316
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 317
ID ADU06304 standard; protein; 742 AA.
DE Novel bronchial cancer-associated human protein SeqID528.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 318
ID ADY15336 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1142.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.3%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 319
ID ADY15338 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1144.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.3%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.2e-10;
RESULT 320
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.2%; Score 202.5; DB 8; Length 330;
Best Local Similarity 25.1%; Pred. No. 3.4e-10;
RESULT 321
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFAStm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.2%; Score 202.5; DB 4; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.9e-10;
RESULT 322
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202.5; DB 6; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.9e-10;
RESULT 323
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 4.3e-10;
RESULT 324
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 361;
Best Local Similarity 24.1%; Pred. No. 4.3e-10;
RESULT 325
ID ADS75483 standard; protein; 361 AA.
DE Human cell surface glycoprotein CD44 amino acid sequence.
PN JP2004275060-A.
PD 07-OCT-2004.
PA (SANY) SANKYO CO LTD.

Query Match 12.2%; Score 202; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 4.3e-10;
RESULT 326
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 327
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 328
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 329
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 330
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 331
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 12.2%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 332
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 333
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 334
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 335
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 336
ID ADW72142 standard; protein; 742 AA.
DE Human CD44 protein as biomarker for colorectal cancer.
PN US2005014165-A1.
PD 20-JAN-2005.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 12.2%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 337
ID ADZ51062 standard; protein; 742 AA.
DE Amino acid sequence of human CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 12.2%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-09;
RESULT 338
ID ABU04617 standard; protein; 425 AA.
DE Human expressed protein tag (EPT) #1283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 201; DB 6; Length 425;
Best Local Similarity 22.0%; Pred. No. 6.6e-10;
RESULT 339
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.1%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.5e-09;
RESULT 340
ID ADW43570 standard; protein; 699 AA.
DE CD44v3-v10.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.1%; Score 200.5; DB 9; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.5e-09;
RESULT 341
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 342
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 343
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.

Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 344
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 345
ID AAY96140 standard; protein; 493 AA.
DE Human epithelial CD44.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 3; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 346
ID AAU02449 standard; protein; 493 AA.
DE Human epithelial antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 4; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 347
ID AAU99123 standard; protein; 493 AA.
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN WO200244342-A2.
PD 06-JUN-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 12.0%; Score 199.5; DB 5; Length 493;
Best Local Similarity 22.2%; Pred. No. 1.1e-09;
RESULT 348
ID ABU04637 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1303.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 349
ID ABU04627 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1293.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 350
ID ABU04639 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1305.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 351
ID ABU04623 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1289.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 1.1e-09;
RESULT 352
ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 353
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 354
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 1.1e-09;
RESULT 355
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 356
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 357
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 22.2%; Pred. No. 1.1e-09;
RESULT 358
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 359
ID AEB87764 standard; protein; 493 AA.
DE Human CD44, breast tumor marker.
PN WO2005071419-A2.
PD 04-AUG-2005.
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES.
Query Match 12.0%; Score 199.5; DB 9; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
RESULT 360
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 7.5e-10;
RESULT 361
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 7.5e-10;
RESULT 362
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 198; DB 6; Length 395;
Best Local Similarity 23.0%; Pred. No. 1.2e-09;
RESULT 363
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.3e-09;
RESULT 364
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.3e-09;
RESULT 365
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.4e-09;
RESULT 366
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.4e-09;
RESULT 367
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 368
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 369
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 370
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 371
ID ADV73230 standard; protein; 699 AA.
DE Human colon tumor cell upregulated protein SEQ ID NO 71.
PN WO2004110345-A2.
PD 23-DEC-2004.
PA (PHAA) PHARMACIA CORP.
Query Match 11.9%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 372
ID ADY16689 standard; protein; 699 AA.
DE PRO polypeptide SEQ ID NO 2495.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 11.9%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 3.5e-09;
RESULT 373
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 374
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1.2e-09;
RESULT 375
ID ABU04624 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.2e-09;
RESULT 376
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.2e-09;
RESULT 377
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.8e-09;
RESULT 378
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 425;

Best Local Similarity 30.9%; Pred. No. 2e-09;
RESULT 379
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 2.4e-09;
RESULT 380
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 5.9e-09;
RESULT 381
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 1e-09;
RESULT 382
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 1.1e-09;
RESULT 383
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 1.7e-09;
RESULT 384
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.6%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 9.9e-09;
RESULT 385
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.6%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 9.9e-09;
RESULT 386
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 3.2e-09;
RESULT 387
ID ABU04606 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 3.2e-09;
RESULT 388
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 6.7e-09;
RESULT 389
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 6.7e-09;
RESULT 390
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.3%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 3.2e-09;
RESULT 391
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.3%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 2.2e-09;
RESULT 392
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.3%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.3%; Pred. No. 2.5e-09;
RESULT 393
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.2%; Score 185; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 3.5e-09;
RESULT 394
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.0%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 5.4e-09;
RESULT 395
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.0%; Score 182; DB 6; Length 112;

Best Local Similarity 34.2%; Pred. No. 6.7e-09;
RESULT 396
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 10.9%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 8.3e-09;
RESULT 397
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 180; DB 4; Length 920;
Best Local Similarity 25.6%; Pred. No. 1.9e-07;
RESULT 398
ID ADI60410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 180; DB 7; Length 920;
Best Local Similarity 25.6%; Pred. No. 1.9e-07;
RESULT 399
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.3%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 400
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.3%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 401
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.1%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 5.7e-05;
RESULT 402
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 9.0%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 6.2e-06;
RESULT 403
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.8%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 3.5e-05;
RESULT 404
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.8%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 5.9e-05;
RESULT 405
ID AAR26044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 406
ID AAW13654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 407
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 408
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 409
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 5; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 410
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 411
ID ABU56653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 412
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 413
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.

PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 414
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 415
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 416
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 417
ID ADW38508 standard; protein; 277 AA.
DE Immunomodulatory gene TNFa induced protein 6.
PN WO2005000099-A2.
PD 06-JAN-2005.
PA (GENZ) GENZYME CORP.
Query Match 8.8%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 418
ID AEA23596 standard; protein; 277 AA.
DE Human PRO polypeptide SEQ ID NO 138.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 8.8%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 7.3e-05;
RESULT 419
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 8.8%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.0016;
RESULT 420
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 8.7%; Score 144; DB 8; Length 275;
Best Local Similarity 33.0%; Pred. No. 9e-05;
RESULT 421
ID ADO09968 standard; protein; 897 AA.
DE Human NOV1c cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.2%; Score 136; DB 8; Length 897;
Best Local Similarity 21.2%; Pred. No. 0.0026;
RESULT 422
ID ABJ10588 standard; protein; 897 AA.
DE Human novel protein NOV1c SEQ ID NO: 211.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 134; DB 5; Length 897;
Best Local Similarity 20.7%; Pred. No. 0.004;
RESULT 423
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 134; DB 8; Length 897;
Best Local Similarity 20.7%; Pred. No. 0.004;
RESULT 424
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 134; DB 8; Length 1502;
Best Local Similarity 20.7%; Pred. No. 0.0081;
RESULT 425
ID ABJ10586 standard; protein; 2675 AA.
DE Human novel protein NOV1a SEQ ID NO: 2.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 134; DB 5; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.018;
RESULT 426
ID ADO09971 standard; protein; 2675 AA.
DE Human NOV1a variant.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.

PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.1%; Score 134; DB 8; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.018;
RESULT 427
ID ADO09836 standard; protein; 2675 AA.
DE Human NOV1a.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.1%; Score 134; DB 8; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.018;
RESULT 428
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 8.0%; Score 133; DB 5; Length 1394;
Best Local Similarity 20.7%; Pred. No. 0.0091;
RESULT 429
ID ABG72499 standard; protein; 1416 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.0%; Score 133; DB 6; Length 1416;
Best Local Similarity 20.7%; Pred. No. 0.0093;
RESULT 430
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 8.0%; Score 133; DB 5; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0095;
RESULT 431
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.0%; Score 133; DB 6; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0095;
RESULT 432
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 133; DB 8; Length 1510;
Best Local Similarity 20.7%; Pred. No. 0.01;
RESULT 433
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.0%; Score 133; DB 6; Length 1653;
Best Local Similarity 20.7%; Pred. No. 0.012;
RESULT 434
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 8.0%; Score 133; DB 8; Length 1895;
Best Local Similarity 20.7%; Pred. No. 0.014;
RESULT 435
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 133; DB 8; Length 2551;
Best Local Similarity 20.7%; Pred. No. 0.021;
RESULT 436
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.0%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.02;
RESULT 437
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.0%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.021;
RESULT 438
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 7.9%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0068;
RESULT 439
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 7.9%; Score 131.5; DB 8; Length 883;

Best Local Similarity 24.3%; Pred. No. 0.0068;
RESULT 440
ID AEB34752 standard; protein; 883 AA.
DE Mammalian mutant BEHAB protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 7.9%; Score 131.5; DB 9; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0068;
RESULT 441
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 4; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0049;
RESULT 442
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 131; DB 6; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0049;
RESULT 443
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0049;
RESULT 444
ID ADF71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0049;
RESULT 445
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 8; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0049;
RESULT 446
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 4; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0052;
RESULT 447
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 131; DB 6; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0052;
RESULT 448
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0052;
RESULT 449
ID ADF71511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0052;
RESULT 450
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 131; DB 8; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0052;
RESULT 451
ID ADH18892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 7.9%; Score 131; DB 8; Length 806;
Best Local Similarity 20.4%; Pred. No. 0.0066;
RESULT 452
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 4; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 453
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 454
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.9%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 455
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 456
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 457
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 458
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 459
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 460
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 461
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 462
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 463
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 464
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 465
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 466
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 467
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 468
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 469
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 470
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 471
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 472
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 473
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 474
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 475
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 476
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 477
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 478
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 479
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 480
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 481
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 482
ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 483
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 484
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 485
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 486
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 487
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 488
ID ADD95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 489
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 490
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 491
ID ADE39444 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;

RESULT 492
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 493
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 494
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 495
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 496
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 497
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 498
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 499
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 500
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 501
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 502
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 503
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 504
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 505
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 506
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 507
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 508
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 509
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 510
ID ADD88932 standard; protein; 911 AA.

DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 511
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 512
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 513
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 514
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 515
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 516
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 517
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 518
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 519
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 520
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 521
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 522
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 523
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 524
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 525
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 526
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 527
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 528
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 529
ID ADH40040 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 530
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 531
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 532
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 533
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 534
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 535
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 536
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 537
ID ADH58488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 538
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 539
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 540
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 541
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 542
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 543
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 544
ID AEA00137 standard; protein; 911 AA.
DE Human TAT145 protein SEQ ID NO:89.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 9; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 545
ID AEA00657 standard; protein; 911 AA.
DE Human TAT145 protein sequence SeqID89.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 9; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0079;
RESULT 546
ID AAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 7.9%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 547
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 548
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0084;
RESULT 549
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevican protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 550
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0084;
RESULT 551
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 552
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0084;
RESULT 553
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0084;
RESULT 554
ID AEB34755 standard; protein; 883 AA.
DE Rat poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 7.9%; Score 130.5; DB 9; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0084;
RESULT 555
ID ABB90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 130.5; DB 5; Length 1082;
Best Local Similarity 20.6%; Pred. No. 0.011;
RESULT 556
ID ADX15811 standard; protein; 2316 AA.
DE Human aggrecan.
PN WO2005012512-A1.
PD 10-FEB-2005.
PA (NAKA/) NAKAMURA N.
Query Match 7.9%; Score 130.5; DB 9; Length 2316;
Best Local Similarity 27.4%; Pred. No. 0.032;
RESULT 557
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 130.5; DB 8; Length 2570;
Best Local Similarity 20.6%; Pred. No. 0.036;
RESULT 558
ID AAY93911 standard; protein; 457 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 7.8%; Score 129.5; DB 3; Length 457;
Best Local Similarity 20.9%; Pred. No. 0.0042;
RESULT 559
ID ABM83434 standard; protein; 761 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 129.5; DB 8; Length 761;
Best Local Similarity 22.8%; Pred. No. 0.0085;
RESULT 560
ID AAY93910 standard; protein; 2157 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 7.8%; Score 129.5; DB 3; Length 2157;
Best Local Similarity 20.9%; Pred. No. 0.036;
RESULT 561
ID ABR82200 standard; protein; 2570 AA.
DE Human CLEVER-1 protein SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Query Match 7.8%; Score 129.5; DB 6; Length 2570;
Best Local Similarity 20.9%; Pred. No. 0.045;
RESULT 562
ID AAB08023 standard; protein; 95 AA.
DE The domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.8%; Score 128.5; DB 3; Length 95;

Best Local Similarity 28.7%; Pred. No. 0.00061;
RESULT 563
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 7.8%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00061;
RESULT 564
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 7.8%; Score 128.5; DB 2; Length 912;
Best Local Similarity 22.0%; Pred. No. 0.014;
RESULT 565
ID ADV70173 standard; protein; 671 AA.
DE Tumor-associated antigenic target polypeptide TAT152.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.011;
RESULT 566
ID AEA00138 standard; protein; 671 AA.
DE Human TAT152 protein SEQ ID NO:90.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.011;
RESULT 567
ID AEA00658 standard; protein; 671 AA.
DE Human TAT152 protein sequence SeqID90.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.011;
RESULT 568
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.7%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.015;
RESULT 569
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.7%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.016;
RESULT 570
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 7.7%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.017;
RESULT 571
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.7%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.017;
RESULT 572
ID ADK67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 7.7%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.017;
RESULT 573
ID AEB34757 standard; protein; 911 AA.
DE Human poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 7.7%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.017;
RESULT 574
ID ABR58557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.7%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0037;
RESULT 575
ID ABU56654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.7%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0037;
RESULT 576
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.7%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0037;
RESULT 577
ID ADO24439 standard; protein; 277 AA.
DE Human PRO87335 protein SEQ ID NO:78.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0037;
RESULT 578
ID ADR14117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.7%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0037;
RESULT 579
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.

PA (BIRS/) BIRSE C E.
Query Match 7.6%; Score 126.5; DB 7; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.0081;
RESULT 580
ID ADJ55382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.6%; Score 126.5; DB 8; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.0081;
RESULT 581
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 126; DB 8; Length 277;
Best Local Similarity 34.1%; Pred. No. 0.0046;
RESULT 582
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.5%; Score 124.5; DB 7; Length 482;
Best Local Similarity 22.1%; Pred. No. 0.014;
RESULT 583
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.3%; Score 121.5; DB 8; Length 259;
Best Local Similarity 34.9%; Pred. No. 0.011;
RESULT 584
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 2; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 585
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 3; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 586
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 587
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 588
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 589
ID ABU58413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 590
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 591
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 592
ID ABU84276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 593
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 594
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 595
ID ABU99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 596
ID ABU82719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 597
ID ABU89840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 598
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 599
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 600
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 601
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 602
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 603
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 604
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 605
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 606
ID ABU85591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 607
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 608
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 609
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 610
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 611
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 612
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 613
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 614
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 615
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 616
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 617
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 618
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 619
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 620
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 621
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 622
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 623
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 624
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 625
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 626
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 627
ID ABU88666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 628
ID ABU83361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 629
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 630
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 631
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 632
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 633
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 634
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 635
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 636
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 637
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 638
ID ABU65582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 639
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 640
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 641
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 642
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 643
ID ABU55949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 644
ID ABU65277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 645
ID ABU95222 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 646
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 647
ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 648
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 649
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 650
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 651
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 652
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 653
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 654
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 655
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 656
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 657
ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 658
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 659
ID ABU83056 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 660
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 661
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 662
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 663
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 664
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 665
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 666
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 667
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 668
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 669
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 670
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 671
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 672
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 673
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 674
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 675
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 676
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 677
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 678
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 679
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.

PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 680
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 681
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 682
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 683
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 684
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 685
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 686
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 687
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 688
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 689
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 690
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 691
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 692
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 693
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 694
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 695
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 696
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 697
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 698
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 699
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 700

ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 701
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 702
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 703
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 704
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 705
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 706
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 707
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 708
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 709
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 710
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 711
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 712
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 713
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 714
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 715
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 716
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 717
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 718
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 719
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 720
ID ABR95533 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 721
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 722
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 723
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 724
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 725
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 726
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 727
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 728
ID ABM07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 729
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 730
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 731
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 732
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 733
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 734
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 735
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 736
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 737
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 738
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 739
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 740
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 741
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 742
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 743
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 744
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 745
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 746
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 747
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 748
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 749
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 750
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 751
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 752
ID ABM11560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 753
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 754
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 755
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 756
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 757
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 758
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 759
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 760
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 761
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 762
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 763
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 764
ID ABM76035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 765
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 766
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 767
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 768
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 769
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 770
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 771
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 772
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 773
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 774
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 775
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 776
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 777
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 778
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 779
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 780
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 781
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 782
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 783
ID ABM04855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 784
ID ABM08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 785
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 786
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 787
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 788
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 789
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 790
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 791
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 792
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 793
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 794
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 795
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 796
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 797
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 798
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 799
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 800
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 801
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 802
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 803
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 804
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 805
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 806
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 807
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 808
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 809
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 810
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 811
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 812
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 813
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 814
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 815
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 816
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 817
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 818
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 819
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 820
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 821
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 822
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 823
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 824
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 825
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 826
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 827
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 828
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 829
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 830
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 831
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 832
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 833
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 834
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 835
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 836
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 837
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 838
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 839
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 840
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 841
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 842
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 843
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 844
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 845
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 846
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 847
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 848
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 849
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 850
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 851
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 852
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 853
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 854
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 855
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 856
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 857
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 858
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 859
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 860
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 861
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 862
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 863
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 864
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 865
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 866
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 867
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 868
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 869
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 870
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 871
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 872
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 873
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 874
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 875
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 876
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 877
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 878
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 879
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 880
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 881
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 882
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 883
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 884
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 885
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 886
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 887
ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 888
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 889

ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 890
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 891
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 892
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 893
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 894
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 895
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 896
ID ABM06680 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 897
ID ABM09120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 898
ID ABO39160 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 899
ID ABM75425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 900
ID ABM25349 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 901
ID ABM19859 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 902
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 903
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 904
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 905
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 906
ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 907
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 908
ID ABO06820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 909
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 910
ID ABR73331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 911
ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 912
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 913
ID ABM18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 914
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 915
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 916
ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 917
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 918
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 919
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 920
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 921
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 922
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 923
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 924
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 925
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 926
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 927
ID ABM08510 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 928
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 929
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 930
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 931
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 932
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 933
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 934
ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 935
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 936
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 937
ID ABR88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 938
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 939
ID ABM03271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 940
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 941
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 942
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 943
ID ABO05247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 944
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 945
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 946
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 947
ID ABM17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 948
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 949
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 950
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 951
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 952
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 953
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 954
ID ABM10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 955
ID ABM76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 956
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 957
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 958
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 959
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 960
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 961
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 962
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 963
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 964
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 965
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 966
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 967
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 968
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 969
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 970
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 971
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 972
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 973
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 974
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 975
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 976
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 977
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 978
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 979
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 980
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 981
ID ABM14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 982
ID ABM09730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 983
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 984
ID ABM34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 985
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 986
ID ADA42820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 987
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 988
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 989
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 990
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 991
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 992
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 993
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 994
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 995
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 996
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 997
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 998
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 999
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1000
ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1001
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1002
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1003
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1004
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1005
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1006
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1007
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1008
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1009
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1010
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1011
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1012
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1013
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1014
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1015
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1016
ID ABM22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1017
ID ABM30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1018
ID ABM21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1019
ID ABM21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1020
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1021
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1022
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1023
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1024
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1025
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1026
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1027
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1028
ID ABM31754 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1029
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1030
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1031
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1032
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1033
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1034
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1035
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1036
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1037
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1038
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1039
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1040
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1041
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1042
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1043
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1044
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1045
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1046
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1047
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1048
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1049
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1050
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1051
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1052
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1053
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1054
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1055
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1056
ID ADF95378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1057
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1058
ID ADH08853 standard; protein; 360 AA.

DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1059
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1060
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1061
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1062
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1063
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1064
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1065
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1066
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1067
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1068
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1069
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1070
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1071
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1072
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1073
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1074
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1075
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1076

ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1077
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1078
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1079
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1080
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1081
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1082
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1083
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1084
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1085
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1086
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1087
ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1088
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1089
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1090
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1091
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1092
ID ADI65842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1093
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1094
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1095
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1096
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1097
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1098
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1099
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1100
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1101
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1102
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1103
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1104
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1105
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1106
ID ADR11100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1107
ID ADR18009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1108
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1109
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1110
ID AEA37923 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 9; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.017;
RESULT 1111
ID AEA20028 standard; protein; 422 AA.
DE Novel human polypeptide SEQ ID NO 722.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.3%; Score 121.5; DB 9; Length 422;
Best Local Similarity 34.9%; Pred. No. 0.022;
RESULT 1112
ID AAW59882 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 7.3%; Score 121; DB 2; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1113
ID AAB61241 standard; protein; 528 AA.
DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.3%; Score 121; DB 4; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1114
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.3%; Score 121; DB 6; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1115
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.3%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1116
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.3%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1117
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.3%; Score 121; DB 8; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.033;
RESULT 1118
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 7.3%; Score 120.5; DB 2; Length 1257;
Best Local Similarity 23.6%; Pred. No. 0.12;
RESULT 1119
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.27;
RESULT 1120
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.27;
RESULT 1121
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.

PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.35;
RESULT 1122
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.35;
RESULT 1123
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1124
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1125
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1126
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1127
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1128
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1129
ID ADZ09841 standard; protein; 3396 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.2%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1130
ID ADZ70548 standard; protein; 3396 AA.
DE Human protein from lung cancer marker gene CSPG2.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 7.2%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1131
ID AEA04473 standard; protein; 3396 AA.
DE Human protein from gene overexpressed in cancer, CSPG2.
PN WO2005044990-A2.
PD 19-MAY-2005.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.2%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1132
ID AEB17604 standard; protein; 3396 AA.
DE Human CSPG2 protein SeqID18.
PN JP2005110602-A.
PD 28-APR-2005.
PA (SUMU) SUMITOMO SEIYAKU KK.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.2%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.73;
RESULT 1133
ID ADZ09886 standard; protein; 6792 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.2%; Score 118.5; DB 9; Length 6792;
Best Local Similarity 25.5%; Pred. No. 1.9;
RESULT 1134
ID ADP71273 standard; protein; 191 AA.
DE Human LP2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 7.1%; Score 117; DB 8; Length 191;
Best Local Similarity 26.5%; Pred. No. 0.019;
RESULT 1135
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 117; DB 8; Length 340;
Best Local Similarity 26.5%; Pred. No. 0.043;
RESULT 1136
ID ABU11635 standard; protein; 343 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 117; DB 6; Length 343;
Best Local Similarity 26.5%; Pred. No. 0.043;
RESULT 1137
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.0%; Score 116; DB 8; Length 2397;
Best Local Similarity 28.4%; Pred. No. 0.78;
RESULT 1138
ID AAR85443 standard; protein; 908 AA.
DE Rat brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 6.9%; Score 115; DB 2; Length 908;
Best Local Similarity 22.2%; Pred. No. 0.25;
RESULT 1139
ID ADO31200 standard; protein; 1257 AA.

DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.9%; Score 114.5; DB 8; Length 1257;
Best Local Similarity 23.1%; Pred. No. 0.44;
RESULT 1140
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.9%; Score 114; DB 7; Length 656;
Best Local Similarity 28.4%; Pred. No. 0.2;
RESULT 1141
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 112.5; DB 4; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.09;
RESULT 1142
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.8%; Score 112.5; DB 5; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.09;
RESULT 1143
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 111.5; DB 6; Length 402;
Best Local Similarity 22.5%; Pred. No. 0.18;
RESULT 1144
ID ADP71271 standard; protein; 200 AA.
DE Human aggrecan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.7%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.076;
RESULT 1145
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match 6.7%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.39;
RESULT 1146
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.7%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.39;
RESULT 1147
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 6.7%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2.3;
RESULT 1148
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.7%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2.3;
RESULT 1149
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2.3;
RESULT 1150
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2.3;
RESULT 1151
ID ADV70260 standard; protein; 2409 AA.
DE Tumor-associated antigenic target polypeptide TAT498.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 6.7%; Score 111; DB 9; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2.3;
RESULT 1152
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 110; DB 3; Length 341;
Best Local Similarity 28.5%; Pred. No. 0.2;
RESULT 1153
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 6.6%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.26;
RESULT 1154
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.6;
RESULT 1155
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.6;
RESULT 1156
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.6;
RESULT 1157
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.6%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.6;
RESULT 1158
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1159
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1160
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1161
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1162
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1163
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1164
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1165
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1166
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1167
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1168
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1169
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1170
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1171
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1172
ID ABJ56899 standard; protein; 354 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1173
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1174
ID ABJ56893 standard; protein; 354 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;

Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1175
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1176
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1177
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1178
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant 121P1F1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1179
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1180
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 108; DB 8; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.32;
RESULT 1181
ID AAR77034 standard; protein; 355 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 6.5%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.32;
RESULT 1182
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.59;
RESULT 1183
ID ABJ56890 standard; protein; 721 AA.
DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.85;
RESULT 1184
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.85;
RESULT 1185
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.85;
RESULT 1186
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 6.5%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.064;
RESULT 1187
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.34;
RESULT 1188
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.34;
RESULT 1189
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 339;
Best Local Similarity 28.6%; Pred. No. 0.38;
RESULT 1190
ID ABJ56915 standard; protein; 354 AA.
DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.4;
RESULT 1191
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.4;
RESULT 1192
ID ABJ56907 standard; protein; 355 AA.
DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.4;

RESULT 1193
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.7;
RESULT 1194
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.7;
RESULT 1195
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1196
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1197
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1198
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1199
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1200
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.73;
RESULT 1201
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.74;
RESULT 1202
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 1.2;
RESULT 1203
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 1.3;
RESULT 1204
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.5%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 2.3;
RESULT 1205
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 107; DB 4; Length 1795;
Best Local Similarity 24.1%; Pred. No. 3.7;
RESULT 1206
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 5.6;
RESULT 1207
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 5.6;
RESULT 1208
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.

PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 6.5%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 5.6;
RESULT 1209
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.91;
RESULT 1210
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.3%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.62;
RESULT 1211
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.62;
RESULT 1212
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104.5; DB 3; Length 330;
Best Local Similarity 18.7%; Pred. No. 0.62;
RESULT 1213
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.21;
RESULT 1214
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.21;
RESULT 1215
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.3%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.21;
RESULT 1216
ID ADY16502 standard; protein; 139 AA.
DE PRO polypeptide SEQ ID NO 2308.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.21;
RESULT 1217
ID AEB29759 standard; protein; 139 AA.
DE Human CD44 isoform RC.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.3%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.21;
RESULT 1218
ID ADP71269 standard; protein; 195 AA.
DE Human LP1 protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.34;
RESULT 1219
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.35;
RESULT 1220
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1221
ID ABB60536 standard; protein; 1712 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 104; DB 4; Length 1712;
Best Local Similarity 22.7%; Pred. No. 6.7;
RESULT 1222
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 102.5; DB 4; Length 183;
Best Local Similarity 29.7%; Pred. No. 0.43;
RESULT 1223
ID ADX72128 standard; protein; 309 AA.
DE Plant full length insert polypeptide seqid 41494.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.2%; Score 102; DB 8; Length 309;
Best Local Similarity 24.6%; Pred. No. 0.98;
RESULT 1224
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 1.5;
RESULT 1225
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.

PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 101.5; DB 3; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.7;
RESULT 1226
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 6.1%; Score 101.5; DB 6; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.7;
RESULT 1227
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 2;
RESULT 1228
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 2;
RESULT 1229
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 2;
RESULT 1230
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 6.1%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 2;
RESULT 1231
ID ABB68940 standard; protein; 1379 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 100.5; DB 4; Length 1379;
Best Local Similarity 20.2%; Pred. No. 11;
RESULT 1232
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 6.0%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 2;
RESULT 1233
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Query Match 6.0%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 2.4;
RESULT 1234
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 1;
RESULT 1235
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 1;
RESULT 1236
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.0%; Score 99; DB 8; Length 410;
Best Local Similarity 22.0%; Pred. No. 2.8;
RESULT 1237
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 4.7;
RESULT 1238
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 15;
RESULT 1239
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 98.5; DB 4; Length 1126;
Best Local Similarity 25.0%; Pred. No. 12;
RESULT 1240
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 2870;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1241
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 2870;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1242
ID ADW79951 standard; protein; 2870 AA.
DE Nematode location of vulva (lov-1) mutant protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 9; Length 2870;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1243
ID AAY95556 standard; protein; 3178 AA.

DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1244
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1245
ID ADW79940 standard; protein; 3178 AA.
DE Nematode location of vulva (lov-1) protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 9; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1246
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 33;
RESULT 1247
ID AAB75555 standard; protein; 298 AA.
DE Gene 1 human secreted protein homologous amino acid sequence #109.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.9%; Score 97.5; DB 4; Length 298;
Best Local Similarity 19.8%; Pred. No. 2.5;
RESULT 1248
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1249
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1250
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1251
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1252
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1253
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1254
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 2.7;
RESULT 1255
ID ADQ67145 standard; protein; 803 AA.
DE Novel human protein sequence #2118.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 94; DB 8; Length 803;
Best Local Similarity 21.9%; Pred. No. 21;
RESULT 1256
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID No 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1257
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1258
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1259
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1260
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID No 144.

PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 5;
RESULT 1261
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 5;
RESULT 1262
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 5;
RESULT 1263
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 5;
RESULT 1264
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 93.5; DB 4; Length 320;
Best Local Similarity 23.2%; Pred. No. 6.6;
RESULT 1265
ID ADE36618 standard; protein; 339 AA.
DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 7.1;
RESULT 1266
ID ADE36592 standard; protein; 339 AA.
DE Human NOV1a protein SEQ ID NO:2.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 7.1;
RESULT 1267
ID ABR58582 standard; protein; 359 AA.
DE Human cancer related protein SEQ ID NO:239.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1268
ID ABP70439 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1269
ID ABP70441 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 4.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1270
ID ABP70438 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1271
ID ABR48174 standard; protein; 359 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:64.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1272
ID AAO26680 standard; protein; 359 AA.
DE KIM-1 related protein, SEQ ID No 8.
PN WO200298920-A1.
PD 12-DEC-2002.
PA (BIOJ) BIOGEN INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1273
ID ADE36594 standard; protein; 359 AA.
DE Human NOV1b protein SEQ ID NO:4.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1274
ID ADN38984 standard; protein; 359 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 7; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1275
ID ADQ76690 standard; protein; 359 AA.
DE Human kidney injury molecule-1 (KIM-1).
PN WO2004060041-A2.
PD 22-JUL-2004.
PA (BIOG-) BIOGEN IDEC MA INC.
Query Match 5.6%; Score 93.5; DB 8; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1276
ID ABR99971 standard; protein; 359 AA.
DE HAVCR1 protein, SEQ ID 25.
PN WO2005001092-A2.
PD 06-JAN-2005.
PA (AMHP) WYETH.
Query Match 5.6%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1277
ID ADY98071 standard; protein; 359 AA.
DE Human TIM-1 allele 1-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.6%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1278

ID ADY98077 standard; protein; 359 AA.
DE Human TIM-1 allele 4-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.6%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1279
ID ADY98073 standard; protein; 359 AA.
DE Human TIM-1 allele 2-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.6%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1280
ID ADZ79370 standard; protein; 359 AA.
DE Human kidney injury molecule-1(b) complete protein.
PN US2005112117-A1.
PD 26-MAY-2005.
PA (BAIL/) BAILLY V.
PA (BONV/) BONVENTRE J.
Query Match 5.6%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 7.7;
RESULT 1281
ID ABG07923 standard; protein; 366 AA.
DE Novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 93.5; DB 4; Length 366;
Best Local Similarity 23.2%; Pred. No. 7.9;
RESULT 1282
ID ADP04445 standard; protein; 1381 AA.
DE Sea squirt protein with tissue specific expression in development Seq40.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.6%; Score 93.5; DB 8; Length 1381;
Best Local Similarity 22.9%; Pred. No. 49;
RESULT 1283
ID ABR63235 standard; protein; 2055 AA.
DE Glucansucrase sequence from strain KG15.
PN WO2003008618-A2.
PD 30-JAN-2003.
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
Query Match 5.6%; Score 93.5; DB 6; Length 2055;
Best Local Similarity 23.3%; Pred. No. 84;
RESULT 1284
ID ADU82549 standard; protein; 311 AA.
DE C. elegans SID-2 polypeptide, SEQ ID 3.
PN WO2004099386-A2.
PD 18-NOV-2004.
PA (HARD) HARVARD COLLEGE.
Query Match 5.6%; Score 93; DB 8; Length 311;
Best Local Similarity 18.4%; Pred. No. 7;
RESULT 1285
ID ADU82552 standard; protein; 311 AA.
DE C. elegans SID-2 polypeptide, SEQ ID 6.
PN WO2004099386-A2.
PD 18-NOV-2004.
PA (HARD) HARVARD COLLEGE.
Query Match 5.6%; Score 93; DB 8; Length 311;
Best Local Similarity 18.4%; Pred. No. 7;
RESULT 1286
ID AAR88466 standard; protein; 629 AA.
DE Drosophila scavenger receptor class CI.
PN WO9600288-A2.
PD 04-JAN-1996.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.6%; Score 93; DB 2; Length 629;
Best Local Similarity 19.9%; Pred. No. 19;
RESULT 1287
ID ABG33057 standard; protein; 629 AA.
DE Fruit fly scavenger receptor type CI (dSR-CI).
PN US6429289-B1.
PD 06-AUG-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.6%; Score 93; DB 5; Length 629;
Best Local Similarity 19.9%; Pred. No. 19;
RESULT 1288
ID AAE21524 standard; protein; 629 AA.
DE Drosophila melanogaster scavenger receptor class CI (dSR-CI).
PN US6350859-B1.
PD 26-FEB-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.6%; Score 93; DB 5; Length 629;
Best Local Similarity 19.9%; Pred. No. 19;
RESULT 1289
ID ABP73157 standard; protein; 40 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 5.6%; Score 92.5; DB 6; Length 40;
Best Local Similarity 54.1%; Pred. No. 0.47;
RESULT 1290
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.6%; Score 92.5; DB 2; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;
RESULT 1291
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 92.5; DB 2; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;
RESULT 1292
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 92.5; DB 7; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;
RESULT 1293
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 5.6%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;
RESULT 1294
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;

RESULT 1295
ID ADU66693 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 5.6%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 7.5;
RESULT 1296
ID ABP70440 standard; protein; 365 AA.
DE Amino acid sequence of human TIM-1 allele 3.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 92.5; DB 6; Length 365;
Best Local Similarity 22.6%; Pred. No. 9.8;
RESULT 1297
ID ADY98075 standard; protein; 365 AA.
DE Human TIM-1 allele 3-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.6%; Score 92.5; DB 9; Length 365;
Best Local Similarity 22.6%; Pred. No. 9.8;
RESULT 1298
ID ABB50001 standard; protein; 569 AA.
DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.6%; Score 92.5; DB 5; Length 569;
Best Local Similarity 21.4%; Pred. No. 18;
RESULT 1299
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 92.5; DB 6; Length 569;
Best Local Similarity 21.4%; Pred. No. 18;
RESULT 1300
ID AAU48553 standard; protein; 706 AA.
DE Propionibacterium acnes immunogenic protein #9449.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 4; Length 706;
Best Local Similarity 25.4%; Pred. No. 24;
RESULT 1301
ID ABM45072 standard; protein; 706 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 6; Length 706;
Best Local Similarity 25.4%; Pred. No. 24;
RESULT 1302
ID ADN18863 standard; protein; 994 AA.
DE Bacterial polypeptide #1516.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.6%; Score 92.5; DB 8; Length 994;
Best Local Similarity 19.7%; Pred. No. 39;
RESULT 1303
ID ABR53566 standard; protein; 1636 AA.
DE Protein sequence #SEQ ID 1997.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 6; Length 1636;
Best Local Similarity 19.7%; Pred. No. 77;
RESULT 1304
ID ADK64364 standard; protein; 1636 AA.
DE Disease treating protein complex-derived protein #1193.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 7; Length 1636;
Best Local Similarity 19.7%; Pred. No. 77;
RESULT 1305
ID ABP70442 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 92; DB 6; Length 364;
Best Local Similarity 21.6%; Pred. No. 11;
RESULT 1306
ID ADY98079 standard; protein; 364 AA.
DE Human TIM-1 allele 5-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.6%; Score 92; DB 9; Length 364;
Best Local Similarity 21.6%; Pred. No. 11;
RESULT 1307
ID ABG93047 standard; protein; 966 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.6%; Score 92; DB 5; Length 966;
Best Local Similarity 20.3%; Pred. No. 41;
RESULT 1308
ID ADT87298 standard; protein; 966 AA.
DE Yeast Stress-related protein from gene YBR112C.
PN WO2004092398-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 5.6%; Score 92; DB 8; Length 966;
Best Local Similarity 20.3%; Pred. No. 41;
RESULT 1309
ID ADL72180 standard; protein; 2829 AA.
DE X. laevis mutated adenomatous polyposis coli (APC) protein.
PN WO2004018677-A1.
PD 04-MAR-2004.
PA (EISA) EISAI CO LTD.
Query Match 5.6%; Score 92; DB 8; Length 2829;
Best Local Similarity 20.7%; Pred. No. 1.8e+02;
RESULT 1310
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 4.1;
RESULT 1311
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 4.1;
RESULT 1312
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.

PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.5%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 4.1;
RESULT 1313
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 4.1;
RESULT 1314
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.5%; Score 91.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 9.3;
RESULT 1315
ID AAM52302 standard; protein; 350 AA.
DE ActA protein fragment #2.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 350;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 1316
ID AAM52301 standard; protein; 376 AA.
DE ActA protein fragment #1.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 376;
Best Local Similarity 22.0%; Pred. No. 13;
RESULT 1317
ID AAM52300 standard; protein; 610 AA.
DE ActA protein.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 610;
Best Local Similarity 22.0%; Pred. No. 25;
RESULT 1318
ID AAG79171 standard; protein; 639 AA.
DE Amino acid sequence of an ActA fragment.
PN WO200174858-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.5%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 26;
RESULT 1319
ID AAU09142 standard; protein; 639 AA.
DE Lysteria monocytogenes ActA.
PN WO200174853-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.5%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 26;
RESULT 1320
ID ABB47677 standard; protein; 639 AA.
DE Listeria monocytogenes protein #381.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.5%; Score 91.5; DB 5; Length 639;
Best Local Similarity 22.0%; Pred. No. 26;
RESULT 1321
ID ADM48341 standard; protein; 681 AA.
DE Marburg virus glycoprotein, GP.
PN US2003215794-A1.
PD 20-NOV-2003.
PA (KAWA/) KAWAOKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Query Match 5.5%; Score 91.5; DB 8; Length 681;
Best Local Similarity 19.2%; Pred. No. 29;
RESULT 1322
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 91.5; DB 8; Length 1103;
Best Local Similarity 24.3%; Pred. No. 55;
RESULT 1323
ID ABP60839 standard; protein; 246 AA.
DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 91; DB 5; Length 246;
Best Local Similarity 27.0%; Pred. No. 7.9;
RESULT 1324
ID AEA08149 standard; protein; 4262 AA.
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 5.5%; Score 91; DB 9; Length 4262;
Best Local Similarity 20.7%; Pred. No. 4e+02;
RESULT 1325
ID AEA08148 standard; protein; 4493 AA.
DE Human mucin 17 protein - SEQ ID 3.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 5.5%; Score 91; DB 9; Length 4493;
Best Local Similarity 20.7%; Pred. No. 4.3e+02;
RESULT 1326
ID ADY11098 standard; protein; 463 AA.
DE Plant full length insert polypeptide seqid 66913.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.5%; Score 90.5; DB 8; Length 463;
Best Local Similarity 23.1%; Pred. No. 21;
RESULT 1327
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brsa-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match 5.5%; Score 90.5; DB 8; Length 505;

Best Local Similarity 27.0%; Pred. No. 24;
RESULT 1328
ID ABB60186 standard; protein; 1714 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 90.5; DB 4; Length 1714;
Best Local Similarity 26.7%; Pred. No. 1.3e+02;
RESULT 1329
ID ABB69419 standard; protein; 1976 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 90.5; DB 4; Length 1976;
Best Local Similarity 38.5%; Pred. No. 1.5e+02;
RESULT 1330
ID ABP70443 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 6.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 90; DB 6; Length 364;
Best Local Similarity 21.6%; Pred. No. 17;
RESULT 1331
ID ADY98081 standard; protein; 364 AA.
DE Human TIM-1 allele 5-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.4%; Score 90; DB 9; Length 364;
Best Local Similarity 21.6%; Pred. No. 17;
RESULT 1332
ID ABB59507 standard; protein; 629 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 90; DB 4; Length 629;
Best Local Similarity 20.7%; Pred. No. 36;
RESULT 1333
ID ADD47260 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12954.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 63;
RESULT 1334
ID ADE58049 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3917.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 63;
RESULT 1335
ID ADD47264 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12958.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 63;
RESULT 1336
ID ADE58045 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3913.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 63;
RESULT 1337
ID ADQ29696 standard; protein; 1217 AA.
DE Human colorectal cancer-associated protein #51.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 5.4%; Score 90; DB 8; Length 1217;
Best Local Similarity 18.3%; Pred. No. 88;
RESULT 1338
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 96;
RESULT 1339
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 96;
RESULT 1340
ID ABP70432 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1341
ID ABP70433 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1342
ID ADY98061 standard; protein; 305 AA.
DE Mouse TIM-2 variant.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.4%; Score 89.5; DB 9; Length 305;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1343
ID ADY98059 standard; protein; 305 AA.
DE Mouse TIM-2.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.4%; Score 89.5; DB 9; Length 305;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1344
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89.5; DB 2; Length 410;
Best Local Similarity 21.0%; Pred. No. 22;

RESULT 1345
ID AAR85213 standard; protein; 480 AA.
DE Blowfly larvae PM95 antigen.
PN AU9517609-A.
PD 02-NOV-1995.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.4%; Score 89.5; DB 2; Length 480;
Best Local Similarity 22.1%; Pred. No. 27;
RESULT 1346
ID ABO84994 standard; protein; 917 AA.
DE Murine cancer-associated protein (CAP) MP07-101.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.4%; Score 89.5; DB 8; Length 917;
Best Local Similarity 21.4%; Pred. No. 67;
RESULT 1347
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 17;
RESULT 1348
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 89; DB 5; Length 343;
Best Local Similarity 27.7%; Pred. No. 19;
RESULT 1349
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1350
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.
PD 18-NOV-1999.
PA (EPIM-) EPIMMUNE INC.
Query Match 5.4%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1351
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.4%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1352
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1353
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;

RESULT 1354
ID ADP23231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1355
ID ADU60107 standard; protein; 416 AA.
DE Housekeeping gene protein, SEQ ID 68.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1356
ID ADW85920 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein-1.
PN WO2005012912-A2.
PD 10-FEB-2005.
PA (CHIR) CHIRON CORP.
Query Match 5.4%; Score 89; DB 9; Length 416;
Best Local Similarity 23.6%; Pred. No. 25;
RESULT 1357
ID ADR86408 standard; protein; 832 AA.
DE Aspergillus fumigatus essential gene protein #458.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.4%; Score 89; DB 8; Length 832;
Best Local Similarity 19.8%; Pred. No. 65;
RESULT 1358
ID ABB70039 standard; protein; 846 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36909.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 846;
Best Local Similarity 22.5%; Pred. No. 66;
RESULT 1359
ID ABB67102 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28098.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 882;
Best Local Similarity 22.5%; Pred. No. 70;
RESULT 1360
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.4%; Score 89; DB 8; Length 951;
Best Local Similarity 22.1%; Pred. No. 78;
RESULT 1361
ID ADM19804 standard; protein; 1076 AA.
DE Protein encoded by novel human channel/transporter gene #122.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 89; DB 4; Length 1076;
Best Local Similarity 21.1%; Pred. No. 92;
RESULT 1362
ID ADX97567 standard; protein; 2624 AA.
DE Pancreatic cancer associated human protein, SEQ ID 115.
PN EP1471075-A2.
PD 27-OCT-2004.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.

PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
Query Match 5.4%; Score 89; DB 8; Length 2624;
Best Local Similarity 27.7%; Pred. No. 3.1e+02;
RESULT 1363
ID AAG39194 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 193;
Best Local Similarity 21.4%; Pred. No. 9.7;
RESULT 1364
ID AAG39193 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 199;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 1365
ID ABG15314 standard; protein; 358 AA.
DE Novel human diagnostic protein #15305.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88.5; DB 4; Length 358;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1366
ID AAR11605 standard; protein; 392 AA.
DE Human 75kD TNF-binding protein.
PN EP417563-A.
PD 20-MAR-1991.
PA (HOFF) HOFFMANN-LA ROCHE AG.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 26;
RESULT 1367
ID AAY30935 standard; protein; 392 AA.
DE Human tumour necrosis factor binding protein fragment.
PN EP939121-A2.
PD 01-SEP-1999.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 26;
RESULT 1368
ID AAB86818 standard; protein; 392 AA.
DE Human TNFBP-associated protein #2.
PN EP1132471-A2.
PD 12-SEP-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 4; Length 392;
Best Local Similarity 21.8%; Pred. No. 26;
RESULT 1369
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.3%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 31;
RESULT 1370
ID ABB63417 standard; protein; 481 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17043.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 88.5; DB 4; Length 481;
Best Local Similarity 21.2%; Pred. No. 34;
RESULT 1371
ID AAG64210 standard; protein; 596 AA.
DE Murine HSP47 interacting protein, M4.
PN JP2001145493-A.
PD 29-MAY-2001.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.3%; Score 88.5; DB 4; Length 596;
Best Local Similarity 21.3%; Pred. No. 46;
RESULT 1372
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.3%; Score 88.5; DB 2; Length 708;
Best Local Similarity 23.6%; Pred. No. 58;
RESULT 1373
ID AAR63068 standard; protein; 905 AA.
DE Human EAA3b excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 88; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 91;
RESULT 1374
ID ADE86597 standard; protein; 995 AA.
DE Frog tail resorption protein.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 5.3%; Score 88; DB 8; Length 995;
Best Local Similarity 19.9%; Pred. No. 1e+02;
RESULT 1375
ID ADN23131 standard; protein; 3507 AA.
DE Bacterial polypeptide #5784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 88; DB 8; Length 3507;
Best Local Similarity 20.1%; Pred. No. 5.8e+02;
RESULT 1376
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88; DB 5; Length 4315;
Best Local Similarity 23.8%; Pred. No. 7.7e+02;
RESULT 1377
ID ADL23265 standard; protein; 5703 AA.
DE Human MUC5B.
PN WO2004019041-A1.
PD 04-MAR-2004.
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
PA (PACK/) PACKER N H.
PA (KARL/) KARLSSON N.
PA (SCHU/) SCHULZ B L.
Query Match 5.3%; Score 88; DB 8; Length 5703;
Best Local Similarity 23.8%; Pred. No. 1.1e+03;
RESULT 1378
ID AEB56507 standard; protein; 5858 AA.
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.
PN WO2005073411-A1.
PD 11-AUG-2005.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.3%; Score 88; DB 9; Length 5858;
Best Local Similarity 23.8%; Pred. No. 1.2e+03;
RESULT 1379

ID AAG13468 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 87.5; DB 3; Length 310;
Best Local Similarity 23.2%; Pred. No. 23;
RESULT 1380
ID AAG13467 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 87.5; DB 3; Length 331;
Best Local Similarity 23.2%; Pred. No. 25;
RESULT 1381
ID AAY52525 standard; protein; 536 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87.5; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 49;
RESULT 1382
ID AAU96329 standard; protein; 536 AA.
DE Der HMW-map polypeptide #16.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87.5; DB 5; Length 536;
Best Local Similarity 23.9%; Pred. No. 49;
RESULT 1383
ID AAY52523 standard; protein; 555 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87.5; DB 3; Length 555;
Best Local Similarity 23.9%; Pred. No. 52;
RESULT 1384
ID AAU96327 standard; protein; 555 AA.
DE Der HMW-map polypeptide #14.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 52;
RESULT 1385
ID AAU96328 standard; protein; 555 AA.
DE Der HMW-map polypeptide #15.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 52;
RESULT 1386
ID ADB64946 standard; protein; 717 AA.
DE Human protein encoded by clone PROST20036350.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.3%; Score 87.5; DB 7; Length 717;
Best Local Similarity 17.8%; Pred. No. 73;
RESULT 1387
ID ADH71768 standard; protein; 904 AA.
DE Human protein of the invention NOV28n SEQ ID NO:664.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.3%; Score 87.5; DB 8; Length 904;
Best Local Similarity 23.8%; Pred. No. 1e+02;
RESULT 1388
ID AAW16313 standard; protein; 906 AA.
DE Yeast alpha factor-G-alpha protein fusion.
PN WO9711159-A1.
PD 27-MAR-1997.
PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.
Query Match 5.3%; Score 87.5; DB 2; Length 906;
Best Local Similarity 19.7%; Pred. No. 1e+02;
RESULT 1389
ID ADZ03664 standard; protein; 981 AA.
DE PRG4-Lub:1 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.3%; Score 87.5; DB 9; Length 981;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1390
ID ADZ03672 standard; protein; 1038 AA.
DE PRG4-Lub:3 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.3%; Score 87.5; DB 9; Length 1038;
Best Local Similarity 22.3%; Pred. No. 1.2e+02;
RESULT 1391
ID ADZ03676 standard; protein; 1069 AA.
DE PRG4-Lub:4 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.3%; Score 87.5; DB 9; Length 1069;
Best Local Similarity 22.3%; Pred. No. 1.3e+02;
RESULT 1392
ID AAW54844 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.3%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1393
ID AAY41778 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.3%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1394
ID AAW89563 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor BoPCaR 1.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.3%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1395
ID AAY51825 standard; protein; 1085 AA.
DE Bovine calcium receptor BoPCaR1 protein.
PN US6031003-A.
PD 29-FEB-2000.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.3%; Score 87.5; DB 3; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1396
ID AAB47820 standard; protein; 1085 AA.
DE BoPCaR1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSP-) NPS PHARM INC.
Query Match 5.3%; Score 87.5; DB 5; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;

RESULT 1397
ID ADJ93194 standard; protein; 1085 AA.
DE Bovine extracellular Ca-sensing receptor.
PN WO200296946-A1.
PD 05-DEC-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.3%; Score 87.5; DB 7; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1398
ID ADI40961 standard; protein; 1085 AA.
DE Bovine GPCR CASR.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.3%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1399
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.3%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.3e+02;
RESULT 1400
ID ADZ03680 standard; protein; 1100 AA.
DE PRG4-Lub:5 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.3%; Score 87.5; DB 9; Length 1100;
Best Local Similarity 22.3%; Pred. No. 1.3e+02;
RESULT 1401
ID ADS24007 standard; protein; 1322 AA.
DE Bacterial polypeptide #13040.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87.5; DB 8; Length 1322;
Best Local Similarity 22.9%; Pred. No. 1.7e+02;
RESULT 1402
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.3%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 18;
RESULT 1403
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1404
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1405
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1406
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1407
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1408
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 23;
RESULT 1409
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.3%; Score 87; DB 8; Length 363;
Best Local Similarity 25.3%; Pred. No. 32;
RESULT 1410
ID ADY37611 standard; protein; 363 AA.
DE Lung cancer related protein, SEQ ID 87.
PN US2005048589-A1.
PD 03-MAR-2005.
PA (JEND/) JENDOUBI M.
Query Match 5.3%; Score 87; DB 9; Length 363;
Best Local Similarity 25.3%; Pred. No. 32;
RESULT 1411
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 5.3%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 39;
RESULT 1412
ID ADX91714 standard; protein; 611 AA.
DE Plant full length insert polypeptide seqid 54378.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.3%; Score 87; DB 8; Length 611;
Best Local Similarity 21.8%; Pred. No. 66;
RESULT 1413
ID AAG83274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PN WO200140474-A2.

PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 631;
Best Local Similarity 28.1%; Pred. No. 69;
RESULT 1414
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 5; Length 631;
Best Local Similarity 28.1%; Pred. No. 69;
RESULT 1415
ID ADD42755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 664;
Best Local Similarity 28.1%; Pred. No. 74;
RESULT 1416
ID AAR63070 standard; protein; 849 AA.
DE Human EAA3d excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 87; DB 2; Length 849;
Best Local Similarity 22.4%; Pred. No. 1e+02;
RESULT 1417
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kB agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 862;
Best Local Similarity 19.1%; Pred. No. 1.1e+02;
RESULT 1418
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 1.1e+02;
RESULT 1419
ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 1.1e+02;
RESULT 1420
ID AAR60112 standard; protein; 905 AA.
DE Human EAA3a excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
RESULT 1421
ID AAR75883 standard; protein; 905 AA.
DE Human EAA3 receptor (Q-591).
PN WO9517508-A2.
PD 29-JUN-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
RESULT 1422
ID AAB19496 standard; protein; 905 AA.
DE The Q591 form of the human EAA3 receptor.
PN US6136544-A.
PD 24-OCT-2000.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 4; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
RESULT 1423
ID ADX26248 standard; protein; 905 AA.
DE Novel cell pain response detection method-related human protein SeqID594.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 5.3%; Score 87; DB 9; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
RESULT 1424
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PN WO200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1425
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PN WO200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 5.3%; Score 87; DB 5; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1426
ID ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1427
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 95.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1428
ID ADW29028 standard; protein; 1016 AA.
DE C_trachomatis polymorphic membrane protein (PmpH) Seq 22.
PN WO2005002619-A2.
PD 13-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 5.3%; Score 87; DB 9; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1429
ID AEA19092 standard; protein; 1016 AA.
DE Chlamydia trachomatis protein - SEQ ID 95.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match 5.3%; Score 87; DB 9; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.3e+02;
RESULT 1430
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.3e+02;
RESULT 1431

ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.3e+02;
RESULT 1432
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.3e+02;
RESULT 1433
ID ABB67362 standard; protein; 1575 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28878.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 87; DB 4; Length 1575;
Best Local Similarity 20.5%; Pred. No. 2.4e+02;
RESULT 1434
ID AAU39177 standard; protein; 238 AA.
DE Propionibacterium acnes immunogenic protein #73.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 4; Length 238;
Best Local Similarity 22.7%; Pred. No. 20;
RESULT 1435
ID ABM35696 standard; protein; 238 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #372.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 6; Length 238;
Best Local Similarity 22.7%; Pred. No. 20;
RESULT 1436
ID AAP91941 standard; peptide; 400 AA.
DE Sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.2%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 41;
RESULT 1437
ID ADN19290 standard; protein; 503 AA.
DE Bacterial polypeptide #1943.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.2%; Score 86.5; DB 8; Length 503;
Best Local Similarity 22.1%; Pred. No. 56;
RESULT 1438
ID ABU25742 standard; protein; 687 AA.
DE Protein encoded by Prokaryotic essential gene #11269.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 86.5; DB 6; Length 687;
Best Local Similarity 23.2%; Pred. No. 86;
RESULT 1439
ID ABG15647 standard; protein; 714 AA.
DE Novel human diagnostic protein #15638.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 91;
RESULT 1440
ID ABG15147 standard; protein; 714 AA.
DE Novel human diagnostic protein #15138.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 91;
RESULT 1441
ID AAY54466 standard; protein; 788 AA.
DE Amino acid sequence of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.2%; Score 86.5; DB 3; Length 788;
Best Local Similarity 27.2%; Pred. No. 1e+02;
RESULT 1442
ID AAY54467 standard; protein; 807 AA.
DE Amini acid sequence of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.2%; Score 86.5; DB 3; Length 807;
Best Local Similarity 27.2%; Pred. No. 1.1e+02;
RESULT 1443
ID ADA14416 standard; protein; 1579 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.
PN WO2003068969-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.2%; Score 86.5; DB 6; Length 1579;
Best Local Similarity 21.1%; Pred. No. 2.7e+02;
RESULT 1444
ID ADT07505 standard; protein; 2109 AA.
DE Human colon-specific polypeptide (CSP) #22.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2109;
Best Local Similarity 26.1%; Pred. No. 4e+02;
RESULT 1445
ID ADT07506 standard; protein; 2254 AA.
DE Human colon-specific polypeptide (CSP) #23.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2254;
Best Local Similarity 26.1%; Pred. No. 4.4e+02;
RESULT 1446
ID ADT07507 standard; protein; 2401 AA.
DE Human colon-specific polypeptide (CSP) #24.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2401;
Best Local Similarity 26.1%; Pred. No. 4.8e+02;
RESULT 1447
ID AAY57453 standard; protein; 2781 AA.
DE Human transcriptional regulatory factor SEQ ID NO:10.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.2%; Score 86.5; DB 3; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.9e+02;
RESULT 1448
ID ADF42724 standard; protein; 2781 AA.
DE Human BPTF amino acid sequence SEQ ID NO:30.

PN WO2003102163-A2.
PD 11-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.9e+02;
RESULT 1449
ID ADO00984 standard; protein; 2781 AA.
DE Human homologue of Fruit fly AD-related protein CG17135.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.9e+02;
RESULT 1450
ID ADQ18653 standard; protein; 2781 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.2%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.9e+02;
RESULT 1451
ID AAY57452 standard; protein; 2907 AA.
DE Human transcriptional regulatory factor SEQ ID NO:1.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.2%; Score 86.5; DB 3; Length 2907;
Best Local Similarity 20.8%; Pred. No. 6.2e+02;
RESULT 1452
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.2%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 58;
RESULT 1453
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.2%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 58;
RESULT 1454
ID AAB98978 standard; protein; 551 AA.
DE Rabbit PCLP1.
PN WO200134797-A1.
PD 17-MAY-2001.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.2%; Score 86; DB 4; Length 551;
Best Local Similarity 26.4%; Pred. No. 71;
RESULT 1455
ID ADD18594 standard; protein; 601 AA.
DE Human disease related protein SeqID25.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.2%; Score 86; DB 7; Length 601;
Best Local Similarity 22.0%; Pred. No. 80;
RESULT 1456
ID AAY05477 standard; protein; 750 AA.
DE C. albicans Rbt1 protein sequence.
PN WO9918115-A1.
PD 15-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.2%; Score 86; DB 2; Length 750;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1457
ID ADX76173 standard; protein; 857 AA.
DE Plant full length insert polypeptide seqid 45539.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.2%; Score 86; DB 8; Length 857;
Best Local Similarity 22.1%; Pred. No. 1.3e+02;
RESULT 1458
ID AAB19499 standard; protein; 905 AA.
DE Amino acid sequence of the R591 form of the human EAA3 receptor.
PN US6136544-A.
PD 24-OCT-2000.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.2%; Score 86; DB 4; Length 905;
Best Local Similarity 22.4%; Pred. No. 1.4e+02;
RESULT 1459
ID ADB79822 standard; protein; 1080 AA.
DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 5.2%; Score 86; DB 7; Length 1080;
Best Local Similarity 20.2%; Pred. No. 1.8e+02;
RESULT 1460
ID ABG28388 standard; protein; 1086 AA.
DE Novel human diagnostic protein #28379.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86; DB 4; Length 1086;
Best Local Similarity 19.8%; Pred. No. 1.8e+02;
RESULT 1461
ID ABG05675 standard; protein; 1190 AA.
DE Novel human diagnostic protein #5666.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 86; DB 4; Length 1190;
Best Local Similarity 19.8%; Pred. No. 2e+02;
RESULT 1462
ID AAG23116 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 193;
Best Local Similarity 20.9%; Pred. No. 19;
RESULT 1463
ID AAG23115 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 199;
Best Local Similarity 20.9%; Pred. No. 20;
RESULT 1464
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 3; Length 346;
Best Local Similarity 22.4%; Pred. No. 42;
RESULT 1465
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 42;
RESULT 1466
ID ABB08065 standard; protein; 346 AA.

DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 42;
RESULT 1467
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 6; Length 346;
Best Local Similarity 22.4%; Pred. No. 42;
RESULT 1468
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 43;
RESULT 1469
ID ABB93134 standard; protein; 649 AA.
DE Herbicidally active polypeptide SEQ ID NO 2345.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 5; Length 649;
Best Local Similarity 23.4%; Pred. No. 99;
RESULT 1470
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 99;
RESULT 1471
ID ABU15839 standard; protein; 686 AA.
DE Protein encoded by Prokaryotic essential gene #1366.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 85.5; DB 6; Length 686;
Best Local Similarity 24.2%; Pred. No. 1.1e+02;
RESULT 1472
ID ADN47243 standard; protein; 695 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.2%; Score 85.5; DB 8; Length 695;
Best Local Similarity 20.6%; Pred. No. 1.1e+02;
RESULT 1473
ID ADD47689 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13385.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.3e+02;
RESULT 1474
ID ADD47692 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13388.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.3e+02;
RESULT 1475
ID AAB07743 standard; protein; 781 AA.
DE A snake venom protease (SVPH-4) polypeptide varaint SVPH-4b.
PN WO200043525-A2.
PD 27-JUL-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 5.2%; Score 85.5; DB 3; Length 781;
Best Local Similarity 17.9%; Pred. No. 1.3e+02;
RESULT 1476
ID ADE71292 standard; protein; 781 AA.
DE Novel human protein #46.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 5.2%; Score 85.5; DB 7; Length 781;
Best Local Similarity 23.2%; Pred. No. 1.3e+02;
RESULT 1477
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 1.4e+02;
RESULT 1478
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 85.5; DB 4; Length 843;
Best Local Similarity 22.5%; Pred. No. 1.4e+02;
RESULT 1479
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 1.7e+02;
RESULT 1480
ID ABU54710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 4e+02;
RESULT 1481
ID ABU54858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 4e+02;
RESULT 1482
ID ABU54707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 4.1e+02;
RESULT 1483
ID ADE40509 standard; protein; 2055 AA.
DE Human nuclear receptor coactivator ARAP3.
PN DE10135787-A1.
PD 13-FEB-2003.
PA (JENP) JENAPHARM GMBH & CO KG.
Query Match 5.2%; Score 85.5; DB 8; Length 2055;
Best Local Similarity 20.5%; Pred. No. 4.8e+02;
RESULT 1484
ID ABG95034 standard; protein; 2311 AA.

DE Human translocation (4; 11)(q21; q23) protein #1.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 2311;
Best Local Similarity 24.3%; Pred. No. 5.7e+02;
RESULT 1485
ID AEB29721 standard; protein; 2448 AA.
DE Human Mucin 5 (subtypes A and C).
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.2%; Score 85.5; DB 9; Length 2448;
Best Local Similarity 24.8%; Pred. No. 6.1e+02;
RESULT 1486
ID ABG31317 standard; protein; 2586 AA.
DE Human 5+3 corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1487
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1488
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1489
ID ADL02234 standard; protein; 2586 AA.
DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1490
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1491
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1492
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2587;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1493
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 5; Length 2589;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1494
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2589;
Best Local Similarity 25.8%; Pred. No. 6.6e+02;
RESULT 1495
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.2%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 2e+03;
RESULT 1496
ID ABU54721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 5.2e+03;
RESULT 1497
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 1.3e+04;
RESULT 1498
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 85; DB 3; Length 280;
Best Local Similarity 23.2%; Pred. No. 35;
RESULT 1499
ID ABM91067 standard; protein; 318 AA.
DE M. xanthus protein sequence, seq id 10266.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 5.1%; Score 85; DB 9; Length 318;
Best Local Similarity 23.7%; Pred. No. 41;
RESULT 1500
ID ABB71546 standard; protein; 326 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 326;
Best Local Similarity 22.8%; Pred. No. 43;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:48 ; Search time 69.4882 Seconds
(without alignments)
3269.333 Million cell updates/sec

Title: US-10-063-510-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLLTSIWTTRLL.....NPEESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1657	100.0	322	2	Q9UNF4_HUMAN	Q9unf4 homo sapien
2	1643	99.2	322	2	Q8TC18_HUMAN	Q8tc18 homo sapien
3	1638	98.9	322	2	Q9Y5Y7_HUMAN	Q9y5y7 homo sapien
4	1174	70.9	322	2	Q6UC88_BOVIN	Q6uc88 bos taurus
5	1103	66.6	318	2	Q8BHC0_MOUSE	Q8bhc0 mus musculu
6	1095	66.1	318	2	Q99NE4_MOUSE	Q99ne4 mus musculu
7	726.5	43.8	201	2	Q7YS22_PIG	Q7ys22 sus scrofa
8	245	14.8	392	2	Q58E15_XENLA	Q58e15 xenopus lae
9	241	14.5	441	2	Q6GM56_XENLA	Q6gm56 xenopus lae
10	233.5	14.1	362	1	CD44_CRIGR	P20944 cricetulus
11	229.5	13.9	437	2	Q6P8A2_XENTR	Q6p8a2 xenopus tro
12	227	13.7	364	2	O70509_RAT	O70509 rattus norv
13	222.5	13.4	362	1	CD44_PAPHA	P14745 papio hamad
14	222	13.4	503	1	CD44_RAT	P26051 rattus norv
15	219.5	13.2	780	2	O08779_RAT	O08779 rattus norv
16	219	13.2	265	2	Q98SR5_ANAPL	Q98sr5 anas platyr
17	217.5	13.1	398	2	Q90ZL8_ANAPL	Q90zl8 anas platyr
18	212.5	12.8	431	1	CD44_MESAU	Q60522 m cd44 anti
19	210	12.7	778	1	CD44_MOUSE	P15379 mus musculu
20	208.5	12.6	366	1	CD44_BOVIN	Q29423 bos taurus
21	206.5	12.5	168	2	Q90ZL6_ANAPL	Q90zl6 anas platyr
22	204	12.3	361	2	Q86T72_HUMAN	Q86t72 homo sapien
23	203.5	12.3	364	2	O97569_CERSI	O97569 ceratotheri
24	203.5	12.3	396	2	Q9W6S4_CHICK	Q9w6s4 gallus gall
25	203	12.3	742	2	Q9UJ36_HUMAN	Q9uj36 homo sapien
26	202.5	12.2	351	1	CD44_CANFA	Q28284 canis famil
27	202	12.2	361	2	Q8N694_HUMAN	Q8n694 homo sapien
28	202	12.2	742	1	CD44_HUMAN	P16070 h cd44 anti
29	201	12.1	580	2	Q80X37_MOUSE	Q80x37 mus musculu
30	199.5	12.0	493	2	Q86Z27_HUMAN	Q86z27 homo sapien
31	199.5	12.0	493	2	Q5R9V4_PONPY	Q5r9v4 pongo pygma
32	199	12.0	338	2	Q9H5A4_HUMAN	Q9h5a4 homo sapien
33	197	11.9	719	2	Q9H5A5_HUMAN	Q9h5a5 homo sapien
34	196	11.8	294	2	Q92493_HUMAN	Q92493 homo sapien
35	191.5	11.6	676	2	Q9H5A7_HUMAN	Q9h5a7 homo sapien
36	191	11.5	271	2	Q9H5A3_HUMAN	Q9h5a3 homo sapien
37	191	11.5	470	2	Q9H5A6_HUMAN	Q9h5a6 homo sapien
38	186	11.2	359	1	CD44_HORSE	Q05078 equus cabal
39	173.5	10.5	153	2	Q4SI95_TETNG	Q4si95 tetraodon n
40	150	9.1	537	1	PGCA_PIG	Q29011 sus scrofa
41	149.5	9.0	2109	2	P79787_CHICK	P79787 gallus gall
42	148.5	9.0	2109	1	PGCA_CHICK	P07898 gallus gall
43	147.5	8.9	243	2	Q4S9S8_TETNG	Q4s9s8 tetraodon n
44	145.5	8.8	494	2	Q9BGH3_PIG	Q9bgh3 sus scrofa
45	145.5	8.8	3562	1	CSPG2_CHICK	Q90953 gallus gall
46	145	8.8	277	1	TSG6_HUMAN	P98066 homo sapien
47	145	8.8	277	2	Q53TI7_HUMAN	Q53ti7 homo sapien
48	144	8.7	275	1	TSG6_MOUSE	O08859 mus musculu
49	144	8.7	280	2	Q5W1C4_BOVIN	Q5w1c4 bos taurus
50	143	8.6	2149	2	Q6XL68_BOVIN	Q6xl68 bos taurus
51	143	8.6	2327	2	Q6XL66_BOVIN	Q6xl66 bos taurus
52	143	8.6	2364	1	PGCA_BOVIN	P13608 bos taurus
53	143	8.6	2365	2	Q6XL67_BOVIN	Q6xl67 bos taurus
54	140.5	8.5	2571	1	STAB1_MOUSE	Q8r4y4 mus musculu
55	139.5	8.4	2333	1	PGCA_CANFA	Q28343 canis famil
56	137	8.3	276	1	TSG6_RABIT	P98065 oryctolagus
57	136	8.2	2559	1	STAB2_MOUSE	Q8r4u0 mus musculu
58	133	8.0	514	2	Q62913_RAT	Q62913 rattus norv
59	133	8.0	1431	1	STAB2_RAT	Q8cfm6 rattus norv
60	133	8.0	2551	1	STAB2_HUMAN	Q8wwq8 h stabilin-
61	132.5	8.0	721	2	Q6PID9_HUMAN	Q6pid9 homo sapien
62	132	8.0	1046	2	Q4S1V9_TETNG	Q4s1v9 tetraodon n
63	131.5	7.9	2124	1	PGCA_RAT	P07897 rattus norv
64	131	7.9	314	2	Q4SE78_TETNG	Q4se78 tetraodon n
65	131	7.9	2132	1	PGCA_MOUSE	Q61282 mus musculu
66	130.5	7.9	883	1	PGCB_MOUSE	Q61361 mus musculu
67	130.5	7.9	883	1	PGCB_RAT	P55068 rattus norv
68	130.5	7.9	883	2	Q80WT7_MOUSE	Q80wt7 mus musculu
69	130.5	7.9	1152	2	Q90WM2_XENLA	Q90wm2 xenopus lae
70	130.5	7.9	2415	1	PGCA_HUMAN	P16112 homo sapien
71	130.5	7.9	2570	1	STAB1_HUMAN	Q9ny15 homo sapien
72	128.5	7.8	912	1	PGCB_BOVIN	Q28062 bos taurus
73	128	7.7	845	2	Q4RV64_TETNG	Q4rv64 tetraodon n
74	127.5	7.7	671	2	Q5T3I5_HUMAN	Q5t3i5 homo sapien
75	127.5	7.7	850	2	Q59F90_HUMAN	Q59f90 homo sapien
76	127.5	7.7	911	1	PGCB_HUMAN	Q96gw7 homo sapien
77	127.5	7.7	911	2	Q5SZ10_HUMAN	Q5sz10 homo sapien
78	127	7.7	266	2	Q5I051_XENLA	Q5i051 xenopus lae
79	126	7.6	3358	1	CSPG2_MOUSE	Q62059 mus musculu
80	125.5	7.6	536	2	Q5RG03_BRARE	Q5rg03 brachydanio
81	124.5	7.5	1515	2	Q4T6A4_TETNG	Q4t6a4 tetraodon n
82	124	7.5	2586	2	Q4RUP1_TETNG	Q4rup1 tetraodon n
83	123.5	7.5	386	2	Q4S472_TETNG	Q4s472 tetraodon n
84	123.5	7.5	2760	2	Q4T8G9_TETNG	Q4t8g9 tetraodon n
85	122	7.4	383	2	Q5BJ60_XENTR	Q5bj60 xenopus tro
86	122	7.4	394	1	PGCA_RABIT	Q28670 oryctolagus
87	121.5	7.3	360	1	HPLN3_HUMAN	Q96s86 homo sapien
88	121.5	7.3	1091	2	Q4SE77_TETNG	Q4se77 tetraodon n
89	121	7.3	516	2	Q8IWX2_HUMAN	Q8iwx2 homo sapien
90	120.5	7.3	1570	2	Q75ZI3_BRARE	Q75zi3 brachydanio
91	120	7.2	313	2	Q4SHL9_TETNG	Q4shl9 tetraodon n
92	119.5	7.2	411	2	Q702X4_HHV1	Q702x4 human herpe
93	119	7.2	359	2	Q7ZX17_XENLA	Q7zx17 xenopus lae
94	119	7.2	1452	2	Q55DV2_DICDI	Q55dv2 dictyosteli
95	118.5	7.2	3396	1	CSPG2_HUMAN	P13611 homo sapien
96	118.5	7.2	3410	2	Q59FG9_HUMAN	Q59fg9 homo sapien
97	118	7.1	341	1	HPLN2_MOUSE	Q9esm3 mus musculu
98	117.5	7.1	397	2	Q702X3_HHV1	Q702x3 human herpe
99	117	7.1	340	1	HPLN2_HUMAN	Q9gzv7 homo sapien
100	117	7.1	340	2	Q5T3J0_HUMAN	Q5t3j0 homo sapien
101	117	7.1	537	2	Q4IQU7_GIBZE	Q4iqu7 gibberella
102	116	7.0	368	2	Q8BS97_MOUSE	Q8bs97 mus musculu
103	116	7.0	368	2	Q4VA91_MOUSE	Q4va91 mus musculu
104	116	7.0	2738	1	CSPG2_RAT	Q9erb4 rattus norv

105	115.5	7.0	744	2	Q4RLD6_TETNG	Q4rld6	tetraodon n
106	115	6.9	370	2	Q7M2W7_PIG	Q7m2w7	sus scrofa
107	115	6.9	394	2	Q6DCI6_XENLA	Q6dci6	xenopus lae
108	115	6.9	3381	1	CSPG2_BOVIN	P81282	bos taurus
109	114.5	6.9	1039	2	Q4S473_TETNG	Q4s473	tetraodon n
110	114.5	6.9	1257	1	CSPG3_RAT	P55067	rattus norv
111	114	6.9	610	2	Q9N3C0_CAEEL	Q9n3c0	caenorhabdi
112	113.5	6.8	289	2	Q60TZ2_CAEBR	Q60tz2	caenorhabdi
113	113.5	6.8	1290	2	Q9W6E1_CHICK	Q9w6e1	gallus gall
114	113	6.8	341	1	HPLN2_RAT	Q9esm2	rattus norv
115	113	6.8	459	2	Q54G90_DICDI	Q54g90	dictyosteli
116	113	6.8	892	1	LDLR2_XENLA	Q99088	xenopus lae
117	112.5	6.8	417	1	PGCB_FELCA	P41725	felis silve
118	112	6.8	210	2	Q8C9U7_MOUSE	Q8c9u7	mus musculu
119	112	6.8	390	1	VGLI_HHV11	P06487	human herpe
120	112	6.8	390	2	Q702X7_HHV1	Q702x7	human herpe
121	111.5	6.7	402	1	ODP2_MYCPN	P75392	mycoplasma
122	111	6.7	354	2	Q86W61_HUMAN	Q86w61	homo sapien
123	111	6.7	359	2	Q5R1X6_RAT	Q5r1x6	rattus norv
124	110	6.6	363	2	Q6NV41_BRARE	Q6nv41	brachydanio
125	109	6.6	816	2	O70474_RAT	O70474	rattus norv
126	109	6.6	1321	1	CSPG3_HUMAN	O14594	homo sapien
127	109	6.6	1335	2	Q4LE67_HUMAN	Q4le67	homo sapien
128	108.5	6.5	397	2	Q702X6_HHV1	Q702x6	human herpe
129	108.5	6.5	1441	2	Q4S3C4_TETNG	Q4s3c4	tetraodon n
130	108	6.5	354	1	HPLN1_HUMAN	P10915	homo sapien
131	108	6.5	359	1	HPLN3_MOUSE	Q80wm5	mus musculu
132	108	6.5	624	2	Q19780_CAEEL	Q19780	caenorhabdi
133	107.5	6.5	739	2	O02360_CAEEL	O02360	caenorhabdi
134	107	6.5	354	1	HPLN1_RAT	P03994	rattus norv
135	107	6.5	355	1	HPLN1_CHICK	P07354	gallus gall
136	107	6.5	356	1	HPLN1_MOUSE	Q9qup5	mus musculu
137	107	6.5	527	2	Q54VQ0_DICDI	Q54vq0	dictyosteli
138	107	6.5	543	2	Q4YVC9_PLABE	Q4yvc9	plasmodium
139	107	6.5	862	2	Q9UF98_HUMAN	Q9uf98	homo sapien
140	107	6.5	956	2	Q60MG7_CAEBR	Q60mg7	caenorhabdi
141	107	6.5	1268	1	CSPG3_MOUSE	P55066	mus musculu
142	107	6.5	1321	1	CSPG3_PANTR	Q5is41	pan troglod
143	107	6.5	1795	2	O76894_DROME	O76894	drosophila
144	106.5	6.4	1390	2	Q54GX9_DICDI	Q54gx9	dictyosteli
145	106	6.4	1059	2	Q5ISN4_MACFA	Q5isn4	macaca fasc
146	106	6.4	1153	2	Q4IAN9_GIBZE	Q4ian9	gibberella
147	105.5	6.4	374	2	Q9Z209_CRIGR	Q9z209	cricetulus
148	105.5	6.4	573	2	Q8CJD9_RAT	Q8cjd9	rattus norv
149	105.5	6.4	830	2	Q6CAY0_YARLI	Q6cay0	yarrowia li
150	105	6.3	354	1	HPLN1_BOVIN	P55252	bos taurus
151	105	6.3	438	2	Q4X548_PLACH	Q4x548	plasmodium
152	105	6.3	463	2	Q7RNE3_PLAYO	Q7rne3	plasmodium
153	105	6.3	480	2	Q5CGY9_CRYHO	Q5cgy9	cryptospori
154	105	6.3	612	2	Q6CD44_YARLI	Q6cd44	yarrowia li
155	104.5	6.3	862	1	CSPG2_MACNE	Q28858	macaca neme
156	104	6.3	139	2	O95370_HUMAN	O95370	homo sapien
157	104	6.3	354	1	HPLN1_HORSE	Q28381	equus cabal
158	104	6.3	354	1	HPLN1_PIG	P10859	sus scrofa
159	104	6.3	627	2	Q8MP19_DICDI	Q8mp19	dictyosteli
160	104	6.3	681	2	Q555L9_DICDI	Q555l9	dictyosteli
161	104	6.3	1716	2	Q9I7Q8_DROME	Q9i7q8	drosophila
162	104	6.3	1912	2	Q9VS99_DROME	Q9vs99	drosophila
163	103.5	6.2	288	2	Q6QPC9_9ADEN	Q6qpc9	simian aden
164	103.5	6.2	616	2	Q58EE4_BRARE	Q58ee4	brachydanio
165	103.5	6.2	952	2	Q86AH0_DICDI	Q86ah0	dictyosteli
166	103.5	6.2	1197	2	Q5IS86_9PRIM	Q5is86	saimiri bol
167	103.5	6.2	1254	2	Q94185_CAEEL	Q94185	caenorhabdi
168	103.5	6.2	1592	2	Q5AWR8_EMENI	Q5awr8	aspergillus
169	103	6.2	80	2	Q86UZ1_HUMAN	Q86uz1	homo sapien
170	103	6.2	231	2	Q5T3I6_HUMAN	Q5t3i6	homo sapien
171	103	6.2	232	2	Q5BDD1_EMENI	Q5bdd1	aspergillus
172	102.5	6.2	182	2	Q8I0D8_DROME	Q8i0d8	drosophila
173	102.5	6.2	183	2	Q9VT37_DROME	Q9vt37	drosophila
174	102.5	6.2	497	2	Q8QVC4_9REOV	Q8qvc4	eyach virus
175	102.5	6.2	553	2	Q8F932_LEPIN	Q8f932	leptospira
176	102.5	6.2	557	2	Q72VI3_LEPIC	Q72vi3	leptospira
177	102.5	6.2	590	2	Q5BG25_EMENI	Q5bg25	aspergillus
178	102.5	6.2	595	2	Q5UPW9_MIMIV	Q5upw9	mimivirus.
179	102.5	6.2	699	2	Q8QVE9_9REOV	Q8qve9	eyach virus
180	102	6.2	391	2	Q753G3_ASHGO	Q753g3	ashbya goss
181	102	6.2	404	2	Q702X0_HHV1	Q702x0	human herpe
182	102	6.2	404	2	Q702Y3_HHV1	Q702y3	human herpe
183	102	6.2	1879	2	Q4VZL0_CUCSA	Q4vzl0	cucumis sat
184	101.5	6.1	380	2	O02343_CAEEL	O02343	caenorhabdi
185	101.5	6.1	768	2	O60279_HUMAN	O60279	homo sapien
186	101.5	6.1	1853	2	Q7KT96_DROME	Q7kt96	drosophila
187	101.5	6.1	1893	2	Q9NKC9_DROME	Q9nkc9	drosophila
188	101.5	6.1	4370	2	Q4Q1Q2_LEIMA	Q4q1q2	leishmania
189	101	6.1	700	2	Q8TG00_ASPFU	Q8tg00	aspergillus
190	101	6.1	700	2	Q4WS89_ASPFU	Q4ws89	aspergillus
191	101	6.1	708	2	Q18175_CAEEL	Q18175	caenorhabdi
192	101	6.1	1777	2	Q54FB8_DICDI	Q54fb8	dictyosteli
193	101	6.1	2535	2	Q755B8_ASHGO	Q755b8	ashbya goss
194	100.5	6.1	353	2	Q4IH62_GIBZE	Q4ih62	gibberella
195	100.5	6.1	402	1	HPLN4_HUMAN	Q86uw8	homo sapien
196	100.5	6.1	411	2	Q702X9_HHV1	Q702x9	human herpe
197	100.5	6.1	841	2	Q4Q5Z4_LEIMA	Q4q5z4	leishmania
198	100.5	6.1	1121	2	Q59YM6_CANAL	Q59ym6	candida alb
199	100.5	6.1	1121	2	Q7Z884_CANAL	Q7z884	candida alb
200	100	6.0	319	2	Q4S1V7_TETNG	Q4s1v7	tetraodon n
201	100	6.0	403	2	Q702W8_HHV1	Q702w8	human herpe
202	100	6.0	404	2	Q702W6_HHV1	Q702w6	human herpe
203	100	6.0	404	2	Q702Y0_HHV1	Q702y0	human herpe
204	100	6.0	441	2	Q5BA48_EMENI	Q5ba48	aspergillus
205	100	6.0	486	2	Q8FRY2_COREF	Q8fry2	corynebacte
206	100	6.0	738	2	Q5WN81_CAEBR	Q5wn81	caenorhabdi
207	100	6.0	1317	1	YQU3_CAEEL	Q09550	caenorhabdi
208	99.5	6.0	335	2	Q60H44_BRARE	Q60h44	brachydanio
209	99.5	6.0	478	2	Q7YX15_CAEEL	Q7yx15	caenorhabdi
210	99.5	6.0	577	2	Q52GY0_CAEEL	Q52gy0	caenorhabdi
211	99.5	6.0	1092	1	NCA12_XENLA	P36335	xenopus lae
212	99.5	6.0	1117	2	Q54SZ6_DICDI	Q54sz6	dictyosteli
213	99.5	6.0	1165	2	Q60NC3_CAEBR	Q60nc3	caenorhabdi
214	99.5	6.0	2297	2	Q5PZ43_BRARE	Q5pz43	brachydanio
215	99	6.0	178	2	Q8FQU3_COREF	Q8fqu3	corynebacte
216	99	6.0	388	2	Q4H2F0_HPV27	Q4h2f0	human papil
217	99	6.0	410	1	GPC5B_MOUSE	Q923z0	mus musculu
218	99	6.0	545	2	Q5A7A3_CANAL	Q5a7a3	candida alb
219	99	6.0	604	2	Q6E9B8_LISMO	Q6e9b8	listeria mo
220	99	6.0	620	2	Q5A7H9_CANAL	Q5a7h9	candida alb
221	99	6.0	896	2	Q20253_CAEEL	Q20253	caenorhabdi
222	99	6.0	1100	2	Q8CCT8_MOUSE	Q8cct8	mus musculu
223	99	6.0	5376	1	ZAN_MOUSE	O88799	mus musculu
224	98.5	5.9	204	2	Q9N5Z8_CAEEL	Q9n5z8	caenorhabdi
225	98.5	5.9	346	2	Q7S973_NEUCR	Q7s973	neurospora
226	98.5	5.9	397	2	Q702W7_HHV1	Q702w7	human herpe
227	98.5	5.9	397	2	Q702X1_HHV1	Q702x1	human herpe
228	98.5	5.9	425	2	Q702W3_HHV1	Q702w3	human herpe
229	98.5	5.9	578	2	Q63ZX6_MOUSE	Q63zx6	mus musculu
230	98.5	5.9	889	2	Q4RUP0_TETNG	Q4rup0	tetraodon n
231	98.5	5.9	1126	2	Q9VGK5_DROME	Q9vgk5	drosophila
232	98.5	5.9	1203	2	Q6ZQ56_MOUSE	Q6zq56	mus musculu
233	98.5	5.9	3178	1	YS89_CAEEL	Q09624	caenorhabdi
234	98	5.9	384	2	Q9DW41_RCMVM	Q9dw41	rat cytomeg
235	98	5.9	390	2	Q702W4_HHV1	Q702w4	human herpe
236	98	5.9	505	2	Q4FYQ6_LEIMA	Q4fyq6	leishmania
237	98	5.9	604	2	Q8GNR7_LISMO	Q8gnr7	listeria mo
238	98	5.9	604	2	Q6E9T6_LISMO	Q6e9t6	listeria mo
239	98	5.9	604	2	Q8GNR1_LISMO	Q8gnr1	listeria mo
240	98	5.9	771	2	Q22783_CAEEL	Q22783	caenorhabdi
241	98	5.9	1015	2	Q54V57_DICDI	Q54v57	dictyosteli
242	98	5.9	2112	2	Q9VEL9_DROME	Q9vel9	drosophila
243	97.5	5.9	297	2	Q7PR65_ANOGA	Q7pr65	anopheles g
244	97.5	5.9	298	2	Q9Z0P0_RAT	Q9z0p0	rattus norv
245	97.5	5.9	318	2	Q86HN3_DICDI	Q86hn3	dictyosteli
246	97.5	5.9	385	2	Q9NHU9_DROMI	Q9nhu9	drosophila
247	97.5	5.9	836	2	Q55DF3_DICDI	Q55df3	dictyosteli
248	97.5	5.9	909	1	LDLR1_XENLA	Q99087	xenopus lae
249	97	5.9	294	2	Q54FY4_DICDI	Q54fy4	dictyosteli
250	97	5.9	316	2	Q9U9J0_TOXCA	Q9u9j0	toxocara ca

251	97	5.9	404	2	Q702Y6_HHV1	Q702y6	human herpe
252	97	5.9	604	2	Q6E9K8_LISMO	Q6e9k8	listeria mo
253	97	5.9	604	2	Q6E9X2_LISMO	Q6e9x2	listeria mo
254	97	5.9	604	2	Q6EAI6_LISMO	Q6eai6	listeria mo
255	97	5.9	648	2	Q4QGJ2_LEIMA	Q4qgj2	leishmania
256	97	5.9	1159	2	Q55GQ9_DICDI	Q55gq9	dictyosteli
257	97	5.9	1604	2	Q4SNA3_TETNG	Q4sna3	tetraodon n
258	96.5	5.8	268	2	Q5ATR9_EMENI	Q5atr9	aspergillus
259	96.5	5.8	276	2	Q54NG3_DICDI	Q54ng3	dictyosteli
260	96.5	5.8	385	2	Q9N666_DROMI	Q9n666	drosophila
261	96.5	5.8	385	2	Q9NHU6_DROMI	Q9nhu6	drosophila
262	96.5	5.8	397	2	Q702Y5_HHV1	Q702y5	human herpe
263	96.5	5.8	407	2	Q564S9_CAEEL	Q564s9	caenorhabdi
264	96.5	5.8	465	1	YHU6_YEAST	P38845	saccharomyc
265	96.5	5.8	604	2	Q8GNS1_LISMO	Q8gns1	listeria mo
266	96.5	5.8	731	1	NOG2_CRYGA	Q6tgj8	cryptococcu
267	96.5	5.8	961	2	Q5ATY9_EMENI	Q5aty9	aspergillus
268	96.5	5.8	961	2	Q92223_EMENI	Q92223	emericella
269	96.5	5.8	1031	2	Q925N8_MOUSE	Q925n8	mus musculu
270	96.5	5.8	1031	2	Q9D071_MOUSE	Q9d071	m mus muscu
271	96.5	5.8	1065	2	Q50ZF1_ENTHI	Q50zf1	entamoeba h
272	96.5	5.8	1403	1	LARP_DROME	Q9vaw5	drosophila
273	96	5.8	173	2	Q4KTX2_CEREL	Q4ktx2	cervus elap
274	96	5.8	232	2	Q4V3Z2_DROME	Q4v3z2	drosophila
275	96	5.8	236	2	Q4V400_DROME	Q4v400	drosophila
276	96	5.8	429	2	O76430_CAEEL	O76430	caenorhabdi
277	96	5.8	449	2	Q71UN8_CAEEL	Q71un8	caenorhabdi
278	96	5.8	481	2	Q9XUF4_CAEEL	Q9xuf4	caenorhabdi
279	96	5.8	549	2	Q54WC8_DICDI	Q54wc8	dictyosteli
280	96	5.8	555	2	Q95XI3_CAEEL	Q95xi3	caenorhabdi
281	96	5.8	556	2	Q6DEK7_BRARE	Q6dek7	brachydanio
282	96	5.8	604	2	Q6E9R2_LISMO	Q6e9r2	listeria mo
283	96	5.8	604	2	Q6E9R8_LISMO	Q6e9r8	listeria mo
284	96	5.8	604	2	Q6EAJ7_LISMO	Q6eaj7	listeria mo
285	96	5.8	604	2	Q724K9_LISMF	Q724k9	listeria mo
286	96	5.8	625	2	Q58SF3_DROSI	Q58sf3	drosophila
287	96	5.8	625	2	Q58SH8_DROSI	Q58sh8	drosophila
288	96	5.8	625	2	Q5ELN3_DROSI	Q5eln3	drosophila
289	96	5.8	625	2	Q6V6E1_DROSI	Q6v6e1	drosophila
290	96	5.8	732	2	Q54FU3_DICDI	Q54fu3	dictyosteli
291	96	5.8	804	2	Q54L26_DICDI	Q54l26	dictyosteli
292	96	5.8	1038	2	Q4T3K8_TETNG	Q4t3k8	tetraodon n
293	96	5.8	1088	1	NCA11_XENLA	P16170	xenopus lae
294	96	5.8	1155	2	Q4JA20_SULAC	Q4ja20	sulfolobus
295	96	5.8	1569	2	Q54DM4_DICDI	Q54dm4	dictyosteli
296	95.5	5.8	266	2	Q4HZD3_GIBZE	Q4hzd3	gibberella
297	95.5	5.8	376	1	MID2_YEAST	P36027	saccharomyc
298	95.5	5.8	385	2	Q9NHU5_DROMI	Q9nhu5	drosophila
299	95.5	5.8	385	2	Q9NHU7_DROMI	Q9nhu7	drosophila
300	95.5	5.8	469	2	Q54P62_DICDI	Q54p62	dictyosteli
301	95.5	5.8	585	2	Q5SE79_9MONO	Q5se79	avian pneum
302	95.5	5.8	996	2	Q5BF33_EMENI	Q5bf33	aspergillus
303	95.5	5.8	1259	2	Q869X4_DICDI	Q869x4	dictyosteli
304	95.5	5.8	5374	2	Q99ND0_MOUSE	Q99nd0	mus musculu
305	95	5.7	273	2	Q61002_MOUSE	Q61002	mus musculu
306	95	5.7	281	2	Q4KSI9_9ADEN	Q4ksi9	human adeno
307	95	5.7	390	2	Q702W9_HHV1	Q702w9	human herpe
308	95	5.7	424	2	Q9FGW0_ARATH	Q9fgw0	arabidopsis
309	95	5.7	538	2	O69379_LISMO	O69379	listeria mo
310	95	5.7	601	2	Q5ZKL1_CHICK	Q5zkl1	gallus gall
311	95	5.7	604	2	Q9RQI3_LISMO	Q9rqi3	listeria mo
312	95	5.7	604	2	Q6EAD8_LISMO	Q6ead8	listeria mo
313	95	5.7	639	2	Q8GNR2_LISMO	Q8gnr2	listeria mo
314	95	5.7	639	2	Q6E904_LISMO	Q6e904	listeria mo
315	95	5.7	639	2	Q6E982_LISMO	Q6e982	listeria mo
316	95	5.7	639	2	Q6E9Q6_LISMO	Q6e9q6	listeria mo
317	95	5.7	753	2	Q6PFP4_BRARE	Q6pfp4	brachydanio
318	95	5.7	1203	2	Q6C028_YARLI	Q6c028	yarrowia li
319	95	5.7	1578	2	Q55C84_DICDI	Q55c84	dictyosteli
320	95	5.7	1748	2	Q54FL9_DICDI	Q54fl9	dictyosteli
321	94.5	5.7	345	2	Q691Y8_ANOSA	Q691y8	anolis sagr
322	94.5	5.7	359	1	TIMD1_HUMAN	Q96d42	homo sapien
323	94.5	5.7	383	2	Q702X5_HHV1	Q702x5	human herpe
324	94.5	5.7	383	2	Q702Y4_HHV1	Q702y4	human herpe
325	94.5	5.7	395	2	Q702Z0_HHV1	Q702z0	human herpe
326	94.5	5.7	405	2	Q4INQ5_GIBZE	Q4inq5	gibberella
327	94.5	5.7	494	2	Q4WG24_ASPFU	Q4wg24	aspergillus
328	94.5	5.7	510	2	Q5YFP0_9VIRU	Q5yfp0	singapore g
329	94.5	5.7	519	2	Q7YTR7_CAEEL	Q7ytr7	caenorhabdi
330	94.5	5.7	539	2	Q54GL8_DICDI	Q54gl8	dictyosteli
331	94.5	5.7	698	2	Q61SH2_CAEBR	Q61sh2	caenorhabdi
332	94.5	5.7	814	2	Q5AG78_CANAL	Q5ag78	candida alb
333	94.5	5.7	1007	2	Q55CR8_DICDI	Q55cr8	dictyosteli
334	94.5	5.7	1007	2	Q5P0E5_AZOSE	Q5p0e5	azoarcus sp
335	94.5	5.7	1066	2	Q76NW3_DICDI	Q76nw3	dictyosteli
336	94.5	5.7	1079	2	Q9N4S7_CAEEL	Q9n4s7	caenorhabdi
337	94.5	5.7	1390	2	Q17602_CAEEL	Q17602	caenorhabdi
338	94.5	5.7	1622	2	Q54G21_DICDI	Q54g21	dictyosteli
339	94.5	5.7	1942	2	Q8GIZ7_LACDL	Q8giz7	lactobacill
340	94.5	5.7	3370	2	Q8I1N9_PLAF7	Q8i1n9	plasmodium
341	94	5.7	239	2	Q55C69_DICDI	Q55c69	dictyosteli
342	94	5.7	639	2	Q8GNR8_LISMO	Q8gnr8	listeria mo
343	94	5.7	639	2	Q6E8W8_LISMO	Q6e8w8	listeria mo
344	94	5.7	639	2	Q6E922_LISMO	Q6e922	listeria mo
345	94	5.7	639	2	Q6E9G6_LISMO	Q6e9g6	listeria mo
346	94	5.7	639	2	Q6EA26_LISMO	Q6ea26	listeria mo
347	94	5.7	639	2	Q6EA68_LISMO	Q6ea68	listeria mo
348	94	5.7	639	2	Q6EAF0_LISMO	Q6eaf0	listeria mo
349	94	5.7	769	2	O00816_TOXGO	O00816	toxoplasma
350	94	5.7	989	2	Q83U76_CHLTR	Q83u76	chlamydia t
351	94	5.7	989	2	Q84FU9_CHLTR	Q84fu9	chlamydia t
352	94	5.7	1067	2	Q5BGE6_EMENI	Q5bge6	aspergillus
353	94	5.7	1241	1	PER_DROPS	P12348	drosophila
354	94	5.7	1241	2	Q75JC0_DICDI	Q75jc0	dictyosteli
355	93.5	5.6	278	2	Q4WIP3_ASPFU	Q4wip3	aspergillus
356	93.5	5.6	296	2	Q6P9X9_RAT	Q6p9x9	rattus norv
357	93.5	5.6	383	2	Q702W5_HHV1	Q702w5	human herpe
358	93.5	5.6	385	2	Q9NHU8_DROMI	Q9nhu8	drosophila
359	93.5	5.6	498	2	Q6FWR9_CANGA	Q6fwr9	candida gla
360	93.5	5.6	607	2	Q8GNS0_LISMO	Q8gns0	listeria mo
361	93.5	5.6	613	2	Q51TE4_MAGGR	Q51te4	magnaporthe
362	93.5	5.6	626	2	Q9NDD1_LEITR	Q9ndd1	leishmania
363	93.5	5.6	802	2	Q60LR3_CAEBR	Q60lr3	caenorhabdi
364	93.5	5.6	980	2	Q54TI9_DICDI	Q54ti9	dictyosteli
365	93.5	5.6	1033	2	Q4HYJ6_GIBZE	Q4hyj6	gibberella
366	93.5	5.6	1595	2	Q5SBM3_LACSK	Q5sbm3	lactobacill
367	93	5.6	261	2	Q70CC2_EIMTE	Q70cc2	eimeria ten
368	93	5.6	311	2	O46019_CAEEL	O46019	caenorhabdi
369	93	5.6	385	2	Q8T8I7_DROPS	Q8t8i7	drosophila
370	93	5.6	385	2	Q8T8I9_DROPS	Q8t8i9	drosophila
371	93	5.6	405	2	Q66HZ2_BRARE	Q66hz2	brachydanio
372	93	5.6	448	2	Q5EFZ7_CHICK	Q5efz7	gallus gall
373	93	5.6	572	2	Q58SM0_DROME	Q58sm0	drosophila
374	93	5.6	572	2	Q58SM7_DROME	Q58sm7	drosophila
375	93	5.6	576	2	Q61MD1_CAEBR	Q61md1	caenorhabdi
376	93	5.6	608	2	Q50MX9_ENTHI	Q50mx9	entamoeba h
377	93	5.6	629	2	Q24017_DROME	Q24017	drosophila
378	93	5.6	629	2	Q5ELT0_DROME	Q5elt0	drosophila
379	93	5.6	629	2	Q5ELT4_DROME	Q5elt4	drosophila
380	93	5.6	629	2	Q5ELV0_DROME	Q5elv0	drosophila
381	93	5.6	639	2	Q8GNR5_LISMO	Q8gnr5	listeria mo
382	93	5.6	639	2	Q8GNR6_LISMO	Q8gnr6	listeria mo
383	93	5.6	639	2	Q6E8X4_LISMO	Q6e8x4	listeria mo
384	93	5.6	758	2	Q54UR7_DICDI	Q54ur7	dictyosteli
385	93	5.6	791	2	Q51UQ4_MAGGR	Q51uq4	magnaporthe
386	93	5.6	916	2	Q7YZI0_MONBE	Q7yzi0	monosiga br
387	93	5.6	928	2	Q4SL40_TETNG	Q4sl40	tetraodon n
388	93	5.6	930	2	Q9YBL5_AERPE	Q9ybl5	aeropyrum p
389	93	5.6	1034	2	Q613E9_CAEBR	Q613e9	caenorhabdi
390	93	5.6	1285	2	Q4RXD7_TETNG	Q4rxd7	tetraodon n
391	93	5.6	1292	2	Q4RHM3_TETNG	Q4rhm3	tetraodon n
392	93	5.6	1349	2	Q8WWQ4_HUMAN	Q8wwq4	homo sapien
393	93	5.6	1413	2	Q54FI2_DICDI	Q54fi2	dictyosteli
394	92.5	5.6	215	2	Q614I3_CAEBR	Q614i3	caenorhabdi
395	92.5	5.6	247	2	Q8MKY7_DROME	Q8mky7	drosophila
396	92.5	5.6	296	2	Q923D3_MOUSE	Q923d3	mus musculu

397	92.5	5.6	299	2	Q4HYT1_GIBZE	Q4hyt1	gibberella
398	92.5	5.6	300	1	JAM1_MOUSE	O88792	mus musculu
399	92.5	5.6	385	2	Q9NHV2_DROMI	Q9nhv2	drosophila
400	92.5	5.6	400	1	HPLN4_MOUSE	Q80wm4	mus musculu
401	92.5	5.6	446	2	Q8EMV3_OCEIH	Q8emv3	oceanobacil
402	92.5	5.6	448	2	Q61C01_CAEBR	Q61c01	caenorhabdi
403	92.5	5.6	453	2	Q5KCR5_CRYNE	Q5kcr5	cryptococcu
404	92.5	5.6	466	2	Q55IY7_CRYNE	Q55iy7	cryptococcu
405	92.5	5.6	466	2	Q5KCR4_CRYNE	Q5kcr4	cryptococcu
406	92.5	5.6	487	2	Q54G14_DICDI	Q54g14	dictyosteli
407	92.5	5.6	487	2	Q4UHA9_THEAN	Q4uha9	theileria a
408	92.5	5.6	569	2	Q9KGV9_LISMO	Q9kgv9	listeria mo
409	92.5	5.6	604	2	Q6EAE4_LISMO	Q6eae4	listeria mo
410	92.5	5.6	623	2	O57602_ICTPU	O57602	ictalurus p
411	92.5	5.6	629	2	Q4QGJ0_LEIMA	Q4qgj0	leishmania
412	92.5	5.6	638	2	Q55FI4_DICDI	Q55fi4	dictyosteli
413	92.5	5.6	708	2	Q73H41_WOLPM	Q73h41	wolbachia p
414	92.5	5.6	784	2	Q7S3V6_NEUCR	Q7s3v6	neurospora
415	92.5	5.6	812	2	Q55D98_DICDI	Q55d98	dictyosteli
416	92.5	5.6	927	2	Q21811_CAEEL	Q21811	caenorhabdi
417	92.5	5.6	1491	2	Q4QDK4_LEIMA	Q4qdk4	leishmania
418	92.5	5.6	1636	1	BUD3_YEAST	P25558	saccharomyc
419	92.5	5.6	2048	2	Q55GC1_DICDI	Q55gc1	dictyosteli
420	92.5	5.6	2338	2	Q759S3_ASHGO	Q759s3	ashbya goss
421	92	5.6	347	2	Q8SYW5_DROME	Q8syw5	drosophila
422	92	5.6	429	2	P79046_9ASCO	P79046	humicola gr
423	92	5.6	500	2	Q864U4_BOVIN	Q864u4	bos taurus
424	92	5.6	504	2	Q54FD8_DICDI	Q54fd8	dictyosteli
425	92	5.6	567	2	Q4P6Q2_USTMA	Q4p6q2	ustilago ma
426	92	5.6	574	2	Q58SM3_DROME	Q58sm3	drosophila
427	92	5.6	586	2	Q5B1Y4_EMENI	Q5b1y4	aspergillus
428	92	5.6	604	2	Q9JNA2_LISMO	Q9jna2	listeria mo
429	92	5.6	629	2	Q5ELR9_DROME	Q5elr9	drosophila
430	92	5.6	629	2	Q5ELS5_DROME	Q5els5	drosophila
431	92	5.6	629	2	Q5ELU4_DROME	Q5elu4	drosophila
432	92	5.6	639	2	Q6EA92_LISMO	Q6ea92	listeria mo
433	92	5.6	644	2	Q6CF33_YARLI	Q6cf33	yarrowia li
434	92	5.6	659	2	Q95XE2_CAEEL	Q95xe2	caenorhabdi
435	92	5.6	668	2	Q4QGK4_LEIMA	Q4qgk4	leishmania
436	92	5.6	741	2	Q6CH88_YARLI	Q6ch88	yarrowia li
437	92	5.6	828	2	Q5B8I9_EMENI	Q5b8i9	aspergillus
438	92	5.6	846	2	O01699_CAEEL	O01699	caenorhabdi
439	92	5.6	907	2	Q6CTD8_KLULA	Q6ctd8	kluyveromyc
440	92	5.6	966	1	SSN6_YEAST	P14922	saccharomyc
441	92	5.6	1170	2	Q54PK2_DICDI	Q54pk2	dictyosteli
442	92	5.6	1269	2	Q54CA1_DICDI	Q54ca1	dictyosteli
443	92	5.6	1343	2	Q54XT5_DICDI	Q54xt5	dictyosteli
444	92	5.6	1505	2	Q54VU4_DICDI	Q54vu4	dictyosteli
445	92	5.6	1720	2	Q8I486_PLAF7	Q8i486	plasmodium
446	92	5.6	2829	1	APC_XENLA	P70039	xenopus lae
447	91.5	5.5	161	2	Q6CPZ3_KLULA	Q6cpz3	kluyveromyc
448	91.5	5.5	198	2	Q7WRT1_LISMO	Q7wrt1	listeria mo
449	91.5	5.5	198	2	Q7X384_LISMO	Q7x384	listeria mo
450	91.5	5.5	300	2	Q8VC39_MOUSE	Q8vc39	mus musculu
451	91.5	5.5	305	2	Q8R183_MOUSE	Q8r183	mus musculu
452	91.5	5.5	338	2	Q6EAH4_LISMO	Q6eah4	listeria mo
453	91.5	5.5	383	2	Q5I693_HHV1	Q5i693	human herpe
454	91.5	5.5	383	2	Q702X8_HHV1	Q702x8	human herpe
455	91.5	5.5	385	2	Q9NHV1_DROMI	Q9nhv1	drosophila
456	91.5	5.5	411	1	LAMP2_RAT	P17046	rattus norv
457	91.5	5.5	411	2	Q6P6W1_RAT	Q6p6w1	rattus norv
458	91.5	5.5	497	2	Q8QVC5_9REOV	Q8qvc5	eyach virus
459	91.5	5.5	538	2	Q76H84_STRMU	Q76h84	streptococc
460	91.5	5.5	573	2	O69380_LISMO	O69380	listeria mo
461	91.5	5.5	579	2	Q5CYK7_CRYPV	Q5cyk7	cryptospori
462	91.5	5.5	588	2	Q5ANG0_CANAL	Q5ang0	candida alb
463	91.5	5.5	604	2	Q8GNR3_LISMO	Q8gnr3	listeria mo
464	91.5	5.5	604	2	Q6E8U4_LISMO	Q6e8u4	listeria mo
465	91.5	5.5	627	2	Q7RWT2_NEUCR	Q7rwt2	neurospora
466	91.5	5.5	633	2	Q9JMY6_LISMO	Q9jmy6	listeria mo
467	91.5	5.5	633	2	Q4TVQ6_LISMO	Q4tvq6	listeria mo
468	91.5	5.5	639	1	ACTA_LISMO	P33379	listeria mo
469	91.5	5.5	639	2	Q8GNR9_LISMO	Q8gnr9	listeria mo
470	91.5	5.5	639	2	Q6E8V0_LISMO	Q6e8v0	listeria mo
471	91.5	5.5	639	2	Q6E9I4_LISMO	Q6e9i4	listeria mo
472	91.5	5.5	639	2	Q6E9X8_LISMO	Q6e9x8	listeria mo
473	91.5	5.5	639	2	Q6EA56_LISMO	Q6ea56	listeria mo
474	91.5	5.5	639	2	Q6EAA4_LISMO	Q6eaa4	listeria mo
475	91.5	5.5	639	2	Q8GNS2_LISMO	Q8gns2	listeria mo
476	91.5	5.5	639	2	Q6E8T8_LISMO	Q6e8t8	listeria mo
477	91.5	5.5	651	2	Q61YZ5_CAEBR	Q61yz5	caenorhabdi
478	91.5	5.5	681	1	VGP_MABVP	P35254	marburg vir
479	91.5	5.5	681	2	Q71VM1_9MONO	Q71vm1	lake victor
480	91.5	5.5	860	2	Q7RZN3_NEUCR	Q7rzn3	neurospora
481	91.5	5.5	1138	2	Q4UNB8_RICFE	Q4unb8	rickettsia
482	91.5	5.5	1148	2	Q6CBJ2_YARLI	Q6cbj2	yarrowia li
483	91.5	5.5	1167	2	Q7RWQ7_NEUCR	Q7rwq7	neurospora
484	91.5	5.5	1481	2	Q4P152_USTMA	Q4p152	ustilago ma
485	91.5	5.5	1783	2	Q51UR4_MAGGR	Q51ur4	magnaporthe
486	91	5.5	174	2	Q7YTP1_CAEEL	Q7ytp1	caenorhabdi
487	91	5.5	198	2	Q7X3M4_LISMO	Q7x3m4	listeria mo
488	91	5.5	213	2	Q5T3I7_HUMAN	Q5t3i7	homo sapien
489	91	5.5	246	2	Q9UAV4_CAEEL	Q9uav4	caenorhabdi
490	91	5.5	346	2	Q52J88_9SAUR	Q52j88	heteronotia
491	91	5.5	346	2	Q52J76_9SAUR	Q52j76	heteronotia
492	91	5.5	450	2	Q8CV85_OCEIH	Q8cv85	oceanobacil
493	91	5.5	488	2	Q09586_CAEEL	Q09586	caenorhabdi
494	91	5.5	591	2	Q4WHJ8_ASPFU	Q4whj8	aspergillus
495	91	5.5	596	2	Q6P1T0_XENTR	Q6p1t0	xenopus tro
496	91	5.5	600	2	Q4VBE0_XENTR	Q4vbe0	xenopus tro
497	91	5.5	620	2	Q8SVR3_ENCCU	Q8svr3	encephalito
498	91	5.5	629	2	Q5ELR5_DROME	Q5elr5	drosophila
499	91	5.5	629	2	Q5ELR7_DROME	Q5elr7	drosophila
500	91	5.5	629	2	Q5ELS3_DROME	Q5els3	drosophila
501	91	5.5	639	2	Q6E964_LISMO	Q6e964	listeria mo
502	91	5.5	639	2	Q6EAI0_LISMO	Q6eai0	listeria mo
503	91	5.5	644	2	Q54D31_DICDI	Q54d31	dictyosteli
504	91	5.5	693	2	Q7PYY7_ANOGA	Q7pyy7	anopheles g
505	91	5.5	701	2	Q8ZWG4_PYRAE	Q8zwg4	pyrobaculum
506	91	5.5	730	2	Q86AZ8_DICDI	Q86az8	dictyosteli
507	91	5.5	876	2	Q619L5_CAEBR	Q619l5	caenorhabdi
508	91	5.5	1246	2	Q51FG7_ENTHI	Q51fg7	entamoeba h
509	91	5.5	1398	2	Q869T5_DICDI	Q869t5	dictyosteli
510	91	5.5	1842	2	Q4N830_THEPA	Q4n830	theileria p
511	91	5.5	2162	2	Q09515_CAEEL	Q09515	caenorhabdi
512	91	5.5	2176	2	Q54VP0_DICDI	Q54vp0	dictyosteli
513	91	5.5	4262	2	Q685J2_HUMAN	Q685j2	homo sapien
514	91	5.5	4493	2	Q685J3_HUMAN	Q685j3	homo sapien
515	90.5	5.5	306	2	Q54UW3_DICDI	Q54uw3	dictyosteli
516	90.5	5.5	336	2	Q4Z0P5_PLABE	Q4z0p5	plasmodium
517	90.5	5.5	360	2	Q4WG94_ASPFU	Q4wg94	aspergillus
518	90.5	5.5	385	2	Q9NHV0_DROMI	Q9nhv0	drosophila
519	90.5	5.5	385	2	Q9NHV3_DROMI	Q9nhv3	drosophila
520	90.5	5.5	406	2	Q528W4_MAGGR	Q528w4	magnaporthe
521	90.5	5.5	408	2	Q6UDF5_9HERP	Q6udf5	psittacid h
522	90.5	5.5	461	2	Q6C2X8_YARLI	Q6c2x8	yarrowia li
523	90.5	5.5	496	2	Q55D06_DICDI	Q55d06	dictyosteli
524	90.5	5.5	575	1	CH61_CUCMA	Q05045	cucurbita m
525	90.5	5.5	595	2	Q5ANA0_CANAL	Q5ana0	candida alb
526	90.5	5.5	659	2	Q59R26_CANAL	Q59r26	candida alb
527	90.5	5.5	662	1	MUC1_XENLA	Q05049	xenopus lae
528	90.5	5.5	678	2	Q54U48_DICDI	Q54u48	dictyosteli
529	90.5	5.5	690	2	Q66S18_9UROC	Q66s18	oikopleura
530	90.5	5.5	862	2	Q615W4_CAEBR	Q615w4	caenorhabdi
531	90.5	5.5	952	2	Q9U3P1_CAEEL	Q9u3p1	caenorhabdi
532	90.5	5.5	972	2	Q60Q42_CAEBR	Q60q42	caenorhabdi
533	90.5	5.5	1084	2	Q55A66_DICDI	Q55a66	dictyosteli
534	90.5	5.5	1084	2	Q86LA6_DICDI	Q86la6	dictyosteli
535	90.5	5.5	1126	2	Q5CIS2_CRYHO	Q5cis2	cryptospori
536	90.5	5.5	1175	2	Q9VRL7_DROME	Q9vrl7	drosophila
537	90.5	5.5	1400	2	Q5FBC4_DICDI	Q5fbc4	dictyosteli
538	90.5	5.5	1711	1	NU214_DROME	Q9w1x4	drosophila
539	90.5	5.5	1976	2	Q9V9I8_DROME	Q9v9i8	drosophila
540	90.5	5.5	2300	2	Q7SFP6_NEUCR	Q7sfp6	neurospora
541	90	5.4	294	2	Q4V3X0_DROME	Q4v3x0	drosophila
542	90	5.4	388	1	VE2_HPV27	P36789	human papil

543	90	5.4	474	2	Q4I7B2_GIBZE	Q4i7b2	gibberella
544	90	5.4	488	2	Q4V3Z8_DROME	Q4v3z8	drosophila
545	90	5.4	508	2	Q54BP8_DICDI	Q54bp8	dictyosteli
546	90	5.4	511	2	Q5A7R7_CANAL	Q5a7r7	candida alb
547	90	5.4	540	2	Q7SFI7_NEUCR	Q7sfi7	neurospora
548	90	5.4	560	2	Q54LP6_DICDI	Q54lp6	dictyosteli
549	90	5.4	572	2	Q58SM4_DROME	Q58sm4	drosophila
550	90	5.4	572	2	Q58SM6_DROME	Q58sm6	drosophila
551	90	5.4	598	2	Q5ELV8_DROSI	Q5elv8	drosophila
552	90	5.4	604	2	Q6E9Q0_LISMO	Q6e9q0	listeria mo
553	90	5.4	612	2	Q7QJB6_ANOGA	Q7qjb6	anopheles g
554	90	5.4	616	2	Q4WC60_ASPFU	Q4wc60	aspergillus
555	90	5.4	626	2	Q8IQJ5_DROME	Q8iqj5	drosophila
556	90	5.4	629	2	Q5ELS7_DROME	Q5els7	drosophila
557	90	5.4	629	2	Q9V3H7_DROME	Q9v3h7	drosophila
558	90	5.4	630	2	Q5ELS1_DROME	Q5els1	drosophila
559	90	5.4	639	2	Q6E8S6_LISMO	Q6e8s6	listeria mo
560	90	5.4	740	2	Q54H84_DICDI	Q54h84	dictyosteli
561	90	5.4	812	2	Q61KE5_CAEBR	Q61ke5	caenorhabdi
562	90	5.4	823	2	Q54Y28_DICDI	Q54y28	dictyosteli
563	90	5.4	877	2	Q9H3Q6_HUMAN	Q9h3q6	homo sapien
564	90	5.4	878	2	Q9H3Q7_HUMAN	Q9h3q7	homo sapien
565	90	5.4	948	2	Q86AV9_DICDI	Q86av9	d phosphati
566	90	5.4	954	2	Q610Z8_CAEBR	Q610z8	caenorhabdi
567	90	5.4	957	2	O14651_HUMAN	O14651	homo sapien
568	90	5.4	965	2	Q22286_CAEEL	Q22286	caenorhabdi
569	90	5.4	1086	2	Q54X99_DICDI	Q54x99	dictyosteli
570	90	5.4	1170	2	Q4IC26_GIBZE	Q4ic26	gibberella
571	90	5.4	1217	2	Q9UKW9_HUMAN	Q9ukw9	homo sapien
572	90	5.4	1293	2	Q4Q6D9_LEIMA	Q4q6d9	leishmania
573	90	5.4	1367	1	MUC1_YEAST	P08640	saccharomyc
574	90	5.4	1367	2	Q6LCS8_SACDI	Q6lcs8	saccharomyc
575	90	5.4	1593	2	Q8SX82_DROME	Q8sx82	drosophila
576	90	5.4	2282	2	Q9NK56_DROME	Q9nk56	drosophila
577	90	5.4	2871	2	Q8IM87_DROME	Q8im87	drosophila
578	90	5.4	2874	2	Q9V483_DROME	Q9v483	drosophila
579	89.5	5.4	195	2	Q9QX82_RAT	Q9qx82	rattus norv
580	89.5	5.4	276	2	Q52BL6_MAGGR	Q52bl6	magnaporthe
581	89.5	5.4	305	2	Q8VBW0_MOUSE	Q8vbw0	mus musculu
582	89.5	5.4	319	1	CJ078_MOUSE	Q8bp27	mus musculu
583	89.5	5.4	326	2	Q7SCW5_NEUCR	Q7scw5	neurospora
584	89.5	5.4	359	2	Q5KCB0_CRYNE	Q5kcb0	cryptococcu
585	89.5	5.4	440	2	Q9P566_NEUCR	Q9p566	neurospora
586	89.5	5.4	443	2	Q6P111_BRARE	Q6p111	brachydanio
587	89.5	5.4	455	2	Q7VNN0_HAEDU	Q7vnn0	haemophilus
588	89.5	5.4	456	2	Q25242_LUCCU	Q25242	lucilia cup
589	89.5	5.4	471	2	Q9VMG7_DROME	Q9vmg7	drosophila
590	89.5	5.4	480	2	Q25241_LUCCU	Q25241	lucilia cup
591	89.5	5.4	492	2	Q6CGC6_YARLI	Q6cgc6	yarrowia li
592	89.5	5.4	510	2	Q6SCJ8_ASPFU	Q6scj8	aspergillus
593	89.5	5.4	548	2	Q61CS6_CAEBR	Q61cs6	caenorhabdi
594	89.5	5.4	558	2	Q4JK70_DERPT	Q4jk70	dermatophag
595	89.5	5.4	604	2	Q6E9W0_LISMO	Q6e9w0	listeria mo
596	89.5	5.4	606	2	Q5ZLR8_CHICK	Q5zlr8	gallus gall
597	89.5	5.4	634	2	Q71T11_MOMCH	Q71t11	momordica c
598	89.5	5.4	659	2	Q556Y6_DICDI	Q556y6	dictyosteli
599	89.5	5.4	659	2	Q86AI8_DICDI	Q86ai8	dictyosteli
600	89.5	5.4	917	2	Q7QJI6_ANOGA	Q7qji6	anopheles g
601	89.5	5.4	1145	2	Q8JKT0_9VIRU	Q8jkt0	heliothis z
602	89.5	5.4	1368	2	Q23821_CAEVU	Q23821	caenorhabdi
603	89.5	5.4	1773	2	Q4N437_THEPA	Q4n437	theileria p
604	89.5	5.4	1816	2	Q4N6E9_THEPA	Q4n6e9	theileria p
605	89	5.4	307	1	SGS3_DROME	P02840	drosophila
606	89	5.4	369	2	Q91E39_9ALPH	Q91e39	phocid herp
607	89	5.4	392	2	Q59FZ0_HUMAN	Q59fz0	homo sapien
608	89	5.4	416	1	LAMP1_HUMAN	P11279	homo sapien
609	89	5.4	417	2	Q8WU33_HUMAN	Q8wu33	homo sapien
610	89	5.4	421	2	Q6KCA6_CANDU	Q6kca6	candida dub
611	89	5.4	422	2	Q5CNT4_CRYHO	Q5cnt4	cryptospori
612	89	5.4	477	2	Q14887_HUMAN	Q14887	homo sapien
613	89	5.4	482	2	Q6BSZ9_DEBHA	Q6bsz9	debaryomyce
614	89	5.4	487	2	Q4U479_ANOGA	Q4u479	anopheles g
615	89	5.4	503	1	NAS14_CAEEL	Q19269	caenorhabdi
616	89	5.4	516	2	Q5CM29_CRYHO	Q5cm29	cryptospori
617	89	5.4	589	2	Q4N7T4_THEPA	Q4n7t4	theileria p
618	89	5.4	603	2	Q6CE49_YARLI	Q6ce49	yarrowia li
619	89	5.4	666	2	Q7QXK0_GIALA	Q7qxk0	giardia lam
620	89	5.4	714	2	Q9NGW9_DICDI	Q9ngw9	dictyosteli
621	89	5.4	770	2	Q55G55_DICDI	Q55g55	dictyosteli
622	89	5.4	833	2	Q8IRC1_DROME	Q8irc1	drosophila
623	89	5.4	851	2	Q9VZI0_DROME	Q9vzi0	drosophila
624	89	5.4	860	2	Q5WNQ1_CAEBR	Q5wnq1	caenorhabdi
625	89	5.4	880	2	Q54UK3_DICDI	Q54uk3	dictyosteli
626	89	5.4	887	2	Q9I7T2_DROME	Q9i7t2	drosophila
627	89	5.4	898	2	Q8IRC0_DROME	Q8irc0	drosophila
628	89	5.4	917	2	Q4X105_ASPFU	Q4x105	aspergillus
629	89	5.4	951	2	Q9FVX8_ORYSA	Q9fvx8	oryza sativ
630	89	5.4	958	2	Q4WTT4_ASPFU	Q4wtt4	aspergillus
631	89	5.4	983	2	Q8IRB9_DROME	Q8irb9	drosophila
632	89	5.4	1081	2	Q59EA1_HUMAN	Q59ea1	homo sapien
633	89	5.4	1116	2	Q5AJH8_CANAL	Q5ajh8	candida alb
634	89	5.4	1473	2	Q54TV0_DICDI	Q54tv0	dictyosteli
635	89	5.4	1483	2	Q7KWU3_DICDI	Q7kwu3	dictyosteli
636	89	5.4	1493	2	Q559I7_DICDI	Q559i7	dictyosteli
637	89	5.4	1521	2	Q7Q1W8_ANOGA	Q7q1w8	anopheles g
638	89	5.4	1708	2	Q7XWZ9_ORYSA	Q7xwz9	oryza sativ
639	89	5.4	2273	2	Q63HU2_BURPS	Q63hu2	burkholderi
640	89	5.4	6994	2	Q17343_CAEEL	Q17343	caenorhabdi
641	89	5.4	6994	2	Q17490_CAEEL	Q17490	caenorhabdi
642	88.5	5.3	193	2	O23366_ARATH	O23366	arabidopsis
643	88.5	5.3	264	2	Q80XS5_MOUSE	Q80xs5	mus musculu
644	88.5	5.3	321	2	Q25939_PLAFA	Q25939	plasmodium
645	88.5	5.3	359	2	Q55JE9_CRYNE	Q55je9	cryptococcu
646	88.5	5.3	389	2	Q611Z9_CAEBR	Q611z9	caenorhabdi
647	88.5	5.3	448	2	Q6AQD8_DESPS	Q6aqd8	desulfotale
648	88.5	5.3	481	2	Q9VWK3_DROME	Q9vwk3	drosophila
649	88.5	5.3	494	2	Q618M1_CAEBR	Q618m1	caenorhabdi
650	88.5	5.3	518	2	Q8NJS3_CANAL	Q8njs3	candida alb
651	88.5	5.3	569	2	Q71XI0_LISMF	Q71xi0	listeria mo
652	88.5	5.3	582	2	Q8IR74_DROME	Q8ir74	drosophila
653	88.5	5.3	596	1	UBQL4_MOUSE	Q99nb8	mus musculu
654	88.5	5.3	598	2	Q9JMY5_LISMO	Q9jmy5	listeria mo
655	88.5	5.3	615	2	Q9M6E8_PHAVU	Q9m6e8	phaseolus v
656	88.5	5.3	622	2	Q58SF6_DROSI	Q58sf6	drosophila
657	88.5	5.3	653	2	Q8IJX0_PLAF7	Q8ijx0	plasmodium
658	88.5	5.3	699	2	Q6CSM7_KLULA	Q6csm7	kluyveromyc
659	88.5	5.3	721	2	Q97UG7_SULSO	Q97ug7	sulfolobus
660	88.5	5.3	722	2	O59644_SULSO	O59644	sulfolobus
661	88.5	5.3	722	2	Q6FTP4_CANGA	Q6ftp4	candida gla
662	88.5	5.3	752	2	Q52CR1_MAGGR	Q52cr1	magnaporthe
663	88.5	5.3	764	2	Q4WYI0_ASPFU	Q4wyi0	aspergillus
664	88.5	5.3	901	2	Q9H195_HUMAN	Q9h195	homo sapien
665	88.5	5.3	980	2	Q84FU6_CHLTR	Q84fu6	chlamydia t
666	88.5	5.3	980	2	Q84FU8_CHLTR	Q84fu8	chlamydia t
667	88.5	5.3	981	2	Q84FU7_CHLTR	Q84fu7	chlamydia t
668	88.5	5.3	1042	2	Q59X21_CANAL	Q59x21	candida alb
669	88.5	5.3	1101	1	GUNC_CELFI	P14090	cellulomona
670	88.5	5.3	1106	2	Q4IAX5_GIBZE	Q4iax5	gibberella
671	88.5	5.3	1224	2	Q54PM6_DICDI	Q54pm6	dictyosteli
672	88.5	5.3	1230	2	Q54JY4_DICDI	Q54jy4	dictyosteli
673	88.5	5.3	1346	2	Q54SH1_DICDI	Q54sh1	dictyosteli
674	88.5	5.3	2122	2	Q54R92_DICDI	Q54r92	dictyosteli
675	88	5.3	103	2	Q9TTB3_PIG	Q9ttb3	sus scrofa
676	88	5.3	161	2	Q9CVT7_MOUSE	Q9cvt7	mus musculu
677	88	5.3	259	2	Q9N3B9_CAEEL	Q9n3b9	caenorhabdi
678	88	5.3	302	2	Q55XK5_CRYNE	Q55xk5	cryptococcu
679	88	5.3	302	2	Q5KMC9_CRYNE	Q5kmc9	cryptococcu
680	88	5.3	345	2	Q690W2_ANOSA	Q690w2	anolis sagr
681	88	5.3	347	2	Q9TZV4_PLAFA	Q9tzv4	plasmodium
682	88	5.3	362	2	Q9TZV3_PLAFA	Q9tzv3	plasmodium
683	88	5.3	382	2	Q6C971_YARLI	Q6c971	yarrowia li
684	88	5.3	385	2	Q8T8I2_DROPB	Q8t8i2	drosophila
685	88	5.3	385	2	Q8T8I4_DROPB	Q8t8i4	drosophila
686	88	5.3	385	2	Q8T8I6_DROPB	Q8t8i6	drosophila
687	88	5.3	385	2	Q8T8J0_DROPB	Q8t8j0	drosophila
688	88	5.3	385	2	Q8T8J1_DROPB	Q8t8j1	drosophila

689	88	5.3	385	2	Q8T8K3_DROPE	Q8t8k3	drosophila
690	88	5.3	447	2	Q6CCR1_YARLI	Q6ccr1	yarrowia li
691	88	5.3	449	2	Q6CWZ6_KLULA	Q6cwz6	kluyveromyc
692	88	5.3	456	2	Q9U2W2_CAEEL	Q9u2w2	caenorhabdi
693	88	5.3	543	2	Q7QK86_ANOGA	Q7qk86	anopheles g
694	88	5.3	564	2	O01627_CAEEL	O01627	caenorhabdi
695	88	5.3	577	2	Q6FSJ1_CANGA	Q6fsj1	candida gla
696	88	5.3	587	2	Q51R09_MAGGR	Q51r09	magnaporthe
697	88	5.3	587	2	Q4QGJ9_LEIMA	Q4qgj9	leishmania
698	88	5.3	588	2	Q813F9_BACCR	Q813f9	bacillus ce
699	88	5.3	601	2	Q6V6S2_DROME	Q6v6s2	drosophila
700	88	5.3	602	2	Q8YV91_ANASP	Q8yv91	anabaena sp
701	88	5.3	604	2	Q6E916_LISMO	Q6e916	listeria mo
702	88	5.3	616	2	Q8R0X0_MOUSE	Q8r0x0	mus musculu
703	88	5.3	656	2	Q8BUE7_MOUSE	Q8bue7	mus musculu
704	88	5.3	716	2	Q9NYE4_HUMAN	Q9nye4	homo sapien
705	88	5.3	761	2	O22271_ARATH	O22271	arabidopsis
706	88	5.3	931	2	Q51LJ1_MAGGR	Q51lj1	magnaporthe
707	88	5.3	995	2	Q91638_XENLA	Q91638	xenopus lae
708	88	5.3	1051	2	Q6C1J9_YARLI	Q6c1j9	yarrowia li
709	88	5.3	1409	2	Q5ALT5_CANAL	Q5alt5	candida alb
710	88	5.3	1630	1	MSP1_PLAFK	P04932	plasmodium
711	88	5.3	1790	2	Q8I816_APLCA	Q8i816	aplysia cal
712	88	5.3	2195	2	Q4SA07_TETNG	Q4sa07	tetraodon n
713	88	5.3	5703	1	MUC5B_HUMAN	Q9hc84	homo sapien
714	87.5	5.3	147	2	O61043_TRYCR	O61043	trypanosoma
715	87.5	5.3	244	2	Q54RQ4_DICDI	Q54rq4	dictyosteli
716	87.5	5.3	283	2	Q5XUY9_ARATH	Q5xuy9	arabidopsis
717	87.5	5.3	283	2	Q9FKU2_ARATH	Q9fku2	arabidopsis
718	87.5	5.3	289	2	Q4IJR0_GIBZE	Q4ijr0	gibberella
719	87.5	5.3	299	2	Q5H2T1_XANOR	Q5h2t1	xanthomonas
720	87.5	5.3	338	2	Q6CY50_KLULA	Q6cy50	kluyveromyc
721	87.5	5.3	345	2	Q56WV8_ARATH	Q56wv8	arabidopsis
722	87.5	5.3	357	2	Q4N8P6_THEPA	Q4n8p6	theileria p
723	87.5	5.3	366	2	Q6FSI8_CANGA	Q6fsi8	candida gla
724	87.5	5.3	383	2	Q702Y9_HHV1	Q702y9	human herpe
725	87.5	5.3	442	2	Q7S2Z3_NEUCR	Q7s2z3	neurospora
726	87.5	5.3	462	2	Q8TUE0_METAC	Q8tue0	methanosarc
727	87.5	5.3	463	2	Q5A3K1_CANAL	Q5a3k1	candida alb
728	87.5	5.3	498	2	Q6FVC8_CANGA	Q6fvc8	candida gla
729	87.5	5.3	542	2	Q4V4X7_DROME	Q4v4x7	drosophila
730	87.5	5.3	555	2	Q9U6R7_DERFA	Q9u6r7	dermatophag
731	87.5	5.3	563	2	Q5LKG3_SILPO	Q5lkg3	silicibacte
732	87.5	5.3	571	2	Q4YHW1_PLABE	Q4yhw1	plasmodium
733	87.5	5.3	622	2	Q58SG2_DROSI	Q58sg2	drosophila
734	87.5	5.3	622	2	Q58SH9_DROSI	Q58sh9	drosophila
735	87.5	5.3	622	2	Q5ELQ5_DROSI	Q5elq5	drosophila
736	87.5	5.3	622	2	Q5ELQ9_DROSI	Q5elq9	drosophila
737	87.5	5.3	623	2	Q6T547_LISMO	Q6t547	listeria mo
738	87.5	5.3	625	2	Q5ELP7_DROSI	Q5elp7	drosophila
739	87.5	5.3	634	2	Q7RWB0_NEUCR	Q7rwb0	neurospora
740	87.5	5.3	639	2	Q6T548_LISMO	Q6t548	listeria mo
741	87.5	5.3	648	2	O44189_CAEEL	O44189	caenorhabdi
742	87.5	5.3	653	2	Q59YC5_CANAL	Q59yc5	candida alb
743	87.5	5.3	653	2	Q8NK55_CANAL	Q8nk55	candida alb
744	87.5	5.3	665	2	Q4IIW3_GIBZE	Q4iiw3	gibberella
745	87.5	5.3	682	2	Q60PP2_CAEBR	Q60pp2	caenorhabdi
746	87.5	5.3	717	2	Q8NAJ6_HUMAN	Q8naj6	homo sapien
747	87.5	5.3	752	2	Q8MNE2_DICDI	Q8mne2	dictyosteli
748	87.5	5.3	785	2	Q7QQI5_GIALA	Q7qqi5	giardia lam
749	87.5	5.3	825	2	Q9LZA6_ARATH	Q9lza6	arabidopsis
750	87.5	5.3	867	2	Q90X49_BRARE	Q90x49	brachydanio
751	87.5	5.3	906	2	Q8UVU1_XENLA	Q8uvu1	xenopus lae
752	87.5	5.3	908	2	Q59PF9_CANAL	Q59pf9	candida alb
753	87.5	5.3	968	2	Q4SSC4_TETNG	Q4ssc4	tetraodon n
754	87.5	5.3	971	2	Q6W3C4_CAEEL	Q6w3c4	caenorhabdi
755	87.5	5.3	989	2	Q19930_CAEEL	Q19930	caenorhabdi
756	87.5	5.3	997	1	VGNM_APMV	P38485	andean pota
757	87.5	5.3	1085	1	CASR_BOVIN	P35384	bos taurus
758	87.5	5.3	1091	1	NCAM1_CHICK	P13590	gallus gall
759	87.5	5.3	1118	2	Q550H5_DICDI	Q550h5	dictyosteli
760	87.5	5.3	1129	2	Q6CB75_YARLI	Q6cb75	yarrowia li
761	87.5	5.3	1313	2	Q55WZ1_CRYNE	Q55wz1	cryptococcu
762	87.5	5.3	1370	2	Q6C3B8_YARLI	Q6c3b8	yarrowia li
763	87.5	5.3	1799	2	Q7KUI0_DROME	Q7kui0	drosophila
764	87.5	5.3	1802	1	HKR1_YEAST	P41809	saccharomyc
765	87.5	5.3	2314	2	Q55F23_DICDI	Q55f23	dictyosteli
766	87.5	5.3	2817	2	Q97K42_CLOAB	Q97k42	clostridium
767	87	5.3	167	2	O65742_CICAR	O65742	cicer ariet
768	87	5.3	235	2	Q63349_RAT	Q63349	rattus norv
769	87	5.3	259	2	Q70CD5_EIMTE	Q70cd5	eimeria ten
770	87	5.3	362	2	Q6CGU2_YARLI	Q6cgu2	yarrowia li
771	87	5.3	363	2	Q91YK8_MOUSE	Q91yk8	mus musculu
772	87	5.3	379	2	Q823B1_CHLCV	Q823b1	chlamydophi
773	87	5.3	385	2	Q8T8J9_DROPS	Q8t8j9	drosophila
774	87	5.3	406	2	Q4I3G6_GIBZE	Q4i3g6	gibberella
775	87	5.3	442	2	Q758Q5_ASHGO	Q758q5	ashbya goss
776	87	5.3	453	2	Q9U301_CAEEL	Q9u301	caenorhabdi
777	87	5.3	456	2	Q5B7G2_EMENI	Q5b7g2	aspergillus
778	87	5.3	478	2	Q55RT1_CRYNE	Q55rt1	cryptococcu
779	87	5.3	484	2	Q4FKQ7_9TRYP	Q4fkq7	trypanosoma
780	87	5.3	532	2	Q4JK69_DERPT	Q4jk69	dermatophag
781	87	5.3	567	2	Q60X66_CAEBR	Q60x66	caenorhabdi
782	87	5.3	585	2	Q58SH0_DROSI	Q58sh0	drosophila
783	87	5.3	639	2	Q6E8S0_LISMO	Q6e8s0	listeria mo
784	87	5.3	661	2	O13444_CLAFU	O13444	cladosporiu
785	87	5.3	686	2	Q61XJ6_CAEBR	Q61xj6	caenorhabdi
786	87	5.3	689	2	Q724Q0_LISMF	Q724q0	listeria mo
787	87	5.3	752	2	Q9YC61_AERPE	Q9yc61	aeropyrum p
788	87	5.3	812	2	Q54G74_DICDI	Q54g74	dictyosteli
789	87	5.3	841	2	Q6AX88_XENLA	Q6ax88	xenopus lae
790	87	5.3	881	2	Q8IMS9_DROME	Q8ims9	drosophila
791	87	5.3	919	2	Q51BH5_ENTHI	Q51bh5	entamoeba h
792	87	5.3	991	2	Q83UW2_CHLTR	Q83uw2	chlamydia t
793	87	5.3	991	2	Q84FV0_CHLTR	Q84fv0	chlamydia t
794	87	5.3	991	2	Q84FV1_CHLTR	Q84fv1	chlamydia t
795	87	5.3	1016	1	PMPH_CHLTR	O84880	chlamydia t
796	87	5.3	1048	2	Q9LAU3_LEGPN	Q9lau3	legionella
797	87	5.3	1055	2	Q55G65_DICDI	Q55g65	dictyosteli
798	87	5.3	1082	1	YK02_SCHPO	Q9hdy9	schizosacch
799	87	5.3	1173	2	Q61A60_CAEBR	Q61a60	caenorhabdi
800	87	5.3	1447	2	Q5B4Q8_EMENI	Q5b4q8	aspergillus
801	87	5.3	1506	2	P79927_XENLA	P79927	xenopus lae
802	87	5.3	1537	1	FLO1_YEAST	P32768	saccharomyc
803	87	5.3	1537	2	Q58HH7_YEAST	Q58hh7	saccharomyc
804	87	5.3	6586	2	Q52FL1_MAGGR	Q52fl1	magnaporthe
805	86.5	5.2	197	2	Q9Z317_MOUSE	Q9z317	mus musculu
806	86.5	5.2	197	2	Q9R0L9_MOUSE	Q9r019	mus musculu
807	86.5	5.2	245	2	Q61MB0_CAEBR	Q61mb0	caenorhabdi
808	86.5	5.2	249	2	Q6BVX5_DEBHA	Q6bvx5	debaryomyce
809	86.5	5.2	277	2	Q4KMD4_BRARE	Q4kmd4	brachydanio
810	86.5	5.2	390	2	Q73JV8_TREDE	Q73jv8	treponema d
811	86.5	5.2	400	1	MUA1_XENLA	P10667	xenopus lae
812	86.5	5.2	401	2	Q6BV71_DEBHA	Q6bv71	debaryomyce
813	86.5	5.2	442	2	Q7M8Z3_WOLSU	Q7m8z3	wolinella s
814	86.5	5.2	451	2	Q6DF68_XENTR	Q6df68	xenopus tro
815	86.5	5.2	461	2	Q21004_CAEEL	Q21004	caenorhabdi
816	86.5	5.2	483	2	Q5AT96_EMENI	Q5at96	aspergillus
817	86.5	5.2	484	1	PAPO2_XENLA	P51005	xenopus lae
818	86.5	5.2	493	2	Q23330_CAEEL	Q23330	caenorhabdi
819	86.5	5.2	503	1	WSC2_YEAST	P53832	saccharomyc
820	86.5	5.2	582	2	Q58SG7_DROSI	Q58sg7	drosophila
821	86.5	5.2	582	2	Q58SG8_DROSI	Q58sg8	drosophila
822	86.5	5.2	582	2	Q58SG9_DROSI	Q58sg9	drosophila
823	86.5	5.2	582	2	Q58SH3_DROSI	Q58sh3	drosophila
824	86.5	5.2	598	2	Q5ELV4_DROSI	Q5elv4	drosophila
825	86.5	5.2	598	2	Q5ELV5_DROSI	Q5elv5	drosophila
826	86.5	5.2	598	2	Q5ELW0_DROSI	Q5elw0	drosophila
827	86.5	5.2	601	2	Q6V6S4_DROME	Q6v6s4	drosophila
828	86.5	5.2	604	2	Q6E8Z8_LISMO	Q6e8z8	listeria mo
829	86.5	5.2	604	2	Q6E928_LISMO	Q6e928	listeria mo
830	86.5	5.2	624	2	Q58SF9_DROSI	Q58sf9	drosophila
831	86.5	5.2	639	2	Q8GNR0_LISMO	Q8gnr0	listeria mo
832	86.5	5.2	639	2	Q6E952_LISMO	Q6e952	listeria mo
833	86.5	5.2	639	2	Q6E976_LISMO	Q6e976	listeria mo
834	86.5	5.2	687	2	Q6NHU1_CORDI	Q6nhu1	corynebacte

835	86.5	5.2	733	2	Q55E25_DICDI	Q55e25	dictyosteli
836	86.5	5.2	739	1	GAG_SMRVH	P21411	squirrel mo
837	86.5	5.2	779	2	Q5TRJ3_ANOGA	Q5trj3	anopheles g
838	86.5	5.2	788	2	O18510_TRINI	O18510	trichoplusi
839	86.5	5.2	790	2	Q8TBZ7_HUMAN	Q8tbz7	homo sapien
840	86.5	5.2	807	2	O18511_TRINI	O18511	trichoplusi
841	86.5	5.2	838	2	Q7UNP4_RHOBA	Q7unp4	rhodopirell
842	86.5	5.2	843	2	Q4RQM0_TETNG	Q4rqm0	tetraodon n
843	86.5	5.2	853	2	Q54S28_DICDI	Q54s28	dictyosteli
844	86.5	5.2	941	2	Q9LTH0_ARATH	Q9lth0	arabidopsis
845	86.5	5.2	970	2	Q4W973_ASPFU	Q4w973	aspergillus
846	86.5	5.2	1300	2	Q6BZP6_YARLI	Q6bzp6	yarrowia li
847	86.5	5.2	1546	2	Q80SS4_MOUSE	Q80ss4	mus musculu
848	86.5	5.2	1579	2	Q99MP1_MOUSE	Q99mp1	mus musculu
849	86.5	5.2	1683	2	Q810D4_MOUSE	Q810d4	mus musculu
850	86.5	5.2	1684	2	Q9WTQ5_MOUSE	Q9wtq5	mus musculu
851	86.5	5.2	1822	2	Q7R0W4_GIALA	Q7r0w4	giardia lam
852	86.5	5.2	1844	2	Q22579_CAEEL	Q22579	caenorhabdi
853	86.5	5.2	1851	2	Q9ESP3_RAT	Q9esp3	rattus norv
854	86.5	5.2	2546	2	Q54ER5_DICDI	Q54er5	dictyosteli
855	86.5	5.2	2781	2	Q9UIG2_HUMAN	Q9uig2	homo sapien
856	86.5	5.2	4509	2	Q54T85_DICDI	Q54t85	dictyosteli
857	86	5.2	337	2	Q5AFI4_CANAL	Q5afi4	candida alb
858	86	5.2	345	2	Q6UJM5_9SAUR	Q6ujm5	diplodactyl
859	86	5.2	346	2	Q52J82_9SAUR	Q52j82	heteronotia
860	86	5.2	347	2	Q9TZV5_PLAFA	Q9tzv5	plasmodium
861	86	5.2	347	2	Q9TZV6_PLAFA	Q9tzv6	plasmodium
862	86	5.2	385	2	Q8T8K4_DROPE	Q8t8k4	drosophila
863	86	5.2	390	2	Q70LM3_PHLRA	Q70lm3	phlebia rad
864	86	5.2	390	2	Q96TS5_PHLRA	Q96ts5	phlebia rad
865	86	5.2	431	2	Q51WX9_MAGGR	Q51wx9	magnaporthe
866	86	5.2	434	2	Q872V2_NEUCR	Q872v2	neurospora
867	86	5.2	460	2	O18984_CERAE	O18984	cercopithec
868	86	5.2	476	2	Q03996_PLACH	Q03996	plasmodium
869	86	5.2	477	2	Q86YC5_HUMAN	Q86yc5	homo sapien
870	86	5.2	495	2	Q6AK33_DESPS	Q6ak33	desulfotale
871	86	5.2	537	2	Q5AHC9_CANAL	Q5ahc9	candida alb
872	86	5.2	537	2	Q5AHQ5_CANAL	Q5ahq5	candida alb
873	86	5.2	551	1	PODXL_RABIT	Q28645	oryctolagus
874	86	5.2	572	2	Q58SM1_DROME	Q58sm1	drosophila
875	86	5.2	598	2	Q4TVQ7_LISMO	Q4tvq7	listeria mo
876	86	5.2	604	2	Q8GNQ9_LISMO	Q8gnq9	listeria mo
877	86	5.2	604	2	Q6E9N2_LISMO	Q6e9n2	listeria mo
878	86	5.2	625	2	Q58SG0_DROSI	Q58sg0	drosophila
879	86	5.2	629	2	Q5ELS8_DROME	Q5els8	drosophila
880	86	5.2	639	2	Q6E8R4_LISMO	Q6e8r4	listeria mo
881	86	5.2	697	2	Q7S009_NEUCR	Q7s009	neurospora
882	86	5.2	709	2	Q4P7Y7_USTMA	Q4p7y7	ustilago ma
883	86	5.2	714	2	Q59TK9_CANAL	Q59tk9	candida alb
884	86	5.2	714	2	Q59TP1_CANAL	Q59tp1	candida alb
885	86	5.2	734	2	Q869R9_DICDI	Q869r9	dictyosteli
886	86	5.2	750	2	Q9HFZ4_CANAL	Q9hfz4	candida alb
887	86	5.2	780	2	Q9LK78_ARATH	Q91k78	arabidopsis
888	86	5.2	799	2	Q8EXF5_LEPIN	Q8exf5	leptospira
889	86	5.2	799	2	Q75FI7_LEPIC	Q75fi7	leptospira
890	86	5.2	843	2	Q7XJ06_ORYSA	Q7xj06	oryza sativ
891	86	5.2	855	2	Q55C58_DICDI	Q55c58	dictyosteli
892	86	5.2	866	2	Q80XL8_MOUSE	Q80xl8	mus musculu
893	86	5.2	955	2	Q55MM6_CRYNE	Q55mm6	cryptococcu
894	86	5.2	955	2	Q5KB01_CRYNE	Q5kb01	cryptococcu
895	86	5.2	1080	1	UBP8_MOUSE	Q80u87	mus musculu
896	86	5.2	1266	2	Q6CAR3_YARLI	Q6car3	yarrowia li
897	86	5.2	1266	2	Q626F7_CAEBR	Q626f7	caenorhabdi
898	86	5.2	1324	2	Q8MMQ2_DICDI	Q8mmq2	dictyosteli
899	86	5.2	1609	2	Q51DL9_ENTHI	Q51dl9	entamoeba h
900	86	5.2	1674	2	Q80Z18_MOUSE	Q80z18	mus musculu
901	86	5.2	1716	2	Q61ZV2_CAEBR	Q61zv2	caenorhabdi
902	86	5.2	1785	2	Q25685_PLACH	Q25685	plasmodium
903	86	5.2	2044	2	Q4HZP9_GIBZE	Q4hzp9	gibberella
904	86	5.2	2247	2	Q55FT4_DICDI	Q55ft4	dictyosteli
905	85.5	5.2	193	2	Q8LB00_ARATH	Q81b00	arabidopsis
906	85.5	5.2	206	2	Q6TVK4_9POXV	Q6tvk4	orf virus.
907	85.5	5.2	224	2	Q8KKT9_RHIET	Q8kkt9	rhizobium e
908	85.5	5.2	269	2	Q9U9J2_TOXCA	Q9u9j2	toxocara ca
909	85.5	5.2	271	2	Q6DGI9_BRARE	Q6dgi9	brachydanio
910	85.5	5.2	345	2	Q691X0_ANOSA	Q691x0	anolis sagr
911	85.5	5.2	346	2	Q5R230_9ZYGO	Q5r230	phycomyces
912	85.5	5.2	370	2	Q7KRX4_DROME	Q7krx4	drosophila
913	85.5	5.2	378	1	FBSH_MOUSE	Q8r089	mus musculu
914	85.5	5.2	379	2	Q8I050_DROME	Q8i050	drosophila
915	85.5	5.2	390	2	Q8IGQ0_DROME	Q8igq0	drosophila
916	85.5	5.2	405	2	Q51PI1_MAGGR	Q51pi1	magnaporthe
917	85.5	5.2	419	2	Q5TZ27_BRARE	Q5tz27	brachydanio
918	85.5	5.2	427	2	Q4STA8_TETNG	Q4sta8	tetraodon n
919	85.5	5.2	453	2	Q4IGE4_GIBZE	Q4ige4	gibberella
920	85.5	5.2	459	2	Q5WG39_BACSK	Q5wg39	bacillus cl
921	85.5	5.2	575	1	CH62_CUCMA	Q05046	cucurbita m
922	85.5	5.2	585	2	Q58SG4_DROSI	Q58sg4	drosophila
923	85.5	5.2	595	2	Q7R2J1_GIALA	Q7r2j1	giardia lam
924	85.5	5.2	622	2	Q6V6D8_DROSI	Q6v6d8	drosophila
925	85.5	5.2	622	2	Q6V6E4_DROSI	Q6v6e4	drosophila
926	85.5	5.2	623	2	Q89QR8_BRAJA	Q89qr8	bradyrhizob
927	85.5	5.2	624	2	Q58SF2_DROSI	Q58sf2	drosophila
928	85.5	5.2	624	2	Q58SG1_DROSI	Q58sg1	drosophila
929	85.5	5.2	624	2	Q5ELN1_DROSI	Q5eln1	drosophila
930	85.5	5.2	624	2	Q5ELN5_DROSI	Q5eln5	drosophila
931	85.5	5.2	624	2	Q5ELN9_DROSI	Q5eln9	drosophila
932	85.5	5.2	625	2	Q9LCJ8_STAAU	Q9lcj8	staphylococ
933	85.5	5.2	643	2	Q5JHI9_PYRKO	Q5jhi9	pyrococcus
934	85.5	5.2	649	2	O49445_ARATH	O49445	arabidopsis
935	85.5	5.2	693	2	Q54LR1_DICDI	Q54lr1	dictyosteli
936	85.5	5.2	716	2	Q54BA1_DICDI	Q54ba1	dictyosteli
937	85.5	5.2	734	2	Q7S939_NEUCR	Q7s939	neurospora
938	85.5	5.2	746	2	Q54N84_DICDI	Q54n84	dictyosteli
939	85.5	5.2	780	1	LMBL3_HUMAN	Q96jm7	homo sapien
940	85.5	5.2	780	2	Q4VXE1_HUMAN	Q4vxe1	homo sapien
941	85.5	5.2	786	2	Q21027_CAEEL	Q21027	caenorhabdi
942	85.5	5.2	841	2	Q6R8J4_BRARE	Q6r8j4	brachydanio
943	85.5	5.2	843	2	Q9VYH8_DROME	Q9vyh8	drosophila
944	85.5	5.2	863	2	Q851G7_ORYSA	Q851g7	oryza sativ
945	85.5	5.2	866	2	Q4PDE9_USTMA	Q4pde9	ustilago ma
946	85.5	5.2	878	2	Q55GH4_DICDI	Q55gh4	dictyosteli
947	85.5	5.2	895	2	O80973_ARATH	O80973	arabidopsis
948	85.5	5.2	935	2	Q6R8J3_BRARE	Q6r8j3	brachydanio
949	85.5	5.2	954	2	Q55FS4_DICDI	Q55fs4	dictyosteli
950	85.5	5.2	977	2	Q6R8J2_BRARE	Q6r8j2	brachydanio
951	85.5	5.2	981	2	Q6GQI9_XENLA	Q6gqi9	xenopus lae
952	85.5	5.2	1052	2	Q91G49_IRV6	Q91g49	chilo iride
953	85.5	5.2	1209	2	Q4SFS8_TETNG	Q4sfs8	tetraodon n
954	85.5	5.2	1868	2	Q5TJ69_9VIRU	Q5tj69	cacao swoll
955	85.5	5.2	2448	2	Q8WWQ5_HUMAN	Q8wwq5	homo sapien
956	85.5	5.2	2482	2	Q61GF0_CAEBR	Q61gf0	caenorhabdi
957	85.5	5.2	3346	2	Q822X0_CHLCV	Q822x0	chlamydophi
958	85.5	5.2	4862	2	Q5RI27_BRARE	Q5ri27	brachydanio
959	85.5	5.2	6995	2	Q96RK2_HUMAN	Q96rk2	homo sapien
960	85	5.1	172	2	Q8VC95_MOUSE	Q8vc95	mus musculu
961	85	5.1	255	2	Q86HS8_DICDI	Q86hs8	dictyosteli
962	85	5.1	265	2	Q9GZE5_CAEEL	Q9gze5	caenorhabdi
963	85	5.1	300	2	Q95XH5_CAEEL	Q95xh5	caenorhabdi
964	85	5.1	317	2	Q8BEK4_COWPX	Q8bek4	cowpox viru
965	85	5.1	320	2	Q4SCG1_TETNG	Q4scg1	tetraodon n
966	85	5.1	326	2	Q9VW89_DROME	Q9vw89	drosophila
967	85	5.1	343	1	HXDAA_BRARE	Q90469	brachydanio
968	85	5.1	346	2	Q52JE0_9SAUR	Q52je0	heteronotia
969	85	5.1	346	2	Q52JD9_9SAUR	Q52jd9	heteronotia
970	85	5.1	346	2	Q52JB6_9SAUR	Q52jb6	heteronotia
971	85	5.1	346	2	Q52J84_9SAUR	Q52j84	heteronotia
972	85	5.1	346	2	Q52J86_9SAUR	Q52j86	heteronotia
973	85	5.1	410	2	Q4R5B5_MACFA	Q4r5b5	macaca fasc
974	85	5.1	456	2	Q5R8Q6_PONPY	Q5r8q6	pongo pygma
975	85	5.1	472	2	Q5B2T1_EMENI	Q5b2t1	aspergillus
976	85	5.1	477	2	Q7MR34_WOLSU	Q7mr34	wolinella s
977	85	5.1	478	2	Q5KG84_CRYNE	Q5kg84	cryptococcu
978	85	5.1	503	2	Q8VCF0_MOUSE	Q8vcf0	mus musculu
979	85	5.1	510	2	Q8NJT3_KLULA	Q8njt3	kluyveromyc
980	85	5.1	526	2	Q51YT8_MAGGR	Q51yt8	magnaporthe

981	85	5.1	531	2	Q5TXG4_ANOGA	Q5txg4	anopheles g
982	85	5.1	573	2	Q8H7K9_ORYSA	Q8h7k9	oryza sativ
983	85	5.1	576	2	Q06604_YEAST	Q06604	saccharomyc
984	85	5.1	597	2	Q5AA66_CANAL	Q5aa66	candida alb
985	85	5.1	599	2	Q6C2K2_YARLI	Q6c2k2	yarrowia li
986	85	5.1	601	2	Q6V6S1_DROME	Q6v6s1	drosophila
987	85	5.1	612	2	Q622S9_CAEBR	Q622s9	caenorhabdi
988	85	5.1	625	2	Q58SF8_DROSI	Q58sf8	drosophila
989	85	5.1	627	1	PKNB_LACLA	Q9cef5	lactococcus
990	85	5.1	629	2	Q7ZTW7_BRARE	Q7ztw7	brachydanio
991	85	5.1	639	2	Q6E9T0_LISMO	Q6e9t0	listeria mo
992	85	5.1	655	2	Q4SQL5_TETNG	Q4sql5	tetraodon n
993	85	5.1	657	2	Q54E45_DICDI	Q54e45	dictyosteli
994	85	5.1	782	2	Q8GX37_ARATH	Q8gx37	arabidopsis
995	85	5.1	852	2	Q6CIA5_YARLI	Q6cia5	yarrowia li
996	85	5.1	860	1	VG12_BPB03	Q37893	bacteriopha
997	85	5.1	879	2	Q4IC17_GIBZE	Q4ic17	gibberella
998	85	5.1	911	2	Q7KWL1_DICDI	Q7kwl1	dictyosteli
999	85	5.1	927	2	Q52F88_MAGGR	Q52f88	magnaporthe
1000	85	5.1	989	2	Q9M1E4_ARATH	Q9m1e4	arabidopsis
1001	85	5.1	990	2	Q91803_XENLA	Q91803	xenopus lae
1002	85	5.1	993	2	Q83TJ6_CHLTR	Q83tj6	chlamydia t
1003	85	5.1	1002	2	Q60YJ3_CAEBR	Q60yj3	caenorhabdi
1004	85	5.1	1004	2	Q4RRX1_TETNG	Q4rrx1	tetraodon n
1005	85	5.1	1013	2	Q6CKC8_KLULA	Q6ckc8	kluyveromyc
1006	85	5.1	1025	2	Q626Q9_CAEBR	Q626q9	caenorhabdi
1007	85	5.1	1049	2	Q960E6_DROME	Q960e6	drosophila
1008	85	5.1	1049	2	Q9V6L1_DROME	Q9v6l1	drosophila
1009	85	5.1	1061	2	Q5RA99_PONPY	Q5ra99	pongo pygma
1010	85	5.1	1139	2	Q54Z39_DICDI	Q54z39	dictyosteli
1011	85	5.1	1170	2	Q95011_CAEEL	Q95011	caenorhabdi
1012	85	5.1	1214	2	Q54LU4_DICDI	Q54lu4	dictyosteli
1013	85	5.1	1286	2	Q9VR49_DROME	Q9vr49	drosophila
1014	85	5.1	1354	2	Q9VKA7_DROME	Q9vka7	drosophila
1015	85	5.1	1429	2	Q61Y04_CAEBR	Q61y04	caenorhabdi
1016	85	5.1	1693	2	Q51ZG9_MAGGR	Q51zg9	magnaporthe
1017	85	5.1	1779	2	O52374_9FIRM	O52374	caldicellul
1018	85	5.1	17352	2	Q95YM2_PROCL	Q95ym2	procambarus
1019	84.5	5.1	187	2	Q5CYR7_CRYPV	Q5cyr7	cryptospori
1020	84.5	5.1	220	2	Q9EQG0_MOUSE	Q9eqg0	mus musculu
1021	84.5	5.1	245	2	Q564Z3_CAEEL	Q564z3	caenorhabdi
1022	84.5	5.1	250	2	Q5AP52_CANAL	Q5ap52	candida alb
1023	84.5	5.1	274	2	Q54WW2_DICDI	Q54ww2	dictyosteli
1024	84.5	5.1	278	2	Q51QC1_MAGGR	Q51qc1	magnaporthe
1025	84.5	5.1	313	2	Q8BEJ1_9POXV	Q8bej1	skunkpox vi
1026	84.5	5.1	333	2	Q60JT6_CAEBR	Q60jt6	caenorhabdi
1027	84.5	5.1	345	2	Q691T8_ANOSA	Q691t8	anolis sagr
1028	84.5	5.1	378	2	Q6FNP6_CANGA	Q6fnp6	candida gla
1029	84.5	5.1	396	2	Q51TI2_MAGGR	Q51ti2	magnaporthe
1030	84.5	5.1	423	2	Q6CTJ9_KLULA	Q6ctj9	kluyveromyc
1031	84.5	5.1	456	2	Q8R5M8_MOUSE	Q8r5m8	mus musculu
1032	84.5	5.1	463	2	Q9JX25_NEIMA	Q9jx25	neisseria m
1033	84.5	5.1	493	1	TNR8_RAT	P97525	rattus norv
1034	84.5	5.1	506	2	Q53QT8_HUMAN	Q53qt8	homo sapien
1035	84.5	5.1	522	2	Q4VAS1_HUMAN	Q4vas1	homo sapien
1036	84.5	5.1	524	2	Q54B97_DICDI	Q54b97	dictyosteli
1037	84.5	5.1	532	2	Q6P7V2_MOUSE	Q6p7v2	mus musculu
1038	84.5	5.1	540	1	CH60_STRAP	Q8kj20	streptococc
1039	84.5	5.1	542	2	Q54PF2_DICDI	Q54pf2	dictyosteli
1040	84.5	5.1	547	2	Q4R5X1_MACFA	Q4r5x1	macaca fasc
1041	84.5	5.1	560	2	Q4VAS3_HUMAN	Q4vas3	homo sapien
1042	84.5	5.1	562	1	NUPL_HUMAN	P52594	homo sapien
1043	84.5	5.1	562	2	Q4VAS0_HUMAN	Q4vas0	homo sapien
1044	84.5	5.1	566	2	Q4UKT5_RICFE	Q4ukt5	rickettsia
1045	84.5	5.1	570	2	Q6GMZ9_XENLA	Q6gmz9	xenopus lae
1046	84.5	5.1	582	2	Q58SG6_DROSI	Q58sg6	drosophila
1047	84.5	5.1	622	2	Q6V6E2_DROSI	Q6v6e2	drosophila
1048	84.5	5.1	624	2	Q58SF4_DROSI	Q58sf4	drosophila
1049	84.5	5.1	624	2	Q675N0_CORSU	Q675n0	cornus suec
1050	84.5	5.1	625	2	Q58SF7_DROSI	Q58sf7	drosophila
1051	84.5	5.1	632	2	Q5ELU2_DROME	Q5elu2	drosophila
1052	84.5	5.1	636	2	Q66HZ5_BRARE	Q66hz5	brachydanio
1053	84.5	5.1	653	2	Q4P8I9_USTMA	Q4p8i9	ustilago ma
1054	84.5	5.1	657	2	Q86ID0_DICDI	Q86id0	dictyosteli
1055	84.5	5.1	658	1	SHK1_SCHPO	P50527	schizosacch
1056	84.5	5.1	706	2	Q5CVY0_CRYPV	Q5cvy0	cryptospori
1057	84.5	5.1	709	2	O16783_CAEEL	O16783	caenorhabdi
1058	84.5	5.1	729	2	Q51WE3_MAGGR	Q51we3	magnaporthe
1059	84.5	5.1	773	2	Q8TGH3_9BASI	Q8tgh3	malassezia
1060	84.5	5.1	803	1	IF2_COXBU	Q83bs1	coxiella bu
1061	84.5	5.1	806	2	Q9VCQ7_DROME	Q9vcq7	drosophila
1062	84.5	5.1	814	2	Q6C247_YARLI	Q6c247	yarrowia li
1063	84.5	5.1	834	2	Q877B7_ASPOR	Q877b7	aspergillus
1064	84.5	5.1	931	2	Q5LHK9_BACFN	Q5lhk9	bacteroides
1065	84.5	5.1	931	2	Q64YI7_BACFR	Q64yi7	bacteroides
1066	84.5	5.1	956	2	Q4P0T6_USTMA	Q4p0t6	ustilago ma
1067	84.5	5.1	956	2	Q4SFS4_TETNG	Q4sfs4	tetraodon n
1068	84.5	5.1	1047	2	Q874L3_CANAL	Q874l3	candida alb
1069	84.5	5.1	1057	2	Q5KE83_CRYNE	Q5ke83	cryptococcu
1070	84.5	5.1	1102	2	Q08964_YEAST	Q08964	saccharomyc
1071	84.5	5.1	1103	2	Q6CA70_YARLI	Q6ca70	yarrowia li
1072	84.5	5.1	1161	1	DAN4_YEAST	P47179	saccharomyc
1073	84.5	5.1	1186	2	Q54I94_DICDI	Q54i94	dictyosteli
1074	84.5	5.1	1189	2	Q54CM2_DICDI	Q54cm2	dictyosteli
1075	84.5	5.1	1218	2	Q54YZ6_DICDI	Q54yz6	dictyosteli
1076	84.5	5.1	1355	2	Q86AM1_DICDI	Q86am1	dictyosteli
1077	84.5	5.1	1380	2	Q556L7_DICDI	Q556l7	dictyosteli
1078	84.5	5.1	1420	2	Q4FWR7_LEIMA	Q4fwr7	leishmania
1079	84.5	5.1	1629	2	Q4IB96_GIBZE	Q4ib96	gibberella
1080	84.5	5.1	1743	2	Q8I1L9_PLAVI	Q8i1l9	plasmodium
1081	84.5	5.1	1827	2	Q4Y6M8_PLACH	Q4y6m8	plasmodium
1082	84.5	5.1	1878	2	Q6CPZ4_KLULA	Q6cpz4	kluyveromyc
1083	84.5	5.1	1984	1	SCN9A_RAT	O08562	rattus norv
1084	84.5	5.1	2163	2	Q61TS1_CAEBR	Q61ts1	caenorhabdi
1085	84.5	5.1	2180	2	Q9VAS8_DROME	Q9vas8	drosophila
1086	84.5	5.1	2205	2	Q54C75_DICDI	Q54c75	dictyosteli
1087	84.5	5.1	2206	2	Q4REQ4_TETNG	Q4req4	tetraodon n
1088	84.5	5.1	2378	2	Q7N7Y6_PHOLL	Q7n7y6	photorhabdu
1089	84.5	5.1	2481	2	Q7A4B1_STAAN	Q7a4b1	staphylococ
1090	84.5	5.1	2481	2	Q99QR6_STAAM	Q99qr6	staphylococ
1091	84.5	5.1	2761	2	Q19522_CAEEL	Q19522	caenorhabdi
1092	84.5	5.1	3443	2	Q8JZM8_MOUSE	Q8jzm8	mus musculu
1093	84.5	5.1	22152	2	Q8WXI7_HUMAN	Q8wxi7	homo sapien
1094	84	5.1	197	2	Q54GR3_DICDI	Q54gr3	dictyosteli
1095	84	5.1	262	2	P74577_SYNY3	P74577	synechocyst
1096	84	5.1	305	2	Q4WUZ7_ASPFU	Q4wuz7	aspergillus
1097	84	5.1	309	2	Q63549_RAT	Q63549	rattus norv
1098	84	5.1	335	2	Q9C7W2_ARATH	Q9c7w2	arabidopsis
1099	84	5.1	346	2	Q52J83_9SAUR	Q52j83	heteronotia
1100	84	5.1	346	2	Q52J75_9SAUR	Q52j75	heteronotia
1101	84	5.1	346	2	Q52J73_9SAUR	Q52j73	heteronotia
1102	84	5.1	359	1	MTDH_MEDSA	O82515	medicago sa
1103	84	5.1	359	2	Q53X16_MEDSA	Q53x16	medicago sa
1104	84	5.1	376	2	Q54N82_DICDI	Q54n82	dictyosteli
1105	84	5.1	385	2	Q8T8I3_DROPB	Q8t8i3	drosophila
1106	84	5.1	385	2	Q8T8I5_DROPB	Q8t8i5	drosophila
1107	84	5.1	385	2	Q8T8K2_DROPE	Q8t8k2	drosophila
1108	84	5.1	385	2	Q8T8L0_DROPE	Q8t810	drosophila
1109	84	5.1	399	2	Q5MJ02_TETPY	Q5mj02	tetrahymena
1110	84	5.1	420	2	Q8N7W9_HUMAN	Q8n7w9	homo sapien
1111	84	5.1	420	2	Q8YMH1_ANASP	Q8ymh1	anabaena sp
1112	84	5.1	456	1	NRX3B_BOVIN	Q28143	bos taurus
1113	84	5.1	464	2	Q9VX42_DROME	Q9vx42	drosophila
1114	84	5.1	475	2	Q8FQJ1_COREF	Q8fqj1	corynebacte
1115	84	5.1	487	2	Q8E1P9_STRA5	Q8e1p9	streptococc
1116	84	5.1	487	2	Q8E764_STRA3	Q8e764	streptococc
1117	84	5.1	543	2	Q14879_HUMAN	Q14879	homo sapien
1118	84	5.1	598	2	Q5ELV9_DROSI	Q5elv9	drosophila
1119	84	5.1	610	2	Q4IL56_GIBZE	Q4il56	gibberella
1120	84	5.1	625	2	Q58SH7_DROSI	Q58sh7	drosophila
1121	84	5.1	625	2	Q5ELP1_DROSI	Q5elp1	drosophila
1122	84	5.1	636	1	ENV_MCFF	P15073	mink cell f
1123	84	5.1	639	2	Q6E934_LISMO	Q6e934	listeria mo
1124	84	5.1	640	2	Q55G71_DICDI	Q55g71	dictyosteli
1125	84	5.1	641	2	Q6AJU8_DESPS	Q6aju8	desulfotale
1126	84	5.1	648	2	Q95QX0_CAEEL	Q95qx0	caenorhabdi

1127	84	5.1	668	2	Q5B5D4_EMENI	Q5b5d4	aspergillus
1128	84	5.1	677	2	Q5B9K5_EMENI	Q5b9k5	aspergillus
1129	84	5.1	713	2	Q55RT5_CRYNE	Q55rt5	cryptococcu
1130	84	5.1	730	2	Q6CPU9_KLULA	Q6cpu9	kluyveromyc
1131	84	5.1	758	2	Q51JF4_MAGGR	Q51jf4	magnaporthe
1132	84	5.1	793	2	Q8YAG7_LISMO	Q8yag7	listeria mo
1133	84	5.1	809	2	Q54J73_DICDI	Q54j73	dictyosteli
1134	84	5.1	812	2	Q5TT09_ANOGA	Q5tt09	anopheles g
1135	84	5.1	827	2	Q6IWN3_USTMA	Q6iwn3	ustilago ma
1136	84	5.1	827	2	Q4PBV7_USTMA	Q4pbv7	ustilago ma
1137	84	5.1	836	2	Q56DP0_PLABE	Q56dp0	plasmodium
1138	84	5.1	854	2	Q5ZKA3_CHICK	Q5zka3	gallus gall
1139	84	5.1	855	2	Q4P3C5_USTMA	Q4p3c5	ustilago ma
1140	84	5.1	864	1	AT7L1_HUMAN	Q9ulk2	homo sapien
1141	84	5.1	880	2	Q7YU85_DROME	Q7yu85	drosophila
1142	84	5.1	933	2	Q6ZMZ5_HUMAN	Q6zmz5	h cdna flj1
1143	84	5.1	961	1	BNC1_MOUSE	O35914	mus musculu
1144	84	5.1	996	1	LRP8_MOUSE	Q924x6	mus musculu
1145	84	5.1	1021	2	Q6CXY2_KLULA	Q6cxy2	kluyveromyc
1146	84	5.1	1075	1	FLO5_YEAST	P38894	saccharomyc
1147	84	5.1	1085	2	Q5BLF7_BRARE	Q5blf7	brachydanio
1148	84	5.1	1153	2	Q6A1Q0_DROME	Q6a1q0	drosophila
1149	84	5.1	1326	2	Q5KJA8_CRYNE	Q5kja8	cryptococcu
1150	84	5.1	1331	1	MANB_CALSA	P22533	caldocellum
1151	84	5.1	1343	2	Q960V6_DROME	Q960v6	drosophila
1152	84	5.1	1343	2	Q9W2G6_DROME	Q9w2g6	drosophila
1153	84	5.1	1362	2	Q9V294_PYRAB	Q9v294	pyrococcus
1154	84	5.1	1366	2	Q86AM2_DICDI	Q86am2	dictyosteli
1155	84	5.1	1601	2	Q54L90_DICDI	Q54l90	dictyosteli
1156	84	5.1	1645	2	Q9U263_CAEEL	Q9u263	caenorhabdi
1157	84	5.1	1649	2	Q54LW8_DICDI	Q54lw8	dictyosteli
1158	84	5.1	1832	2	O96503_CRYPV	O96503	cryptospori
1159	84	5.1	2044	2	Q55CR5_DICDI	Q55cr5	dictyosteli
1160	84	5.1	2215	2	Q8IIZ6_PLAF7	Q8iiz6	plasmodium
1161	84	5.1	2233	2	Q7PRT5_ANOGA	Q7prt5	anopheles g
1162	84	5.1	2306	2	Q4WYG2_ASPFU	Q4wyg2	aspergillus
1163	84	5.1	2447	2	Q4RIS7_TETNG	Q4ris7	tetraodon n
1164	83.5	5.0	198	2	Q4WAE1_ASPFU	Q4wae1	aspergillus
1165	83.5	5.0	203	2	Q4VHF5_9MONO	Q4vhf5	bovine resp
1166	83.5	5.0	216	2	Q28501_MACMU	Q28501	macaca mula
1167	83.5	5.0	274	2	Q9EX24_STRCO	Q9ex24	streptomyce
1168	83.5	5.0	279	2	Q14888_HUMAN	Q14888	homo sapien
1169	83.5	5.0	292	2	O68668_BACME	O68668	bacillus me
1170	83.5	5.0	306	2	Q88V34_LACPL	Q88v34	lactobacill
1171	83.5	5.0	306	2	Q9QYL4_MOUSE	Q9qyl4	mus musculu
1172	83.5	5.0	352	1	MYB86_ARATH	Q8lph6	arabidopsis
1173	83.5	5.0	385	2	Q8T8L3_DROMI	Q8t8l3	drosophila
1174	83.5	5.0	385	2	Q83NC5_TROW8	Q83nc5	tropheryma
1175	83.5	5.0	405	2	Q95XV0_CAEEL	Q95xv0	caenorhabdi
1176	83.5	5.0	446	2	Q9Y849_KLULA	Q9y849	kluyveromyc
1177	83.5	5.0	448	2	Q83FT5_TROWT	Q83ft5	tropheryma
1178	83.5	5.0	455	2	Q4INK6_GIBZE	Q4ink6	gibberella
1179	83.5	5.0	465	2	Q84DR0_LISMO	Q84dr0	listeria mo
1180	83.5	5.0	476	2	Q7SEJ2_NEUCR	Q7sej2	neurospora
1181	83.5	5.0	476	2	Q6AYP5_RAT	Q6ayp5	rattus norv
1182	83.5	5.0	486	2	Q84DR1_LISMO	Q84dr1	listeria mo
1183	83.5	5.0	498	1	TNR8_MOUSE	Q60846	mus musculu
1184	83.5	5.0	498	2	Q6C977_YARLI	Q6c977	yarrowia li
1185	83.5	5.0	516	2	Q7YYC5_CRYPV	Q7yyc5	cryptospori
1186	83.5	5.0	575	2	Q58SM2_DROME	Q58sm2	drosophila
1187	83.5	5.0	585	2	Q5SE80_9MONO	Q5se80	avian pneum
1188	83.5	5.0	585	2	Q5SE81_9MONO	Q5se81	avian pneum
1189	83.5	5.0	623	2	Q7XND3_ORYSA	Q7xnd3	oryza sativ
1190	83.5	5.0	624	2	Q58SF5_DROSI	Q58sf5	drosophila
1191	83.5	5.0	624	2	Q5ELP3_DROSI	Q5elp3	drosophila
1192	83.5	5.0	624	2	Q5VFJ5_9ASTE	Q5vfj5	cornus cf.
1193	83.5	5.0	632	2	Q5ELT8_DROME	Q5elt8	drosophila
1194	83.5	5.0	641	2	Q86SD2_CIOIN	Q86sd2	ciona intes
1195	83.5	5.0	669	2	Q7EZY9_ORYSA	Q7ezy9	oryza sativ
1196	83.5	5.0	674	2	Q6APL0_DESPS	Q6apl0	desulfotale
1197	83.5	5.0	789	2	Q57ZE5_9TRYP	Q57ze5	trypanosoma
1198	83.5	5.0	791	2	Q66VC3_9ALPH	Q66vc3	equid herpe
1199	83.5	5.0	800	2	Q8TFG4_SCHPO	Q8tfg4	schizosacch
1200	83.5	5.0	812	2	Q86AW3_DICDI	Q86aw3	dictyosteli
1201	83.5	5.0	822	2	Q54Z52_DICDI	Q54z52	dictyosteli
1202	83.5	5.0	838	2	Q90YM1_BRARE	Q90ym1	brachydanio
1203	83.5	5.0	899	2	Q58CJ5_DROME	Q58cj5	drosophila
1204	83.5	5.0	915	2	Q54BC9_DICDI	Q54bc9	dictyosteli
1205	83.5	5.0	935	2	Q9VGN4_DROME	Q9vgn4	drosophila
1206	83.5	5.0	967	2	Q08294_YEAST	Q08294	saccharomyc
1207	83.5	5.0	976	2	Q9A531_CAUCR	Q9a531	caulobacter
1208	83.5	5.0	984	2	Q4UEB9_THEAN	Q4ueb9	theileria a
1209	83.5	5.0	1001	2	Q05164_YEAST	Q05164	saccharomyc
1210	83.5	5.0	1043	2	Q97E41_CLOAB	Q97e41	clostridium
1211	83.5	5.0	1056	2	Q55P74_CRYNE	Q55p74	cryptococcu
1212	83.5	5.0	1255	2	Q54HF3_DICDI	Q54hf3	dictyosteli
1213	83.5	5.0	1286	2	Q9TXR6_CAEEL	Q9txr6	caenorhabdi
1214	83.5	5.0	1570	2	Q61L27_CAEBR	Q61l27	caenorhabdi
1215	83.5	5.0	1589	2	Q54I34_DICDI	Q54i34	dictyosteli
1216	83.5	5.0	1607	2	Q6CDM9_YARLI	Q6cdm9	yarrowia li
1217	83.5	5.0	1713	2	Q8TGE1_YEAST	Q8tge1	saccharomyc
1218	83.5	5.0	1765	2	Q54WL2_DICDI	Q54wl2	dictyosteli
1219	83.5	5.0	1820	2	Q54F55_DICDI	Q54f55	dictyosteli
1220	83.5	5.0	1855	2	Q4L3P2_STAHJ	Q4l3p2	staphylococ
1221	83.5	5.0	2623	2	Q54SZ1_DICDI	Q54sz1	dictyosteli
1222	83.5	5.0	2656	2	Q4UEK8_THEAN	Q4uek8	theileria a
1223	83.5	5.0	2764	2	Q7Z7D6_HUMAN	Q7z7d6	homo sapien
1224	83.5	5.0	3026	2	Q8ILS9_PLAF7	Q8ils9	plasmodium
1225	83.5	5.0	3175	1	RPOA_EAVBU	P19811	e replicase
1226	83.5	5.0	3372	2	Q864S8_FELCA	Q864s8	felis silve
1227	83.5	5.0	5179	1	MUC2_HUMAN	Q02817	homo sapien
1228	83	5.0	197	2	Q8JL62_GVCF	Q8jl62	choristoneu
1229	83	5.0	198	2	Q7QB72_ANOGA	Q7qb72	anopheles g
1230	83	5.0	207	2	Q4X0I5_ASPFU	Q4x0i5	aspergillus
1231	83	5.0	257	2	Q54HH8_DICDI	Q54hh8	dictyosteli
1232	83	5.0	262	2	Q7PRG9_ANOGA	Q7prg9	anopheles g
1233	83	5.0	277	2	Q5A5U6_CANAL	Q5a5u6	candida alb
1234	83	5.0	291	2	Q6QPG5_9ADEN	Q6qpg5	simian aden
1235	83	5.0	309	2	Q6IEL3_ORYSA	Q6iel3	oryza sativ
1236	83	5.0	309	2	Q7XNY3_ORYSA	Q7xny3	oryza sativ
1237	83	5.0	314	2	Q9H8R7_HUMAN	Q9h8r7	homo sapien
1238	83	5.0	316	2	Q8TD14_HUMAN	Q8td14	homo sapien
1239	83	5.0	337	2	Q7Z5K8_HUMAN	Q7z5k8	homo sapien
1240	83	5.0	342	2	Q54LV1_DICDI	Q54lv1	dictyosteli
1241	83	5.0	345	2	Q691Y6_ANOSA	Q691y6	anolis sagr
1242	83	5.0	346	2	Q8SHB2_RHABR	Q8shb2	rhampholeon
1243	83	5.0	378	2	Q8SXS5_DROME	Q8sxs5	drosophila
1244	83	5.0	382	2	Q9XZZ8_LITSI	Q9xzz8	litomosoide
1245	83	5.0	385	2	Q8T8K5_DROPE	Q8t8k5	drosophila
1246	83	5.0	409	1	RD23B_HUMAN	P54727	homo sapien
1247	83	5.0	409	2	Q53F10_HUMAN	Q53f10	homo sapien
1248	83	5.0	410	2	Q5AYD3_EMENI	Q5ayd3	aspergillus
1249	83	5.0	419	2	Q8TD11_HUMAN	Q8td11	homo sapien
1250	83	5.0	422	2	Q8TD13_HUMAN	Q8td13	homo sapien
1251	83	5.0	463	2	O42665_SCHPO	O42665	schizosacch
1252	83	5.0	485	2	Q9V8B0_DROME	Q9v8b0	drosophila
1253	83	5.0	512	2	Q4I756_GIBZE	Q4i756	gibberella
1254	83	5.0	542	2	Q54SA9_DICDI	Q54sa9	dictyosteli
1255	83	5.0	547	2	Q623V9_CAEBR	Q623v9	caenorhabdi
1256	83	5.0	552	2	Q4N6B9_THEPA	Q4n6b9	theileria p
1257	83	5.0	559	2	Q9VN36_DROME	Q9vn36	drosophila
1258	83	5.0	564	2	Q5CQC1_CRYPV	Q5cqc1	cryptospori
1259	83	5.0	585	2	Q58SG3_DROSI	Q58sg3	drosophila
1260	83	5.0	585	2	Q58SG5_DROSI	Q58sg5	drosophila
1261	83	5.0	585	2	Q58SH2_DROSI	Q58sh2	drosophila
1262	83	5.0	599	2	Q5ELY7_DROME	Q5ely7	drosophila
1263	83	5.0	599	2	Q5ELY8_DROME	Q5ely8	drosophila
1264	83	5.0	600	2	Q59F94_HUMAN	Q59f94	homo sapien
1265	83	5.0	601	1	UBQL4_HUMAN	Q9nrr5	homo sapien
1266	83	5.0	601	2	Q5VYA1_HUMAN	Q5vya1	homo sapien
1267	83	5.0	605	1	WSC4_YEAST	P38739	saccharomyc
1268	83	5.0	632	2	Q5ELU0_DROME	Q5elu0	drosophila
1269	83	5.0	632	2	Q5ELU8_DROME	Q5elu8	drosophila
1270	83	5.0	639	2	Q6E8Z2_LISMO	Q6e8z2	listeria mo
1271	83	5.0	653	1	NUMB_MOUSE	Q9qzs3	mus musculu
1272	83	5.0	661	2	Q9V8S2_DROME	Q9v8s2	drosophila

1273	83	5.0	679	2	Q59DM1_CAEEL	Q59dm1	caenorhabdi
1274	83	5.0	737	1	KNS1_YEAST	P32350	saccharomyc
1275	83	5.0	738	1	VU47_HHV6Z	P52549	human herpe
1276	83	5.0	762	2	Q86AG3_DICDI	Q86ag3	dictyosteli
1277	83	5.0	769	2	Q17921_CAEEL	Q17921	caenorhabdi
1278	83	5.0	771	2	Q4WCD2_ASPFU	Q4wcd2	aspergillus
1279	83	5.0	786	2	Q9FDM5_STRAG	Q9fdm5	streptococc
1280	83	5.0	794	2	Q55CQ4_DICDI	Q55cq4	dictyosteli
1281	83	5.0	797	1	VGLX_EHV1B	P28968	equine herp
1282	83	5.0	806	2	Q5R6R3_PONPY	Q5r6r3	pongo pygma
1283	83	5.0	814	2	Q55AJ1_DICDI	Q55aj1	dictyosteli
1284	83	5.0	826	2	Q8V0L5_9ALPH	Q8v0l5	equid herpe
1285	83	5.0	832	2	Q60J61_CAEBR	Q60j61	caenorhabdi
1286	83	5.0	858	2	Q9H8D9_HUMAN	Q9h8d9	homo sapien
1287	83	5.0	866	1	VGLX_EHV1V	Q6s6w0	equine herp
1288	83	5.0	866	2	O39781_9ALPH	O39781	equid herpe
1289	83	5.0	867	2	O39782_9ALPH	O39782	equid herpe
1290	83	5.0	904	2	Q5SW65_HUMAN	Q5sw65	homo sapien
1291	83	5.0	955	2	Q5SQZ9_HUMAN	Q5sqz9	homo sapien
1292	83	5.0	963	1	LRP8_HUMAN	Q14114	homo sapien
1293	83	5.0	963	2	Q5SW67_HUMAN	Q5sw67	homo sapien
1294	83	5.0	985	2	Q5KL22_CRYNE	Q5kl22	cryptococcu
1295	83	5.0	985	2	Q55V60_CRYNE	Q55v60	cryptococcu
1296	83	5.0	1002	2	Q6CBD5_YARLI	Q6cbd5	yarrowia li
1297	83	5.0	1030	2	Q7QV30_GIALA	Q7qv30	giardia lam
1298	83	5.0	1069	2	Q519R3_ENTHI	Q519r3	entamoeba h
1299	83	5.0	1080	2	Q510Y4_ENTHI	Q510y4	entamoeba h
1300	83	5.0	1126	2	Q8E6U1_STRA3	Q8e6u1	streptococc
1301	83	5.0	1183	2	Q8GCD1_CHLAU	Q8gcd1	chloroflexu
1302	83	5.0	1184	2	Q4IHX0_GIBZE	Q4ihx0	gibberella
1303	83	5.0	1215	1	GP158_HUMAN	Q5t848	homo sapien
1304	83	5.0	1221	2	Q4X1D8_ASPFU	Q4x1d8	aspergillus
1305	83	5.0	1265	2	Q9P2G7_HUMAN	Q9p2g7	homo sapien
1306	83	5.0	1266	2	Q4X245_ASPFU	Q4x245	aspergillus
1307	83	5.0	1377	2	Q54ND2_DICDI	Q54nd2	dictyosteli
1308	83	5.0	1458	2	Q54PJ4_DICDI	Q54pj4	dictyosteli
1309	83	5.0	1646	2	Q5CFZ6_CRYHO	Q5cfz6	cryptospori
1310	83	5.0	1686	2	Q7RZE6_NEUCR	Q7rze6	neurospora
1311	83	5.0	2081	2	Q5SQZ8_HUMAN	Q5sqz8	homo sapien
1312	83	5.0	2162	2	Q8N3U0_HUMAN	Q8n3u0	homo sapien
1313	83	5.0	2210	2	Q7Z3E7_HUMAN	Q7z3e7	homo sapien
1314	83	5.0	2478	2	Q9LCH2_STAAU	Q9lch2	staphylococ
1315	83	5.0	2478	2	Q9RL69_STAAU	Q9rl69	staphylococ
1316	83	5.0	2478	2	Q5HE44_STAAC	Q5he44	staphylococ
1317	83	5.0	3300	2	Q4N127_THEPA	Q4n127	theileria p
1318	83	5.0	6011	2	Q4U447_POLCB	Q4u447	polyangium
1319	82.5	5.0	184	2	Q7PRM2_ANOGA	Q7prm2	anopheles g
1320	82.5	5.0	197	2	Q26878_TRYCR	Q26878	trypanosoma
1321	82.5	5.0	231	2	Q86LC2_9CNID	Q86lc2	zoanthus sp
1322	82.5	5.0	252	2	Q6GZ06_9MONO	Q6gz06	avian pneum
1323	82.5	5.0	258	2	Q7SGP8_NEUCR	Q7sgp8	neurospora
1324	82.5	5.0	286	2	Q7SAZ7_NEUCR	Q7saz7	neurospora
1325	82.5	5.0	290	1	LECR_CLALU	Q39527	cladrastis
1326	82.5	5.0	308	2	Q7XA59_LILLO	Q7xa59	lilium long
1327	82.5	5.0	326	2	Q9NFX5_CERCA	Q9nfx5	ceratitis c
1328	82.5	5.0	345	2	Q690V6_ANOSA	Q690v6	anolis sagr
1329	82.5	5.0	345	2	Q690V7_ANOSA	Q690v7	anolis sagr
1330	82.5	5.0	345	2	Q690X3_ANOSA	Q690x3	anolis sagr
1331	82.5	5.0	345	2	Q691U6_ANOSA	Q691u6	anolis sagr
1332	82.5	5.0	345	2	Q691Z2_ANOSA	Q691z2	anolis sagr
1333	82.5	5.0	345	2	Q692A4_ANOSA	Q692a4	anolis sagr
1334	82.5	5.0	345	2	Q692C2_9SAUR	Q692c2	anolis quad
1335	82.5	5.0	346	2	Q5CE07_CRYHO	Q5ce07	cryptospori
1336	82.5	5.0	383	1	VE2_HPV57	P22155	human papil
1337	82.5	5.0	389	2	Q64BB8_9ARCH	Q64bb8	uncultured
1338	82.5	5.0	389	2	Q6GXX0_9VIRU	Q6gxx0	swine hepat
1339	82.5	5.0	389	2	Q6GXX2_9VIRU	Q6gxx2	swine hepat
1340	82.5	5.0	389	2	Q6GXX3_9VIRU	Q6gxx3	swine hepat
1341	82.5	5.0	391	2	Q54XF0_DICDI	Q54xf0	dictyosteli
1342	82.5	5.0	400	2	Q9SQF7_BRAJU	Q9sqf7	brassica ju
1343	82.5	5.0	416	2	Q9K8G4_BACHD	Q9k8g4	bacillus ha
1344	82.5	5.0	425	2	Q54VC3_DICDI	Q54vc3	dictyosteli
1345	82.5	5.0	452	2	Q6CE56_YARLI	Q6ce56	yarrowia li
1346	82.5	5.0	456	1	Y883_HAEIN	P44917	haemophilus
1347	82.5	5.0	456	2	Q4QM25_HAEI8	Q4qm25	haemophilus
1348	82.5	5.0	459	2	Q55SZ8_CRYNE	Q55sz8	cryptococcu
1349	82.5	5.0	464	2	Q9C247_NEUCR	Q9c247	neurospora
1350	82.5	5.0	508	2	Q6VNX4_DROSA	Q6vnx4	drosophila
1351	82.5	5.0	517	2	Q5AF50_CANAL	Q5af50	candida alb
1352	82.5	5.0	540	1	CH60_STRA3	Q8cx22	streptococc
1353	82.5	5.0	540	1	CH60_STRA5	Q8cx00	streptococc
1354	82.5	5.0	540	2	Q7UPM2_RHOBA	Q7upm2	rhodopirell
1355	82.5	5.0	569	2	Q9SL10_ARATH	Q9sl10	arabidopsis
1356	82.5	5.0	582	2	Q54W91_DICDI	Q54w91	dictyosteli
1357	82.5	5.0	598	2	Q5ELW5_DROSI	Q5elw5	drosophila
1358	82.5	5.0	599	2	Q5ELY0_DROME	Q5ely0	drosophila
1359	82.5	5.0	602	2	Q4V707_DROME	Q4v707	drosophila
1360	82.5	5.0	607	2	Q8GNR4_LISMO	Q8gnr4	listeria mo
1361	82.5	5.0	623	2	Q5LYX7_STRT1	Q5lyx7	streptococc
1362	82.5	5.0	623	2	Q5M3J0_STRT2	Q5m3j0	streptococc
1363	82.5	5.0	624	2	Q5VFJ4_CORSU	Q5vfj4	cornus suec
1364	82.5	5.0	624	2	Q5VFJ6_CORSU	Q5vfj6	cornus suec
1365	82.5	5.0	624	2	Q5VFJ7_CORSU	Q5vfj7	cornus suec
1366	82.5	5.0	624	2	Q5VFJ9_9ASTE	Q5vfj9	cornus unal
1367	82.5	5.0	624	2	Q5VFK1_9ASTE	Q5vfk1	cornus cf.
1368	82.5	5.0	624	2	Q675N1_CORSU	Q675n1	cornus suec
1369	82.5	5.0	635	2	O66065_FIBSU	O66065	fibrobacter
1370	82.5	5.0	639	2	Q6E910_LISMO	Q6e910	listeria mo
1371	82.5	5.0	639	2	Q6E940_LISMO	Q6e940	listeria mo
1372	82.5	5.0	641	2	Q5KHD0_CRYNE	Q5khd0	cryptococcu
1373	82.5	5.0	646	2	Q4J6E4_SULAC	Q4j6e4	sulfolobus
1374	82.5	5.0	686	2	Q8NVE4_STAAW	Q8nve4	staphylococ
1375	82.5	5.0	698	2	Q74LM8_LACJO	Q74lm8	lactobacill
1376	82.5	5.0	706	2	Q5CL90_CRYHO	Q5cl90	cryptospori
1377	82.5	5.0	711	2	Q7YYX9_CRYPV	Q7yyx9	cryptospori
1378	82.5	5.0	726	1	NFI1_YEAST	Q12216	saccharomyc
1379	82.5	5.0	728	2	Q7NB51_MYCGA	Q7nb51	mycoplasma
1380	82.5	5.0	782	2	Q6CNV3_KLULA	Q6cnv3	kluyveromyc
1381	82.5	5.0	790	1	ADA30_HUMAN	Q9ukf2	homo sapien
1382	82.5	5.0	790	2	Q5T3X6_HUMAN	Q5t3x6	homo sapien
1383	82.5	5.0	808	2	Q8I123_CAEEL	Q8i123	caenorhabdi
1384	82.5	5.0	825	2	Q03088_YEAST	Q03088	saccharomyc
1385	82.5	5.0	833	2	Q602T7_METCA	Q602t7	methylococc
1386	82.5	5.0	848	2	Q6GP20_XENLA	Q6gp20	xenopus lae
1387	82.5	5.0	871	1	POB1_SCHPO	O74653	schizosacch
1388	82.5	5.0	876	2	Q6XLI5_BRARE	Q6xli5	brachydanio
1389	82.5	5.0	896	2	Q52B52_MAGGR	Q52b52	magnaporthe
1390	82.5	5.0	988	2	Q8UVU2_XENLA	Q8uvu2	xenopus lae
1391	82.5	5.0	993	2	Q92JC5_RICCN	Q92jc5	rickettsia
1392	82.5	5.0	1042	2	Q54IH7_DICDI	Q54ih7	dictyosteli
1393	82.5	5.0	1091	2	Q7SDT8_NEUCR	Q7sdt8	neurospora
1394	82.5	5.0	1124	2	Q50XX8_ENTHI	Q50xx8	entamoeba h
1395	82.5	5.0	1163	2	Q7PY32_ANOGA	Q7py32	anopheles g
1396	82.5	5.0	1167	2	Q54CK8_DICDI	Q54ck8	dictyosteli
1397	82.5	5.0	1181	2	Q52A92_MAGGR	Q52a92	magnaporthe
1398	82.5	5.0	1206	1	FMN1B_MOUSE	Q05859	mus musculu
1399	82.5	5.0	1258	2	Q4HVR5_GIBZE	Q4hvr5	gibberella
1400	82.5	5.0	1258	2	Q86IA2_DICDI	Q86ia2	dictyosteli
1401	82.5	5.0	1259	2	Q614L3_CAEBR	Q614l3	caenorhabdi
1402	82.5	5.0	1260	2	Q55G51_DICDI	Q55g51	dictyosteli
1403	82.5	5.0	1261	2	Q7R2F4_GIALA	Q7r2f4	giardia lam
1404	82.5	5.0	1267	2	Q54VU8_DICDI	Q54vu8	dictyosteli
1405	82.5	5.0	1343	2	Q61MH3_CAEBR	Q61mh3	caenorhabdi
1406	82.5	5.0	1371	2	Q9VU22_DROME	Q9vu22	drosophila
1407	82.5	5.0	1383	2	Q5B1U5_EMENI	Q5b1u5	aspergillus
1408	82.5	5.0	1460	1	PMPC_CHLMU	Q9pjy1	chlamydia m
1409	82.5	5.0	1468	1	FMN1A_MOUSE	Q05860	mus musculu
1410	82.5	5.0	1472	2	Q6V9R4_STRPU	Q6v9r4	strongyloce
1411	82.5	5.0	1478	1	LPHN2_BOVIN	O97817	bos taurus
1412	82.5	5.0	1809	2	Q4Q8Z9_LEIMA	Q4q8z9	leishmania
1413	82.5	5.0	1969	2	Q7SEZ5_NEUCR	Q7sez5	neurospora
1414	82.5	5.0	2311	1	ROS_CHICK	P08941	gallus gall
1415	82.5	5.0	2381	2	Q54QC0_DICDI	Q54qc0	dictyosteli
1416	82.5	5.0	4483	2	Q51QB7_MAGGR	Q51qb7	magnaporthe
1417	82	4.9	166	2	Q5IE00_PINTA	Q5ie00	pinus taeda
1418	82	4.9	166	2	Q5IE20_PINTA	Q5ie20	pinus taeda

1419	82	4.9	166	2	Q56VT9_9STRA	Q56vt9 pythium aph
1420	82	4.9	208	2	Q8IWS2_HUMAN	Q8iws2 homo sapien
1421	82	4.9	208	2	Q8N131_HUMAN	Q8n131 homo sapien
1422	82	4.9	219	2	Q61B16_CAEBR	Q61b16 caenorhabdi
1423	82	4.9	226	2	Q5A1Y4_CANAL	Q5a1y4 candida alb
1424	82	4.9	235	2	Q5TM43_MACMU	Q5tm43 macaca mula
1425	82	4.9	236	2	Q9LM00_PINTA	Q9lm00 pinus taeda
1426	82	4.9	250	2	Q8FSI6_COREF	Q8fsi6 corynebacte
1427	82	4.9	255	2	Q8I1N1_DROER	Q8i1n1 drosophila
1428	82	4.9	260	2	O27007_METTH	O27007 methanobact
1429	82	4.9	282	2	Q9FSR0_ORYSA	Q9fsr0 oryza sativ
1430	82	4.9	288	2	Q4YH55_PLABE	Q4yh55 plasmodium
1431	82	4.9	301	2	Q4I1K5_GIBZE	Q4i1k5 gibberella
1432	82	4.9	302	2	Q4I5S3_GIBZE	Q4i5s3 gibberella
1433	82	4.9	311	2	Q55LZ4_CRYNE	Q55lz4 cryptococcu
1434	82	4.9	311	2	Q5K8S4_CRYNE	Q5k8s4 cryptococcu
1435	82	4.9	323	2	Q9W1I7_DROME	Q9w1i7 drosophila
1436	82	4.9	338	2	Q8T8J5_DROPS	Q8t8j5 drosophila
1437	82	4.9	339	2	Q9VUX8_DROME	Q9vux8 drosophila
1438	82	4.9	345	2	Q4FKI2_9TRYP	Q4fki2 trypanosoma
1439	82	4.9	345	2	Q690W9_ANOSA	Q690w9 anolis sagr
1440	82	4.9	345	2	Q691G8_ANOSA	Q691g8 anolis sagr
1441	82	4.9	346	2	Q52JD1_9SAUR	Q52jd1 heteronotia
1442	82	4.9	361	2	Q514P3_ENTHI	Q514p3 entamoeba h
1443	82	4.9	367	2	Q59KD1_CANAL	Q59kd1 candida alb
1444	82	4.9	385	2	Q8T8K9_DROPE	Q8t8k9 drosophila
1445	82	4.9	385	2	Q8T8L2_DROPE	Q8t8l2 drosophila
1446	82	4.9	388	2	Q60KQ3_CAEBR	Q60kq3 caenorhabdi
1447	82	4.9	389	2	O76573_CAEEL	O76573 caenorhabdi
1448	82	4.9	392	2	Q5A484_CANAL	Q5a484 candida alb
1449	82	4.9	397	2	Q55DL3_DICDI	Q55dl3 dictyosteli
1450	82	4.9	410	1	LAMP2_HUMAN	P13473 homo sapien
1451	82	4.9	411	2	Q6Q3G8_HUMAN	Q6q3g8 homo sapien
1452	82	4.9	466	2	Q4PCZ4_USTMA	Q4pcz4 ustilago ma
1453	82	4.9	475	2	Q50ST5_ENTHI	Q50st5 entamoeba h
1454	82	4.9	477	1	MYBPH_HUMAN	Q13203 homo sapien
1455	82	4.9	479	2	Q61AU9_CAEBR	Q61au9 caenorhabdi
1456	82	4.9	483	2	Q9W4M2_DROME	Q9w4m2 drosophila
1457	82	4.9	490	2	Q7PV84_ANOGA	Q7pv84 anopheles g
1458	82	4.9	491	2	Q50RL8_ENTHI	Q50rl8 entamoeba h
1459	82	4.9	495	2	Q4RZZ8_TETNG	Q4rzz8 tetraodon n
1460	82	4.9	520	2	Q4XP68_PLACH	Q4xp68 plasmodium
1461	82	4.9	538	2	Q75JS0_DICDI	Q75js0 dictyosteli
1462	82	4.9	544	2	Q8IG67_CAEEL	Q8ig67 caenorhabdi
1463	82	4.9	562	2	Q51ND8_MAGGR	Q51nd8 magnaporthe
1464	82	4.9	584	1	CEJ1_CAEEL	Q17802 caenorhabdi
1465	82	4.9	588	2	Q4S6Y8_TETNG	Q4s6y8 tetraodon n
1466	82	4.9	599	2	Q5ELX9_DROME	Q5elx9 drosophila
1467	82	4.9	599	2	Q9V680_DROME	Q9v680 drosophila
1468	82	4.9	599	2	Q5ELY3_DROME	Q5ely3 drosophila
1469	82	4.9	600	2	Q4PHL9_USTMA	Q4phl9 ustilago ma
1470	82	4.9	601	2	Q6V6S0_DROME	Q6v6s0 drosophila
1471	82	4.9	625	2	Q5VFL0_9ASTE	Q5vfl0 cornus cf.
1472	82	4.9	630	2	Q96YH6_SULTO	Q96yh6 sulfolobus
1473	82	4.9	641	2	Q83363_9GAMR	Q83363 murine leuk
1474	82	4.9	670	2	Q9YWM0_GALV	Q9ywm0 gibbon ape
1475	82	4.9	673	2	Q91VK6_MOUSE	Q91vk6 mus musculu
1476	82	4.9	693	2	Q27394_CAEEL	Q27394 caenorhabdi
1477	82	4.9	704	2	Q4QGK1_LEIMA	Q4qgk1 leishmania
1478	82	4.9	713	2	Q5KG88_CRYNE	Q5kg88 cryptococcu
1479	82	4.9	720	1	NUP2_YEAST	P32499 saccharomyc
1480	82	4.9	746	2	Q82GM0_STRAW	Q82gm0 streptomyce
1481	82	4.9	761	2	Q9C9S3_ARATH	Q9c9s3 arabidopsis
1482	82	4.9	763	2	Q5A8K3_CANAL	Q5a8k3 candida alb
1483	82	4.9	771	2	Q86NN7_DROME	Q86nn7 drosophila
1484	82	4.9	776	2	Q4RHT1_TETNG	Q4rht1 tetraodon n
1485	82	4.9	780	2	Q5CHI0_CRYHO	Q5chi0 cryptospori
1486	82	4.9	789	2	Q9VY98_DROME	Q9vy98 drosophila
1487	82	4.9	824	2	Q6CY28_KLULA	Q6cy28 kluyveromyc
1488	82	4.9	846	2	O57577_CYNPY	O57577 cynops pyrr
1489	82	4.9	847	2	Q6ZQ82_MOUSE	Q6zq82 mus musculu
1490	82	4.9	894	2	Q7FL10_ARATH	Q7fl10 arabidopsis
1491	82	4.9	894	2	Q9C8I6_ARATH	Q9c8i6 arabidopsis
1492	82	4.9	911	2	Q8GWK9_ARATH	Q8gwk9 arabidopsis
1493	82	4.9	911	2	Q9SA18_ARATH	Q9sa18 arabidopsis
1494	82	4.9	926	1	YIY8_SCHPO	Q9uui5 schizosacch
1495	82	4.9	926	2	Q7LDM3_HUMAN	Q7ldm3 homo sapien
1496	82	4.9	939	2	Q592W9_BRARE	Q592w9 brachydanio
1497	82	4.9	943	1	YL61_SCHPO	Q8tfg9 schizosacch
1498	82	4.9	957	2	Q9UKN0_HUMAN	Q9ukn0 homo sapien
1499	82	4.9	963	2	Q99MX4_GLAVO	Q99mx4 glaucomys v
1500	82	4.9	971	2	Q6A036_MOUSE	Q6a036 mus musculu

ALIGNMENTS

RESULT 1
Q9UNF4_HUMAN
ID Q9UNF4_HUMAN PRELIMINARY; PRT; 322 AA.
AC Q9UNF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hyaluronic acid receptor (XLKD1).
GN Name=HAR; ORFNames=UNQ230;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF127670; AAD49220.2; -; mRNA.
DR EMBL; AY358925; AAQ89284.1; -; mRNA.
DR HSSP; P98066; 1O7B.
DR Ensembl; ENSG00000133800; Homo sapiens.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR PROSITE; PS50963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;

Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
Db 1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy 61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

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Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              |||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 2
Q8TC18_HUMAN
ID   Q8TC18_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q8TC18;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Extracellular link domain containing 1.
GN   Name=XLKD1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026231; AAH26231.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSG00000133800; Homo sapiens.
DR   HGNC; HGNC:14687; XLKD1.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35183 MW;  0B1EDBD76CE4610A CRC64;

  Query Match             99.2%;  Score 1643;  DB 2;  Length 322;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-124;
  Matches  321;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIRKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              |||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 3
Q9Y5Y7_HUMAN
ID   Q9Y5Y7_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q9Y5Y7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA   Jackson D.G.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
DR   EMBL; AF118108; AAD42764.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006928; P:cell motility; TAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
SQ   SEQUENCE   322 AA;  35238 MW;  0EBEA56729CEFFF7 CRC64;

  Query Match             98.9%;  Score 1638;  DB 2;  Length 322;
  Best Local Similarity   99.1%;  Pred. No. 4.9e-124;
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  Matches  319;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVDTALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              |||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFGAYCYNSSDTWTNSRIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              ||||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 4
Q6UC88_BOVIN
ID   Q6UC88_BOVIN PRELIMINARY;      PRT;   322 AA.
AC   Q6UC88;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cell surface retention sequence binding protein-1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA   Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA   Huang J.S.;
RT   "Cloning, expression, characterization and role in autocrine cell
RT   growth of cell surface retention sequence binding protein-1.";
RL   J. Biol. Chem. 278:43855-43869(2003).
DR   EMBL; AY372937; AAQ85130.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35561 MW;  4901DA1BF92648AE CRC64;

  Query Match           70.9%;  Score 1174;  DB 2;  Length 322;
  Best Local Similarity 71.1%;  Pred. No. 1.6e-86;
  Matches  229;  Conservative   34;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||: ||| ||| |||||||||||||:||:||   |||||:|||:||    ||||||:||
Db          1 MAKFFSLGLLLASIWTTRLLVQGSLRSEEISILGPCRIMGVTLVTKKTQPLLNFTEAQEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              |||:||:|| :|||| | |  ||||||||| : |||| ||  ||||||:||||:||:  :
Db         61 CRLVGLTLASQDQVEEARKFGFETCSYGWVKNQFVVIPRIISNPKCGKSGVGVVIWRSSL 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              | :  :||:|||| | |||:|||||| ||:|||:||| ||: :|||||:|  |
Db        121 SSRHRSYCHNSSDIWINSCLPEIITTDDPLFNTETATYTTKLMVSDSTHSELSTDGPDYV 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGGVPTAL 240
              ||  |  |||| ||::||||:|| ||:|| ::|| |  ::|: |||||| |||||||||
Db        181 TTTVAPPLASTSTPRKRKLICITEAFMDTSAVATERESDIQNRPAFKNEAVGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              |||||||| |||||  ||||||||||||||||||||||||||||:||||||||||
Db        241 LVLALLFFAAAAGLAVCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKADDSNPNEESKKM 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              :| ||| ||| ||||||||||
Db        301 NKTPEEPKSPPKTTVRCLEAEV 322


RESULT 5
Q8BHC0_MOUSE
ID   Q8BHC0_MOUSE PRELIMINARY;      PRT;   318 AA.
AC   Q8BHC0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE   cDNA, RIKEN full-length enriched library, clone:1200012G08
DE   product:extra cellular link domain-containing 1, full insert
DE   sequence).
GN   Name=Xlkd1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
```

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC038653; AAH38653.1; -; mRNA.
DR EMBL; BC038892; AAH38892.1; -; mRNA.
DR EMBL; AK004726; BAC25094.1; -; mRNA.
DR HSSP; P98066; 1O7B.
DR Ensembl; ENSMUSG00000030787; Mus musculus.
DR MGI; MGI:2136348; Xlkd1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS50963; LINK_2; 1.
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

Query Match 66.6%; Score 1103; DB 2; Length 318;
Best Local Similarity 69.7%; Pred. No. 8.9e-81;
Matches 221; Conservative 30; Mismatches 62; Indels 4; Gaps 3;

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Qy          6 SLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG 65
              |||||| ||||||  |||:   ::|||  :|||||: || :  | |:||||| |||::||
Db          6 SLVLLLASIWTTRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLG 64

Qy         66 LSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFA 125
              |:|| :||||:| |: |||||||||: | || ||  ||:||||| |||||  | |::|
Db         65 LTLASRDQVESAQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFK 124

Qy        126 AYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTP 185
              |||:|||||| |||||||:||  |: :||  |  ||| || | |  :|| || |   ||
Db        125 AYCHNSSDTWVNSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT- 181

Qy        186 PAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLAL 245
              ||  ||: |: | ||:|||: |  ||:|||| || : ||||||||||||||||||||||
Db        182 RAPPLTSMARKTKKICITEVYTEPITMATETEAFVASGAAFKNEAAGFGGVPTALLVLAL 241

Qy        246 LFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPE 305
              ||||||| |  |||||||||||||| ||||||||||||||||:| | ||||||| ||||
Db        242 LFFGAAAVLAVCYVKRYVKAFPFTTKNQQKEMIETKVVKEEKADDVNANEESKKTIKNPE 301

Qy        306 ESKSPSKTTVRCLEAEV 322
              |:||| ||||||||||
Db        302 EAKSPPKTTVRCLEAEV 318
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RESULT 6
Q99NE4_MOUSE
ID Q99NE4_MOUSE PRELIMINARY; PRT; 318 AA.
AC Q99NE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hyaluronan receptor precursor.
GN   Name=Xlkd1; Synonyms=LYVE-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;
RA   Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT   "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT   endothelium.";
RL   J. Biol. Chem. 276:19420-19430(2001).
DR   EMBL; AJ311501; CAC33082.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   MGI; MGI:2136348; Xlkd1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR   GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor; Signal.
FT   SIGNAL       1     23       Potential.
FT   CHAIN       24    318       LYVE-1.
SQ   SEQUENCE   318 AA;  34641 MW;  1248974A16113330 CRC64;

  Query Match             66.1%;  Score 1095;  DB 2;  Length 318;
  Best Local Similarity   69.1%;  Pred. No. 4e-80;
  Matches  219;  Conservative   30;  Mismatches   64;  Indels    4;  Gaps    3;

Qy          6 SLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG 65
              |||  | ||||||  |||:   ::|||  :|||||: || :  | |:||||| |||::||
Db          6 SLVFFLASIWTTRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLG 64

Qy         66 LSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFA 125
              |:|| :||||:| |: |||||||||||: | || ||  ||:|||| |||||  | |::|
Db         65 LTLASRDQVESAQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFK 124

Qy        126 AYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTP 185
              |||:|||||| |||||||:||  |: :||  |  ||| || | |  :|| || |   ||
Db        125 AYCHNSSDTWVNSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT- 181

Qy        186 PAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLAL 245
              ||  ||: |: | ||:|||: |  ||:|||| || : ||||||||||||||||||||
Db        182 RAPPLTSMARKTKKICITEVYTEPITMATETEAFVASGAAFKNEAAGFGGVPTALLVLAL 241

Qy        246 LFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPE 305
              ||||||| |  |||||||||||||| ||||||||||||||||:| | ||||||| ||||
Db        242 LFFGAAAVLAVCYVKRYVKAFPFTTKNQQKEMIETKVVKEEKADDVNANEESKKTIKNPE 301

Qy        306 ESKSPSKTTVRCLEAEV 322
              |:||| ||||||||||
Db        302 EAKSPPKTTVRCLEAEV 318
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RESULT 7
Q7YS22_PIG
ID   Q7YS22_PIG  PRELIMINARY;      PRT;   201 AA.
AC   Q7YS22;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA   Sellke F.W., Bianchi C.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY304537; AAP69946.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
FT   NON_TER      1      1
FT   NON_TER    201    201
SQ   SEQUENCE   201 AA;  22219 MW;  BAAF34E7EACBBAE3 CRC64;

  Query Match             43.8%;  Score 726.5;  DB 2;  Length 201;
  Best Local Similarity   70.1%;  Pred. No. 1.4e-50;
  Matches  141;  Conservative   21;  Mismatches   36;  Indels    3;  Gaps    2;

Qy         81 SFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI 140
              |||||||||| | |:|| || ||||||||| |||:|:  :|::| |||:||||| |||||
Db          1 SFETCSYGWVKDQFLVIPRIYPNPKCGKNGKGVLVWRHSLSQKFEAYCHNSSDTRTNSCI 60

Qy        141 PEIITTKDPIFNTQTATQTTEFIVSDSTYSVAS--PYSTI-PAPTTTPPAPASTSIPRRK 197
              |||| | || ||| ||  |||  |:| | | ::  | |:: |   ||    |:|| ||::
Db         61 PEIIPTNDPTFNTNTAPYTTEMTVNDRTSSSSTNGPSSSVMPTVVTTSLPLATTSTPRKR 120

Qy        198 KLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFC 257
              ||||:|| |||||:||||| ::||: |||||| ||||:|||||||||||| |||||  |
Db        121 KLICITEAFMETSTISTETELYIENRTAFKNEAIGFGGIPTALLVLALLFFAAAAGLAVC 180

Qy        258 YVKRYVKAFPFTNKNQQKEMI 278
              |||||||||||||||||||||
Db        181 YVKRYVKAFPFTNKNQQKEMI 201
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RESULT 8
Q58E15_XENLA
ID   Q58E15_XENLA PRELIMINARY;      PRT;   392 AA.
AC   Q58E15;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
```

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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092113; AAH92113.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1       1
FT   NON_TER     392     392
SQ   SEQUENCE   392 AA;  43658 MW;  AF47C05AC550C6A1 CRC64;

  Query Match             14.8%;  Score 245;  DB 2;  Length 392;
  Best Local Similarity   34.9%;  Pred. No. 2.8e-11;
  Matches   58;  Conservative   18;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         34 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 93
              :|||  |:  | |     ||  :| : | :|  |:|    |:| ||   |||| |||: |
Db         33 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTSIANYTQLEIALDFGFETCRYGWIEDR 92

Qy         94 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 143
               |:| || ||| |  |  |:       | ::  ||||:|:|   ||:| :
Db         93 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 151

Qy        144 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 188
               | : ||  :||           ||          | |||    | |
Db        152 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 189


RESULT 9
Q6GM56_XENLA
ID   Q6GM56_XENLA PRELIMINARY;      PRT;   441 AA.
AC   Q6GM56;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC443701 protein (Fragment).
GN   Name=LOC443701;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC074228; AAH74228.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   441 AA;  49207 MW;  DF9AA596D506D1A1 CRC64;

  Query Match             14.5%;  Score 241;  DB 2;  Length 441;
  Best Local Similarity   34.3%;  Pred. No. 6.7e-11;
  Matches   57;  Conservative   19;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         34 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 93
              :|||  |:  | |     ||  :| : | :|  ::|    |:| ||   |||| |||: |
Db         32 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTTIASYAQLEIALDFGFETCRYGWIEDR 91

Qy         94 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 143
               |:| || ||| |  |  |:       | ::  ||||:|:|   ||:| :
Db         92 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 150

Qy        144 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 188
               | : ||  :||           ||          | |||    | |
Db        151 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 188


RESULT 10
CD44_CRIGR
ID   CD44_CRIGR     STANDARD;      PRT;   362 AA.
AC   P20944;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
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```
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN   Name=CD44;
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90304889; PubMed=1694723; DOI=10.1016/0092-8674(90)90694-A;
RA   Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
RT   "CD44 is the principal cell surface receptor for hyaluronate.";
RL   Cell 61:1303-1313(1990).
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- INDUCTION: By EBV.
CC   -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC       addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC       of phosphate to cytoplasmic domain serine residues.
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M33827; AAA36967.1; -; mRNA.
DR   PIR; A35616; A35616.
DR   HSSP; P98066; 1TSG.
DR   SMR; P20944; 23-170.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW   Transmembrane.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    362       CD44 antigen.
FT   TOPO_DOM    23    269       Extracellular (Potential).
FT   TRANSMEM   270    290       Potential.
FT   TOPO_DOM   291    362       Cytoplasmic (Potential).
FT   DOMAIN      34    122       Link.
FT   REGION     226    269       Stem.
FT   COMPBIAS   152    160       Arg/Lys-rich (basic).
FT   MOD_RES     23     23       Pyrrolidone carboxylic acid (By
FT                               similarity).
FT   MOD_RES    292    292       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES    326    326       Phosphoserine (By similarity).
FT   CARBOHYD    27     27       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    59     59       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   112    112       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   122    122       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   174    174       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   256    256       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    55    120       By similarity.
FT   DISULFID    79     99       By similarity.
SQ   SEQUENCE   362 AA;  39775 MW;  E89EB434E9EEC948 CRC64;

  Query Match           14.1%;  Score 233.5;  DB 1;  Length 362;
  Best Local Similarity  26.3%;  Pred. No. 2.1e-10;
  Matches   91;  Conservative   45;  Mismatches  147;  Indels   63;  Gaps   12;

Qy         24 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFE 83
              ||  |:: : ::||  |:  | |     :: ||| : |:    :|   ||:  ||   ||
Db         18 SLAHEQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVMALSKGFE 77

Qy         84 TCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI 143
              || ||:: :| ||| || ||  |  |  || |     |  :  ||:|:|     |
Db         78 TCRYGFI-EGHVVIPRIQPNAICAANHTGVYILTSNTS-HYDTYCFNASAPLEEDC---- 131

Qy        144 ITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPTTTPPAPAS-------- 190
               |:   : |:     |   :  | | ||    | |    | |  ||    :|
Db        132 -TSVTDLPNSFEGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNTTDDDVSSGSSSEKST 190

Qy        191 -------TSIPRRKKLICVTEVFMETSTMSTE--------------------TEPFVEN 222
                    | :|          : :   |||:|                      ||   |
Db        191 SGGYVFHTYLPTIHSTADQDDPYFIGSTMATRDQDSSMDPRGNSLTVTDGSKLTEHSSGN 250

Qy        223 KAAFKNEAAGFGG---VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 279
              : :  |  :  ||   ||  |:||| |    | | |     :                |:|:::
Db        251 QDSGLNSTSRPGGKPRVPEWLIVLASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 304

Qy        280 TKVVKEEKANDSNPNEESKKTDKNPE----ESKSPSKTTVRCLEAE 321
                  |  |  |:| : :  |: |     :| ||:|  : : |:
Db        305 NS--GNGKVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQFMTAD 348


RESULT 11
Q6P8A2_XENTR
ID   Q6P8A2_XENTR PRELIMINARY;      PRT;   437 AA.
AC   Q6P8A2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75816.
GN   Name=MGC75816;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061327; AAH61327.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
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```
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   437 AA;  49108 MW;  7088441D0E138C10 CRC64;

  Query Match           13.9%;  Score 229.5;  DB 2;  Length 437;
  Best Local Similarity  26.3%;  Pred. No. 5.6e-10;
  Matches   82;  Conservative   34;  Mismatches  111;  Indels   85;  Gaps   10;

Qy         34 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 93
              :|||  |:  | |    ||  :| : |  |  ::|    :| |    ||||:|||: |
Db         24 ISCRFKGVFHVEKYDRYALNREDAIKLCHELNTTIANLTLMEIAQDIGFETCRYGWIEDR 83

Qy         94 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIP----------E 142
               ||| || ||| |  |  |:       | :: |||||:|:|   || |          :
Db         84 -VVIPRIKPNPICAANYTGIFTLGNNDSLRYDAYCYNASETEDKSCEPVLLLNETDLSHK 142

Qy        143 IITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAP---------TTTPPA-PASTS 192
              | : ||  :||   :|     |  | :   |    | |          || |   | ||
Db        143 TIDSYDPTLDTQNPFRTQNSDKSGDTVTDPGPAMITPDPGQDWDDIQGTTDPHGDPFSTK 202

Qy        193 IPRRKKLICVTEVFMETSTMSTE--TEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGA 250
                          : |||   || :::       :|:  ||
Db        203 ---------------GDGSDSTEQTNEPGIDH--------SGYQEVPG------------ 227

Qy        251 AAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKK---------- 299
                           ||    ::  |  :|:    | ::||: : |  :
Db        228 -------------HHFPEGTDHEVNE-FDTEHTTTENSHDSDGHYEHPRHHDHQDNTGRD 273

Qy        300 -TDKNPEESKSP 310
               |  : | || |
Db        274 YTRPDDESSKEP 285


RESULT 12
O70509_RAT
ID   O70509_RAT  PRELIMINARY;      PRT;   364 AA.
AC   O70509;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Glycoprotein CD44s (Cd44 protein).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA   Stevens J.W.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney, and Pituitary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065147; AAC17117.1; -; mRNA.
DR   EMBL; BC061531; AAH61531.1; -; mRNA.
DR   EMBL; BC085703; AAH85703.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O70509; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   364 AA;  39725 MW;  BA249776C4419AA7 CRC64;

  Query Match           13.7%;  Score 227;  DB 2;  Length 364;
  Best Local Similarity  24.3%;  Pred. No. 7.2e-10;
  Matches   86;  Conservative   55;  Mismatches  153;  Indels   60;  Gaps   13;

Qy         15 WTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQV 74
              |    |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:
Db         10 WGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQM 69

Qy         75 ETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDT 134
              | ||   |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|
Db         70 ELALSKGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAP 128

Qy        135 WTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------- 182
                  |      |:   : |:          |    :  | | ||    | |    | |
Db        129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVS 183

Qy        183 -------TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFK-----N 228
                    :||       | :|  :       : |    ||::| : :  :: : |     :
Db        184 SGSTIEKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATSDGDSSMDPRGGFDTVTHGS 243

Qy        229 EAAGFGG------------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTN 270
              | ||                      :|  |::|| |    |  | |     :
Db        244 ELAGHSSGNQDSGVTTTSGPARRPQIPEWLIILASL-LALALILAVC-----IAVNSRRR 297

Qy        271 KNQQKEMIETK---VVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 321
                |:|:::       |:: | :: |  | || :     :| |::|  : : |:
Db        298 CGQKKKLVINSGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPTETPDQFMTAD 350
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```
RESULT 13
CD44_PAPHA
ID   CD44_PAPHA     STANDARD;      PRT;   362 AA.
AC   P14745;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN   Name=CD44;
OS   Papio hamadryas (Hamadryas baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9557;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 66-74.
RX   MEDLINE=89282830; PubMed=2471974;
RA   Idzerda R.L., Carter W.G., Nottenburg C., Wayner E.A., Gallatin W.M.,
RA   St John T.;
RT   "Isolation and DNA sequence of a cDNA clone encoding a lymphocyte
RT   adhesion receptor for high endothelium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663(1989).
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC       addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC       of phosphate to cytoplasmic domain serine residues.
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M22452; AAA35385.1; -; mRNA.
DR   HSSP; P98066; 1TSG.
DR   SMR; P14745; 20-168.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Direct protein sequencing;
KW   Glycoprotein; Phosphorylation; Proteoglycan;
KW   Pyrrolidone carboxylic acid; Receptor; Signal; Transmembrane.
FT   SIGNAL        1     20       By similarity.
FT   CHAIN        21    362       CD44 antigen.
FT   TOPO_DOM     21    269       Extracellular (Potential).
FT   TRANSMEM    270    290       Potential.
FT   TOPO_DOM    291    362       Cytoplasmic (Potential).
FT   DOMAIN       32    120       Link.
FT   REGION      225    269       Stem.
FT   COMPBIAS    150    158       Arg/Lys-rich (basic).
FT   MOD_RES      21     21       Pyrrolidone carboxylic acid (Probable).
FT   MOD_RES     292    292       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES     326    326       Phosphoserine (By similarity).
FT   CARBOHYD     25     25       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     57     57       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    100    100       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    110    110       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    120    120       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     53    118       By similarity.
FT   DISULFID     77     97       By similarity.
FT   CONFLICT     67     67       E -> V (in Ref. 1; AA sequence).
SQ   SEQUENCE   362 AA;  39379 MW;  578BFCE7C3D52FFF CRC64;

  Query Match            13.4%;  Score 222.5;  DB 1;  Length 362;
  Best Local Similarity  25.5%;  Pred. No. 1.7e-09;
  Matches   92;  Conservative   43;  Mismatches  127;  Indels   99;  Gaps   16;

Qy         20 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 79
              ||| ||   :: : ::||  ||  | |     :: ||| : |:    :|    |:| ||
Db         14 LVQLSL--AQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS 71

Qy         80 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 139
              |||| ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPGEDC 129

Qy        140 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP------APT---------- 182
               |:   : |      |   :  | | |     | | |      :||
Db        130 -----TSVTDLPNAFDGPITITIVNRDGTRYVKKGEYRTNPEDINPSSPTDDDVSSGSSS 184

Qy        183 ---------------TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAF 226
                            |:|| |                    | ||:  |   :: ||
Db        185 ERSSTLGGYIFYNHFSTSPPIPDEDG--------------PWITDSTDRTPATRDQGAF 229

Qy        227 K----------NEAAGF------GG------------VPTALLVLALLFFGAAAGLGFCY 258
                       :|:||       ||            :|  |::|| |    |  | |
Db        230 DPSGGSHTTHGSESAGHSHGSREGGANTTSGPLRTPQIPEWLIILASL-LALALILAVC- 287

Qy        259 VKRYVKAFPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----NPEESKSPS 311
                 :          |:|:::      |:: |::  |  | ||  :     | | |::|
Db        288 ----IAVNSRRRCGQKKKLVINNGNGAVEDRKSSGLN-GEASKSQEMVHLVNKESSETPD 342

Qy        312 K 312
               :
Db        343 Q 343


RESULT 14
CD44_RAT
ID   CD44_RAT       STANDARD;      PRT;   503 AA.
AC   P26051; Q99021;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE   24).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC   STRAIN=BDIX; TISSUE=Pancreas;
RX   MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA   Guenthert U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA   Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT   "A new variant of glycoprotein CD44 confers metastatic potential to
RT   rat carcinoma cells.";
RL   Cell 65:13-24(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RA   Stevens J.W., Midura R.J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SULFATION OF TYR-288.
RX   PubMed=9692903;
RA   Sleeman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT   "CD44 variant exon v5 encodes a tyrosine that is sulphated.";
RL   Eur. J. Biochem. 255:74-80(1998).
```

```
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=2; Synonyms=Long, Meta-1;
CC         IsoId=P26051-1; Sequence=Displayed;
CC       Name=1; Synonyms=Short;
CC         IsoId=P26051-2; Sequence=VSP_005330;
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC       can be more or less sulfated (By similarity).
CC   -!- PTM: Phosphorylated; activation of PKC results in the
CC       dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC       and the phosphorylation of Ser-433 (By similarity).
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M61875; AAA53532.1; -; mRNA.
DR   EMBL; M61874; AAA53534.1; -; mRNA.
DR   EMBL; U52179; AAA97915.1; -; mRNA.
DR   EMBL; U46957; AAA92920.1; -; mRNA.
DR   PIR; B38745; B38745.
DR   HSSP; P98066; 1TSG.
DR   SMR; P26051; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0007155; P:cell adhesion; NAS.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW   Sulfation; Transmembrane.
FT   SIGNAL        1     21
FT   CHAIN        22    503       CD44 antigen.
FT   TOPO_DOM     22    410       Extracellular (Potential).
FT   TRANSMEM    411    431       Potential.
FT   TOPO_DOM    432    503       Cytoplasmic (Potential).
FT   DOMAIN       35    124       Link.
FT   REGION      228    410       Stem.
FT   COMPBIAS    154    162       Arg/Lys-rich (basic).
FT   MOD_RES      22     22       Pyrrolidone carboxylic acid (Probable).
FT   MOD_RES     288    288       Sulfotyrosine (in isoform 2).
FT   MOD_RES     433    433       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES     467    467       Phosphoserine (By similarity).
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     60     60       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    114    114       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    124    124       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    266    266       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     56    122       By similarity.
FT   DISULFID     80    100       By similarity.
FT   VARSPLIC    224    385       IATTPWVSAHTKQNQERTQWNPIHSNPEVLLQTTTRMTDID
FT                                RNSTSAHGENWTQEPQPPFNNHEYQDEEETPHATSTTWADP
FT                                NSTTEEAATQKEKWFENEWQGKNPPTPSEDSHVTEGTTASA
FT                                HNNHPSQRMTTQSQEDVSWTDFFDPISHPMGQGHQTESK
FT                                -> SDGDSSMDPRGGFDTVTHGSELA (in isoform
FT                                1).
FT                                /FTId=VSP_005330.
FT   CONFLICT     74     74       R -> S (in Ref. 2).
SQ   SEQUENCE   503 AA;  55946 MW;  FB489D009BD4EE22 CRC64;

  Query Match             13.4%;  Score 222;  DB 1;  Length 503;
  Best Local Similarity   25.7%;  Pred. No. 2.7e-09;
  Matches   84;  Conservative   40;  Mismatches  165;  Indels   38;  Gaps   11;

Qy         15 WTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQV 74
              |    |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:
Db         10 WGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQM 69

Qy         75 ETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDT 134
              | ||:  |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|
Db         70 ELALRKGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAP 128

Qy        135 WTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------- 182
                |      |:   : |:     |   :  | | ||    | |    | |
Db        129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVS 183

Qy        183 -------TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFKNEAAGF 233
                    :||      | :|  :      : |   ||::|  | |:|        |  :
Db        184 SGSTIEKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATIATTPWVSAHTKQNQERTQW 243

Qy        234 GGV---PTALLVLALLFFGAAAGLGFCYVKRYVK--AFPFTNKNQQKEMIETKVVKEEKA 288
               :   | ||                  : : : :    || |   | |  ||
Db        244 NPIHSNPEVLLQTTTRMTDIDRNSTSAHGENWTQEPQPPFNNHEYQDEE-ETPHATSTTW 302

Qy        289 NDSNPNEESKKTDK-----NPEESKSP 310
               | |   |   | |     |  : |:|
Db        303 ADPNSTTEEAATQKEKWFENEWQGKNP 329


RESULT 15
O08779_RAT
ID   O08779_RAT  PRELIMINARY;      PRT;   780 AA.
AC   O08779;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD44 protein.
GN   Name=CD44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BDX; TISSUE=Pancreas;
RA   Hofmann M.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U96138; AAB54002.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O08779; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   780 AA;  85917 MW;  CC4D35AB1EA7377C CRC64;
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Query Match 13.2%; Score 219.5; DB 2; Length 780;
Best Local Similarity 24.9%; Pred. No. 7.3e-09;
Matches 86; Conservative 45; Mismatches 144; Indels 71; Gaps 13;

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Qy         15 WTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQV 74
Db         10 WGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQM 69

Qy         75 ETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDT 134
Db         70 ELALRKGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAP 128

Qy        135 WTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------- 182
Db        129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVS 183

Qy        183 -------TTPPA-PASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAG-- 232
Db        184 SGSTIEKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLAT-----IASTVYSKSHATAQK 238

Qy        233 --------FGG---------VPTALLVLALLFFGAA------AGLGFCYVKRYVKAFPFT 269
Db        239 QNNWIWSWFGNSQSTTQTQDSPTTTATTALMTTPETPPKRQEAQNWFSW---------FF 289

Qy        270 NKNQQKEMIETKVVKEEKANDSN-----PNEESK-KTDKNPEESKS 309
Db        290 QPSESKSHLHTTTKMPGTESNTNPTGWKPNEENEDETDKYPNFSGS 335
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Search completed: March 20, 2006, 14:12:56
Job time : 127.488 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:29 ; Search time 14.4292 Seconds
(without alignments)
2147.153 Million cell updates/sec

Title: US-10-063-510-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLLTSIWTTRLL.....NPEESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	229.5	13.9	363	2	A37009	CD44 homolog membr
2	222.5	13.4	362	2	A30901	lymphocyte adhesio
3	222.5	13.4	365	2	A34424	CD44 membrane glyc
4	222	13.4	503	2	B38745	cell adhesion mole
5	217.5	13.1	362	2	A35616	T-cell surface gly
6	208.5	12.6	366	2	A53286	cell-surface glyco
7	205	12.4	361	2	JH0417	cell adhesion mole
8	202.5	12.2	351	2	S45305	CD44 antigen precu
9	202	12.2	742	2	A47195	lymphocyte homing
10	199.5	12.0	426	2	JH0518	lymphocyte homing
11	199.5	12.0	493	2	S13530	CD44E protein, epi
12	198	11.9	395	2	I77371	CD44R5 - human
13	196.5	11.9	699	2	I37369	epican - human
14	186	11.2	359	2	S24240	lymphocyte surface
15	148.5	9.0	2109	1	I50421	aggrecan precursor
16	145.5	8.8	3562	2	A47171	chondroitin sulfat
17	145	8.8	277	2	A41735	hyaluronate-bindin
18	145	8.8	1069	2	T42681	hypothetical prote
19	144	8.7	275	2	JC6506	tumor necrosis fac
20	143	8.6	2327	2	T42630	aggrecan - bovine
21	137	8.3	276	2	A47290	TSG-6 homolog PS4
22	131.5	7.9	2124	2	A28452	proteoglycan core
23	131	7.9	2132	1	A55182	aggrecan precursor
24	130.5	7.9	883	2	S57653	brevican precursor
25	130.5	7.9	883	2	S49126	brevican precursor
26	130.5	7.9	2415	1	A39086	aggrecan precursor
27	128.5	7.8	912	2	A54423	brevican precursor
28	121	7.3	1340	2	A39808	proteoglycan core
29	117	7.1	340	2	JC7505	brain link protein
30	116	7.0	2397	1	A55535	versican precursor
31	115	6.9	370	2	S29139	aggrecan - pig (fr
32	115	6.9	1643	2	T14274	versican precursor
33	115	6.9	3381	2	T42389	versican precursor
34	114.5	6.9	1257	2	S28764	neurocan precursor
35	112	6.8	390	1	QQBE77	glycoprotein I pre
36	111.5	6.7	402	2	S73773	dihydrolipoamide a
37	111.5	6.7	909	1	QRXLL2	LDL receptor 2 pre
38	111	6.7	2409	1	A60979	versican precursor
39	108	6.5	354	1	LKHU	proteoglycan link
40	108	6.5	645	2	T29818	hypothetical prote
41	107.5	6.5	739	2	T21769	hypothetical prote
42	107	6.5	355	1	LKCH	proteoglycan link
43	107	6.5	371	2	A53908	brevican precursor
44	107	6.5	408	1	LKRT2	proteoglycan link
45	107	6.5	1268	2	S52781	neurocan - mouse
46	105.5	6.4	113	2	A55885	chondroitin sulfat
47	104.5	6.3	862	2	S43922	versican - pig-tai
48	104	6.3	354	1	S04243	proteoglycan link
49	104	6.3	354	1	S42938	proteoglycan link
50	103.5	6.2	1229	2	T25697	hypothetical prote
51	101.5	6.1	380	2	T28081	hypothetical prote
52	101.5	6.1	768	2	T00073	hypothetical prote
53	101	6.1	708	2	T19474	hypothetical prote
54	100	6.0	378	2	I46268	brevican precursor
55	100	6.0	1251	2	T21389	hypothetical prote
56	99.5	6.0	1092	1	JN0635	neural cell adhesi
57	99	6.0	896	2	T22061	hypothetical prote
58	99	6.0	5376	2	T42215	zonadhesin - mouse
59	98.5	5.9	796	2	T21460	hypothetical prote
60	98	5.9	771	2	T34376	hypothetical prote
61	97.5	5.9	909	1	QRXLL1	LDL receptor 1 pre
62	96.5	5.8	465	2	S46759	hypothetical prote
63	96.5	5.8	660	2	JW0067	chitinase (EC 3.2.
64	96	5.8	449	2	T33257	hypothetical prote
65	96	5.8	1088	1	IJXLNL	neural cell adhesi
66	95.5	5.8	376	2	S52137	MID2 protein - yea
67	95.5	5.8	1471	2	B48218	neurexin III-alpha
68	94.5	5.7	1272	2	S26180	neurofascin - chic
69	94.5	5.7	1390	2	T18883	hypothetical prote
70	94	5.7	1241	2	S01827	period clock prote
71	93	5.6	930	2	B72537	hypothetical prote
72	92.5	5.6	477	2	S53362	mucin 5AC (clone J
73	92.5	5.6	569	2	AI1347	hypothetical prote
74	92.5	5.6	851	2	T22696	hypothetical prote
75	92.5	5.6	927	2	T24031	hypothetical prote
76	92.5	5.6	1367	2	S74285	BUD3 protein - yea
77	92	5.6	429	1	JC5861	endo-1,4-beta-xyla
78	92	5.6	846	2	T21700	hypothetical prote
79	92	5.6	966	2	S25365	CYC8 protein - yea
80	91.5	5.5	411	2	A33664	96K lysosomal memb
81	91.5	5.5	639	2	S20887	actA protein precu
82	91.5	5.5	639	2	AE1100	actin-assembly ind
83	91.5	5.5	672	2	T32557	hypothetical prote
84	91.5	5.5	681	2	S33316	structural protein
85	91	5.5	246	2	T33965	hypothetical prote
86	91	5.5	747	2	T34329	hypothetical prote
87	91	5.5	2172	2	T20145	hypothetical prote
88	90.5	5.5	575	2	S29315	chaperonin 60 - cu
89	90.5	5.5	662	2	A45155	mucin FIM-C.1 - Af
90	90	5.4	388	2	S36500	E2 protein - human
91	90	5.4	1007	2	T24643	hypothetical prote
92	90	5.4	1367	1	S48478	glucan 1,4-alpha-g
93	89.5	5.4	518	2	T49778	hypothetical prote
94	89.5	5.4	1369	2	S70713	protein-tyrosine k
95	89	5.4	307	1	GSPF3	salivary glue prot
96	89	5.4	416	1	A31959	lysosome-associate
97	89	5.4	517	2	T20658	probable zinc meta
98	89	5.4	5170	2	T15348	hypothetical prote
99	88.5	5.3	193	2	A71415	hypothetical prote
100	88.5	5.3	721	2	B90487	hypothetical prote
101	88.5	5.3	770	2	T22808	hypothetical prote
102	88.5	5.3	1101	2	S15271	endoglucanase C (E

103	88	5.3	456	2	T31483	hypothetical prote
104	88	5.3	564	2	T25945	hypothetical prote
105	88	5.3	602	2	AD2067	hypothetical prote
106	88	5.3	761	2	T00940	hypothetical prote
107	88	5.3	1631	1	SAZQK1	major merozoite su
108	88	5.3	3507	2	T34513	hypothetical prote
109	88	5.3	3570	2	T45025	mucin MUC5B, trach
110	87.5	5.3	825	2	T48431	hypothetical prote
111	87.5	5.3	1085	2	S40476	Ca(2+)-sensing rec
112	87.5	5.3	1091	1	IJCHNL	neural cell adhesi
113	87.5	5.3	1802	2	S69703	HKR1 protein precu
114	87.5	5.3	2817	2	B97033	uncharacterized pr
115	87	5.3	235	2	PC2022	mucin like protein
116	87	5.3	752	2	E72616	hypothetical prote
117	87	5.3	1016	2	H71460	probable outer mem
118	87	5.3	1506	2	T30886	integumentary muci
119	87	5.3	1537	2	S53465	flocculation prote
120	86.5	5.2	400	1	A28172	spasmolysin precur
121	86.5	5.2	461	2	T22946	hypothetical prote
122	86.5	5.2	503	2	S63257	probable membrane
123	86.5	5.2	550	2	T29919	hypothetical prote
124	86.5	5.2	740	1	FOLJHD	gag polyprotein -
125	86.5	5.2	1777	2	T34369	hypothetical prote
126	86.5	5.2	2616	2	A57096	nudel protein prec
127	86	5.2	333	2	T27883	hypothetical prote
128	86	5.2	1785	2	A45546	major merozoite su
129	85.5	5.2	575	2	S29316	chaperonin 60 - cu
130	85.5	5.2	649	2	T04606	protein kinase hom
131	85.5	5.2	786	2	T16509	hypothetical prote
132	85.5	5.2	895	2	T02597	Mutator-like trans
133	85	5.1	265	2	T33695	hypothetical prote
134	85	5.1	576	2	S59829	hypothetical prote
135	85	5.1	627	2	G86860	serine/threonine p
136	85	5.1	989	2	T47503	hypothetical prote
137	85	5.1	990	2	I51618	nucleolar phosphop
138	85	5.1	1162	2	T21557	hypothetical prote
139	85	5.1	1779	2	T31085	xylanase - Caldice
140	84.5	5.1	463	2	B82001	probable amino-aci
141	84.5	5.1	493	2	JC5486	membrane glycoprot
142	84.5	5.1	562	2	A57088	nucleoporin-like p
143	84.5	5.1	658	2	T39500	serine/threonine-s
144	84.5	5.1	658	2	S60170	protein kinase Pak
145	84.5	5.1	709	2	T28712	hypothetical prote
146	84.5	5.1	1102	2	S65235	probable membrane
147	84.5	5.1	1161	2	S57180	probable membrane
148	84.5	5.1	2481	2	D90011	FmtB protein [impo
149	84.5	5.1	2761	2	T21064	hypothetical prote
150	84	5.1	262	2	S76772	hypothetical prote
151	84	5.1	335	2	H96667	AP2-containing DNA
152	84	5.1	420	2	AB2426	hypothetical prote
153	84	5.1	426	2	B53580	neurexin III beta
154	84	5.1	543	2	S35047	mucin JUL7 - human
155	84	5.1	636	1	VCVWFS	env polyprotein -
156	84	5.1	793	2	AH1094	probable peptidogl
157	84	5.1	996	2	JE0237	apolipoprotein E r
158	84	5.1	1075	2	S48992	flocculation prote
159	84	5.1	1331	2	A48954	mannan endo-1,4-be
160	84	5.1	1362	2	A75207	amylopullulanase P
161	84	5.1	1832	2	T31113	mucin-like glycopr
162	84	5.1	3020	2	A43932	mucin 2 precursor,
163	83.5	5.0	216	2	I51920	mucin - rhesus mac
164	83.5	5.0	279	2	S53363	mucin 5AC (clone J
165	83.5	5.0	446	2	T45525	WSC4 homolog [impo
166	83.5	5.0	967	2	S66852	hypothetical prote
167	83.5	5.0	976	2	A87576	peptidase, M16 fam
168	83.5	5.0	1043	2	F97302	hypothetical prote
169	83.5	5.0	1286	2	A88396	protein M01E10.2 [
170	83.5	5.0	3175	1	RRWVEV	genome polyprotein
171	83	5.0	221	2	S53649	ribosomal protein
172	83	5.0	409	2	S44346	RAD23 protein homo
173	83	5.0	463	2	T38444	hypothetical prote
174	83	5.0	605	2	S48940	hypothetical prote
175	83	5.0	737	1	S64767	probable serine/th
176	83	5.0	738	2	T44194	hypothetical prote
177	83	5.0	797	1	VGBEX1	glycoprotein X pre
178	83	5.0	866	2	T45462	membrane glycoprot
179	83	5.0	867	2	T45463	membrane glycoprot
180	83	5.0	977	2	T16232	hypothetical prote
181	82.5	5.0	290	2	S66355	lectin-related sto
182	82.5	5.0	383	1	S15624	E2 protein - human
183	82.5	5.0	416	2	B84030	stage VI sporulati
184	82.5	5.0	456	1	H64099	probable amino aci
185	82.5	5.0	569	2	B84470	Mutator-like trans
186	82.5	5.0	726	2	S67044	NFI1 protein - yea
187	82.5	5.0	825	2	S62042	probable membrane
188	82.5	5.0	871	2	T43427	pob1 protein - fis
189	82.5	5.0	993	2	F97717	hypothetical prote
190	82.5	5.0	1206	2	S24407	formin isoform IV
191	82.5	5.0	1407	2	T18381	latrophilin-2 (spl
192	82.5	5.0	1420	2	T18385	latrophilin-2 (spl
193	82.5	5.0	1422	2	T18383	latrophilin-2, spl
194	82.5	5.0	1435	2	T18387	latrophilin-2 (spl
195	82.5	5.0	1450	2	T18382	latrophilin-2 (spl
196	82.5	5.0	1460	2	D81675	polymorphic membra
197	82.5	5.0	1463	2	T18386	latrophilin-2 (spl
198	82.5	5.0	1465	2	T18384	latrophilin-2 (spl
199	82.5	5.0	1468	2	S11515	formin - mouse
200	82.5	5.0	1478	2	T18388	latrophilin-2 (spl
201	82.5	5.0	2311	1	TVCHSR	kinase-related pro
202	82	4.9	260	1	G69223	molybdate-binding
203	82	4.9	389	2	T33340	hypothetical prote
204	82	4.9	410	1	B31959	lysosome-associate
205	82	4.9	410	1	JC4317	lysosome-associate
206	82	4.9	476	2	A46118	myosin-binding pro
207	82	4.9	544	2	T15175	hypothetical prote
208	82	4.9	577	2	G89430	protein K02E2.3 [i
209	82	4.9	584	2	T19061	hypothetical prote
210	82	4.9	693	2	T19551	mucin-like protein
211	82	4.9	720	2	S51340	nucleoporin NUP2 -
212	82	4.9	761	2	A96810	probable Mutator-l
213	82	4.9	894	2	B96557	probable receptor
214	82	4.9	911	2	E86438	hypothetical prote
215	82	4.9	926	2	T38198	COPII coated vesic
216	82	4.9	973	2	A97522	ribonuclease E, RN
217	82	4.9	977	2	AC2741	ribonuclease E [im
218	82	4.9	1021	2	S64506	protein kinase BUB
219	82	4.9	1023	2	JC4013	major acidic nucle
220	82	4.9	1083	2	S59780	hypothetical prote
221	82	4.9	1127	2	T25804	hypothetical prote
222	82	4.9	1672	2	C81675	polymorphic membra
223	82	4.9	2738	2	E88320	protein F07A11.6 [
224	82	4.9	26926	1	I38344	titin, cardiac mus
225	81.5	4.9	235	2	T47379	hypothetical prote
226	81.5	4.9	369	2	T01196	transcription fact
227	81.5	4.9	386	2	B97212	protein containing
228	81.5	4.9	463	2	B81228	sodium/alanine sym
229	81.5	4.9	636	2	S63131	probable membrane
230	81.5	4.9	687	2	A40711	RNA polymerase II
231	81.5	4.9	860	2	AG1612	DNA mismatch repai
232	81.5	4.9	869	2	T22422	hypothetical prote
233	81.5	4.9	1151	2	T18297	zinc-finger protei
234	81.5	4.9	1212	2	T13804	shs protein - frui
235	81.5	4.9	1216	2	F88473	protein F40H6.5 [i
236	81.5	4.9	1419	2	T30531	agglutinin-like ad
237	81.5	4.9	1445	1	A48148	protein-tyrosine-p
238	81.5	4.9	1513	2	T23681	hypothetical prote
239	81.5	4.9	2282	2	T42717	DNA-binding protei
240	81	4.9	339	2	T25562	hypothetical prote
241	81	4.9	413	2	S55890	plasma protein rec
242	81	4.9	422	1	BMRT2Y	synaptotagmin II -
243	81	4.9	651	2	C56653	membrane glycoprot
244	81	4.9	683	2	T10720	NADPH-ferrihemopro
245	81	4.9	683	2	E86358	F12K8.13 protein -
246	81	4.9	911	2	S46497	aspartate kinase (
247	81	4.9	1047	2	A55617	masquerade precurs
248	81	4.9	1128	2	A49960	bud emergence prot

249	81	4.9	1169	2	S38181	flocculation prote
250	81	4.9	1367	2	S51959	hypothetical prote
251	81	4.9	1609	2	S25345	probable membrane
252	81	4.9	1726	2	A39401	merozoite surface
253	81	4.9	6642	2	T29757	protein UNC-89 - C
254	80.5	4.9	148	1	S07723	immediate-early se
255	80.5	4.9	391	1	S15617	E2 protein - human
256	80.5	4.9	441	2	T31482	hypothetical prote
257	80.5	4.9	543	2	T22585	hypothetical prote
258	80.5	4.9	592	2	T34446	hypothetical prote
259	80.5	4.9	595	2	A42086	CD30 antigen precu
260	80.5	4.9	742	2	T33514	hypothetical prote
261	80.5	4.9	798	2	T34248	hypothetical prote
262	80.5	4.9	918	2	I58178	glutamate receptor
263	80.5	4.9	1124	2	F71719	hypothetical prote
264	80.5	4.9	1159	1	A44280	inner layer protei
265	80.5	4.9	2225	2	T26063	hypothetical prote
266	80	4.8	153	2	S67294	hypothetical prote
267	80	4.8	177	1	RGBYGI	regulatory protein
268	80	4.8	345	2	T21776	hypothetical prote
269	80	4.8	359	2	T13478	hypothetical prote
270	80	4.8	415	2	AE2237	hypothetical prote
271	80	4.8	451	2	S71754	cellular hepatitis
272	80	4.8	468	2	A55116	vacuolar ATPase (E
273	80	4.8	521	2	S69559	hypothetical prote
274	80	4.8	650	2	T41681	probable serine/th
275	80	4.8	667	2	A40713	cylicin I - bovine
276	80	4.8	688	2	T18263	S-layer protein -
277	80	4.8	702	2	T34313	hypothetical prote
278	80	4.8	725	2	A41258	a-agglutinin core
279	80	4.8	881	2	S56032	probable membrane
280	80	4.8	1013	1	S04200	NAD ADP-ribosyltra
281	80	4.8	1348	2	S27812	probable epidermal
282	79.5	4.8	152	2	T15170	hypothetical prote
283	79.5	4.8	165	2	A27195	histone H1 - Tetra
284	79.5	4.8	194	2	F72525	hypothetical prote
285	79.5	4.8	354	2	T46740	microfilarial shea
286	79.5	4.8	461	1	A35356	tumor necrosis fac
287	79.5	4.8	510	2	B72007	conserved hypothet
288	79.5	4.8	510	2	A86618	CT861 hypothetical
289	79.5	4.8	534	2	G84713	hypothetical prote
290	79.5	4.8	554	2	JW0094	neurofilament prot
291	79.5	4.8	580	2	T20716	hypothetical prote
292	79.5	4.8	693	2	T25878	hypothetical prote
293	79.5	4.8	827	2	T04789	hypothetical prote
294	79.5	4.8	860	2	AC1250	DNA mismatch repai
295	79.5	4.8	998	2	S31735	NAD ADP-ribosyltra
296	79.5	4.8	1011	2	T20785	hypothetical prote
297	79.5	4.8	1280	2	E95031	alkaline amylopull
298	79.5	4.8	1365	2	S14871	suppressor two of
299	79	4.8	215	2	S26363	histone H1.1 - hum
300	79	4.8	249	2	G84781	hypothetical prote
301	79	4.8	352	2	T51659	myb-related transc
302	79	4.8	534	2	T39903	serine-rich protei
303	79	4.8	575	2	T21775	hypothetical prote
304	79	4.8	611	2	AB1497	internalin protein
305	79	4.8	710	2	S67098	probable membrane
306	79	4.8	738	2	T44007	hypothetical prote
307	79	4.8	739	2	T49456	hypothetical prote
308	79	4.8	822	2	JC4076	dextranase (EC 3.2
309	79	4.8	836	2	S49940	cell division cont
310	79	4.8	949	2	S19808	glutamate receptor
311	79	4.8	1098	2	T08599	probable transcrip
312	79	4.8	1849	2	C41859	IgA-specific metal
313	79	4.8	1904	2	T13256	tail-host specific
314	78.5	4.7	152	2	T28759	hypothetical prote
315	78.5	4.7	164	2	I53641	mucin 5AC - human
316	78.5	4.7	232	2	A60095	larval glue protei
317	78.5	4.7	294	2	A37232	mucin, tracheal (A
318	78.5	4.7	314	1	HNVZVW	hemagglutinin prec
319	78.5	4.7	314	1	JQ1793	hemagglutinin prec
320	78.5	4.7	322	2	A53715	apomucin precursor
321	78.5	4.7	387	2	A53586	albumin-binding pr
322	78.5	4.7	423	2	S69583	hypothetical prote
323	78.5	4.7	542	2	S64030	probable membrane
324	78.5	4.7	591	1	WMBPQ2	gene P2 protein -
325	78.5	4.7	599	2	S46630	hypothetical prote
326	78.5	4.7	688	2	B42161	cGMP-gated cation
327	78.5	4.7	815	2	JG0197	myosin-light-chain
328	78.5	4.7	825	2	T29634	hypothetical prote
329	78.5	4.7	919	1	PXZP1P	H+-exporting ATPas
330	78.5	4.7	1011	1	JH0581	NAD ADP-ribosyltra
331	78.5	4.7	1356	2	T16754	hypothetical prote
332	78.5	4.7	1420	2	T17158	CL2AB protein - ra
333	78.5	4.7	1435	2	T46611	CL2BB protein - ra
334	78.5	4.7	1452	2	T17157	CL2AA protein - ra
335	78.5	4.7	1463	2	T17159	CL2AC protein - ra
336	78.5	4.7	1467	2	T17160	CL2BA protein - ra
337	78.5	4.7	1478	2	T17185	CL2BC protein - ra
338	78.5	4.7	1487	2	T14324	alpha-latrotoxin r
339	78.5	4.7	1876	2	E97944	zinc metalloprotei
340	78.5	4.7	3224	1	S58884	Ran-binding protei
341	78	4.7	253	2	S76719	hypothetical prote
342	78	4.7	260	2	AG2238	hypothetical prote
343	78	4.7	266	2	T30919	hypothetical prote
344	78	4.7	287	2	T12471	hypothetical prote
345	78	4.7	293	2	G87018	probable membrane
346	78	4.7	321	2	T26152	hypothetical prote
347	78	4.7	340	2	AH0940	probable ABC trans
348	78	4.7	372	2	T48660	heat shock protein
349	78	4.7	373	2	F81333	chaperone DnaJ Cj1
350	78	4.7	384	2	T21929	hypothetical prote
351	78	4.7	425	2	T48724	hypothetical prote
352	78	4.7	434	2	B84684	hypothetical prote
353	78	4.7	530	2	A45690	transactivator EBN
354	78	4.7	627	1	VCVWM2	env polyprotein -
355	78	4.7	655	2	T30044	hypothetical prote
356	78	4.7	786	1	A47547	serine proteinease
357	78	4.7	1050	2	T31853	hypothetical prote
358	78	4.7	1337	2	T30291	dextranase - Strep
359	78	4.7	1360	2	T33922	hypothetical prote
360	78	4.7	1442	1	B48148	protein-tyrosine-p
361	78	4.7	1634	2	T26517	hypothetical prote
362	78	4.7	1723	2	H86557	polymorphic membra
363	78	4.7	1723	2	E72067	polymorphic membra
364	78	4.7	1732	2	C81601	polymorphic membra
365	78	4.7	1955	1	AGCH	agrin precursor -
366	78	4.7	1995	2	T08166	probable membrane
367	78	4.7	5327	2	T13564	microtubule-associ
368	77.5	4.7	275	2	T21933	hypothetical prote
369	77.5	4.7	396	2	F83130	probable MFS trans
370	77.5	4.7	401	2	AG3552	brancheD-chain ami
371	77.5	4.7	474	1	BMFFSY	synaptotagmin - fr
372	77.5	4.7	476	2	T32032	hypothetical prote
373	77.5	4.7	496	2	B41322	N-acetylmuramoyl-L
374	77.5	4.7	514	2	JQ1317	activin receptor p
375	77.5	4.7	519	2	T45764	hypothetical prote
376	77.5	4.7	526	2	A56573	nuclear pore compl
377	77.5	4.7	607	2	S01939	hypothetical prote
378	77.5	4.7	623	2	T18892	hypothetical prote
379	77.5	4.7	816	2	S64439	hypothetical prote
380	77.5	4.7	860	2	JC4566	chitinase (EC 3.2.
381	77.5	4.7	906	2	G90281	conserved hypothet
382	77.5	4.7	938	2	A56731	chromatin assembly
383	77.5	4.7	975	2	T08606	protein phosphatas
384	77.5	4.7	993	1	P1VXTA	RNA 1 protein - to
385	77.5	4.7	1127	2	E86386	probable mutator-l
386	77.5	4.7	1156	2	T23748	hypothetical prote
387	77.5	4.7	1312	2	A97879	beta-N-acetylhexos
388	77.5	4.7	1475	2	S42718	nuclear pore compl
389	77.5	4.7	3968	2	A44265	trithorax homolog
390	77	4.6	257	2	G72690	probable spermidin
391	77	4.6	350	2	E75341	peptidyl-prolyl ci
392	77	4.6	353	2	S22805	env polyprotein -
393	77	4.6	453	2	F75206	maltose-binding pe
394	77	4.6	528	2	S69589	hypothetical prote

395	77	4.6	553	2	T19894	hypothetical prote
396	77	4.6	598	2	T22610	hypothetical prote
397	77	4.6	623	2	A48123	cell cycle regulat
398	77	4.6	639	2	T33166	hypothetical prote
399	77	4.6	669	1	VCVWEK	env polyprotein -
400	77	4.6	734	2	B42680	nucleolus-cytoplas
401	77	4.6	750	2	T42614	probable envelope
402	77	4.6	771	2	JC7388	M83 protein - huma
403	77	4.6	861	2	T23810	hypothetical prote
404	77	4.6	862	2	B36786	hypothetical prote
405	77	4.6	892	2	T09193	ataxin 7 - human
406	77	4.6	897	2	S50550	SIN1-associated pr
407	77	4.6	967	2	G86229	hypothetical prote
408	77	4.6	977	2	S49004	tyrosine kinase Mp
409	77	4.6	1016	2	T41720	hypothetical prote
410	77	4.6	1237	2	T14633	hypothetical prote
411	77	4.6	1401	2	T30247	Werner syndrome pr
412	77	4.6	1513	2	A54895	mucin 2, intestina
413	77	4.6	2187	2	T30826	nascent polypeptid
414	76.5	4.6	284	2	T42367	a-agglutinin core
415	76.5	4.6	349	2	T43457	hypothetical prote
416	76.5	4.6	382	2	S27388	neuropeptide Y rec
417	76.5	4.6	391	2	C69673	penicillin-binding
418	76.5	4.6	421	2	A60058	neural cell adhesi
419	76.5	4.6	433	2	H84120	methyl-accepting c
420	76.5	4.6	482	2	AG1147	P60 extracellular
421	76.5	4.6	484	2	A41487	protein P60 precur
422	76.5	4.6	505	2	B46629	mucin 6, gastric (
423	76.5	4.6	518	2	G88961	protein F59A7.8 [i
424	76.5	4.6	542	2	I39540	chitinase (EC 3.2.
425	76.5	4.6	549	2	S04845	Ig heavy chain pre
426	76.5	4.6	640	1	VCVWM1	env polyprotein -
427	76.5	4.6	679	2	S64258	hypothetical prote
428	76.5	4.6	718	2	T29708	hypothetical prote
429	76.5	4.6	727	2	A88131	protein F10G7.9 [i
430	76.5	4.6	749	2	B86403	probable mutator-l
431	76.5	4.6	773	2	T00502	probable receptor-
432	76.5	4.6	806	2	E69424	hypothetical prote
433	76.5	4.6	990	2	T16554	hypothetical prote
434	76.5	4.6	1154	1	VGIHIB	E2 glycoprotein pr
435	76.5	4.6	1379	2	T45119	FIM protein [impor
436	76.5	4.6	1736	2	F86178	hypothetical prote
437	76.5	4.6	1946	2	JC6032	lactocepin (EC 3.4
438	76.5	4.6	3869	2	A48205	All-1 protein +GTE
439	76.5	4.6	5037	2	B35041	ryanodine receptor
440	76	4.6	167	2	A33532	mucin SMUC-40 - hu
441	76	4.6	172	2	T21753	hypothetical prote
442	76	4.6	243	2	B41710	promastigote surfa
443	76	4.6	356	2	D88979	protein F37B4.9 [i
444	76	4.6	368	2	S36564	E2 protein - human
445	76	4.6	378	2	AI2180	hypothetical prote
446	76	4.6	382	2	B88561	protein F58A4.7b [
447	76	4.6	384	2	A41710	promastigote surfa
448	76	4.6	389	2	E97305	NADH-dependent but
449	76	4.6	389	2	A47013	butanol dehydrogen
450	76	4.6	499	2	T47722	probable protein k
451	76	4.6	515	2	AD1162	flagellar motor sw
452	76	4.6	532	2	T28784	hypothetical prote
453	76	4.6	536	2	T37544	hypothetical serin
454	76	4.6	539	2	T02512	hypothetical prote
455	76	4.6	549	2	T49298	hypothetical prote
456	76	4.6	592	2	T16725	hypothetical prote
457	76	4.6	615	2	T47395	hypothetical prote
458	76	4.6	687	2	A49636	soluble vascular e
459	76	4.6	699	2	I38073	nucleolar phosphop
460	76	4.6	700	2	A54641	interspersed repea
461	76	4.6	763	2	T08929	hypothetical prote
462	76	4.6	766	2	B85440	receptor kinase-li
463	76	4.6	824	2	T23923	hypothetical prote
464	76	4.6	929	2	G72677	hypothetical prote
465	76	4.6	940	2	AD1374	internalin protein
466	76	4.6	960	1	JN0677	protein-tyrosine k
467	76	4.6	994	1	MNWVM	nonstructural prot
468	76	4.6	1014	1	A29725	NAD ADP-ribosyltra
469	76	4.6	1041	2	H71617	SERA antigen/papai
470	76	4.6	1046	2	T29776	hypothetical prote
471	76	4.6	1216	2	B90580	hypothetical prote
472	76	4.6	1263	2	AH2011	heterocyst glycoli
473	76	4.6	1338	2	S09982	protein-tyrosine k
474	76	4.6	1348	2	A43917	probable epidermal
475	76	4.6	1388	2	A53317	collagen alpha 1(X
476	76	4.6	1401	2	T17452	Werner syndrome pr
477	76	4.6	1422	2	T42636	protein-tyrosine-p
478	76	4.6	1438	2	B71610	WD40 WEB-1 homolog
479	76	4.6	1489	2	G71406	probable retroviru
480	76	4.6	1513	2	T44045	hypothetical prote
481	76	4.6	1890	2	T04556	hypothetical prote
482	76	4.6	2570	2	T17451	fimbriae-associate
483	75.5	4.6	261	2	T30170	hypothetical prote
484	75.5	4.6	273	2	T44657	protein GP80 [impo
485	75.5	4.6	319	1	A35163	carbonate dehydrat
486	75.5	4.6	343	2	T40306	hypothetical prote
487	75.5	4.6	348	1	B46216	transcription fact
488	75.5	4.6	364	1	OOHUG	opsin, green-sensi
489	75.5	4.6	387	2	A86302	hypothetical prote
490	75.5	4.6	411	2	T03154	DNA polymerase pro
491	75.5	4.6	412	2	E97279	TPR-repeat-contain
492	75.5	4.6	430	1	A46216	transcription fact
493	75.5	4.6	435	2	S40993	hypothetical prote
494	75.5	4.6	443	2	D72383	NADH oxidase - The
495	75.5	4.6	445	2	I38521	inwardly rectifyin
496	75.5	4.6	448	2	S17370	DNA-binding protei
497	75.5	4.6	468	2	S70297	SPS2 protein homol
498	75.5	4.6	511	1	VGBEF4	glycoprotein C - h
499	75.5	4.6	609	2	G87496	peptidase, M23/M37
500	75.5	4.6	639	2	T13151	adapter protein CM
501	75.5	4.6	665	2	G97213	probable membrane-
502	75.5	4.6	709	2	T32089	hypothetical prote
503	75.5	4.6	778	2	T43223	hypothetical prote
504	75.5	4.6	780	2	A48143	HF-1 regulatory el
505	75.5	4.6	963	2	T40290	hypothetical prote
506	75.5	4.6	1131	2	T41144	hypothetical serin
507	75.5	4.6	1166	2	S37692	probable tumor sup
508	75.5	4.6	1235	2	T13710	protein-tyrosine k
509	75.5	4.6	1237	2	E86457	probable RNA helic
510	75.5	4.6	1473	2	T31422	C-terminal domain-
511	75.5	4.6	1655	2	T32633	hypothetical prote
512	75.5	4.6	1737	2	A59235	unconventional myo
513	75.5	4.6	1881	2	H95076	zinc metalloprotei
514	75.5	4.6	2526	2	T20531	hypothetical prote
515	75.5	4.6	3176	2	CGHU3A	collagen alpha 3(V
516	75	4.5	94	2	S53365	mucin 5AC (clone C
517	75	4.5	128	2	T05035	hypothetical prote
518	75	4.5	205	2	S55670	hypothetical prote
519	75	4.5	248	2	AF1914	carbon dioxide con
520	75	4.5	256	2	T09034	hypothetical prote
521	75	4.5	295	2	T28078	hypothetical prote
522	75	4.5	310	1	H71054	hypothetical prote
523	75	4.5	313	2	AH0734	probable bacteriop
524	75	4.5	353	2	S33322	(S)-2-hydroxy-acid
525	75	4.5	388	2	T16861	hypothetical prote
526	75	4.5	390	2	A72108	hypothetical prote
527	75	4.5	390	2	B86514	hypothetical prote
528	75	4.5	418	2	T16713	hypothetical prote
529	75	4.5	425	1	A26431	nerve growth facto
530	75	4.5	453	2	C40511	hypothetical prote
531	75	4.5	475	2	E84745	probable splicing
532	75	4.5	477	2	T32938	hypothetical prote
533	75	4.5	481	2	T38149	pre-mrna splicing
534	75	4.5	554	2	A56596	chitinase (EC 3.2.
535	75	4.5	604	2	T37994	probable splicing
536	75	4.5	607	2	S63395	probable membrane
537	75	4.5	651	2	T16450	hypothetical prote
538	75	4.5	679	2	T19703	hypothetical prote
539	75	4.5	739	2	I56187	transcription fact
540	75	4.5	775	1	WMBE19	ribonucleoside-dip

541	75	4.5	778	2	T45221	DNA damage checkpo
542	75	4.5	796	2	E96654	hypothetical prote
543	75	4.5	858	1	IJRTNC	neural cell adhesi
544	75	4.5	904	2	T03806	hypothetical prote
545	75	4.5	916	2	T20909	hypothetical prote
546	75	4.5	940	2	D89723	protein F39D8.1b [
547	75	4.5	945	2	T21998	hypothetical prote
548	75	4.5	1048	1	S61388	dotA protein - Leg
549	75	4.5	1118	2	A48292	mucin, tracheobron
550	75	4.5	1253	2	T18528	probable pyruvate
551	75	4.5	1741	2	T13610	parallel sister ch
552	75	4.5	1768	2	T13349	parallel sister ch
553	75	4.5	1838	1	CGHU1V	collagen alpha 1(V
554	75	4.5	1979	2	C71622	hypothetical prote
555	75	4.5	3122	2	T17202	DNA-directed DNA p
556	75	4.5	3375	2	T19821	hypothetical prote
557	74.5	4.5	148	2	S50653	hypothetical prote
558	74.5	4.5	211	2	S28046	TUB8 protein - pot
559	74.5	4.5	254	2	D88560	protein F58A4.1 [i
560	74.5	4.5	262	2	T33597	hypothetical prote
561	74.5	4.5	276	2	T51685	myb-related transc
562	74.5	4.5	281	2	T49537	hypothetical prote
563	74.5	4.5	294	2	AI2016	hypothetical prote
564	74.5	4.5	310	1	YAZQ31	300K antigen Ag231
565	74.5	4.5	321	2	T50966	hypothetical prote
566	74.5	4.5	382	2	T25280	hypothetical prote
567	74.5	4.5	396	2	T50229	probable transmemb
568	74.5	4.5	407	2	T26938	hypothetical prote
569	74.5	4.5	416	2	T20448	hypothetical prote
570	74.5	4.5	429	2	S29044	endoglucanase A pr
571	74.5	4.5	432	2	T08771	hypothetical prote
572	74.5	4.5	478	2	A32555	major merozoite su
573	74.5	4.5	482	2	T22754	hypothetical prote
574	74.5	4.5	520	2	S14598	E2 glycoprotein -
575	74.5	4.5	531	2	S09859	hypothetical prote
576	74.5	4.5	551	2	S52287	urbain - silkworm
577	74.5	4.5	636	2	T23232	hypothetical prote
578	74.5	4.5	713	2	JE0230	NADPH-cytochrome P
579	74.5	4.5	802	2	T21315	hypothetical prote
580	74.5	4.5	808	2	T23129	hypothetical prote
581	74.5	4.5	884	2	AE3166	ATP-dependent DNA
582	74.5	4.5	998	2	S37627	protein-tyrosine k
583	74.5	4.5	1042	2	T48801	hypothetical prote
584	74.5	4.5	1595	2	T31082	endo-1,4-beta-xyla
585	74.5	4.5	1630	2	A53577	ascites sialoglyco
586	74.5	4.5	1902	2	C97702	cell surface antig
587	74.5	4.5	1965	2	T33216	hypothetical prote
588	74.5	4.5	2688	2	I49477	alpha-A-crystallin
589	74.5	4.5	3828	2	T13857	trithorax protein
590	74.5	4.5	3944	2	T19997	hypothetical prote
591	74	4.5	147	2	S09762	hypothetical prote
592	74	4.5	223	2	T21930	hypothetical prote
593	74	4.5	257	1	MGNZBR	major surface glyc
594	74	4.5	264	2	A49149	mesoderm developme
595	74	4.5	286	2	S44835	F54H12.3 protein -
596	74	4.5	305	2	AB2149	hypothetical prote
597	74	4.5	317	2	C85432	hypothetical prote
598	74	4.5	332	2	T31928	hypothetical prote
599	74	4.5	339	1	JT0756	group-V allergen i
600	74	4.5	339	2	A56274	sulfur-regulated 3
601	74	4.5	344	2	T13975	NADH2 dehydrogenas
602	74	4.5	346	2	H84512	hypothetical prote
603	74	4.5	390	2	C97889	UDPglucose 6-dehyd
604	74	4.5	397	2	E97176	N-terminal domain
605	74	4.5	412	1	AJBORS	argininosuccinate
606	74	4.5	413	2	S28066	sexual differentia
607	74	4.5	417	2	T20327	hypothetical prote
608	74	4.5	435	2	AG1028	prepilin [imported
609	74	4.5	454	2	T02100	hypothetical prote
610	74	4.5	540	1	FOMVHL	gag polyprotein -
611	74	4.5	575	2	S39484	DNA-binding protei
612	74	4.5	586	2	S66697	probable membrane
613	74	4.5	600	2	T06292	hypothetical prote
614	74	4.5	621	2	T20307	hypothetical prote
615	74	4.5	622	2	AC1236	acyltransferase (t
616	74	4.5	665	1	VCMVKA	env polyprotein pr
617	74	4.5	672	2	T20310	hypothetical prote
618	74	4.5	681	2	A45705	type I transmembra
619	74	4.5	689	2	B43491	env polyprotein -
620	74	4.5	731	2	T04455	hypothetical prote
621	74	4.5	739	1	A34873	transcription fact
622	74	4.5	775	2	A32494	transposable eleme
623	74	4.5	823	2	G90848	probable exonuclea
624	74	4.5	823	2	E85706	probable exonuclea
625	74	4.5	852	2	T06310	hypothetical prote
626	74	4.5	862	2	S51493	major nitrogen reg
627	74	4.5	903	2	T00705	N-chimerin homolog
628	74	4.5	1016	2	T19006	ankyrin related pr
629	74	4.5	1018	2	T40253	hypothetical prote
630	74	4.5	1099	2	G90546	conserved hypothet
631	74	4.5	1104	2	S59310	probable membrane
632	74	4.5	1110	2	I51116	NF-180 - sea lampr
633	74	4.5	1115	1	IJMSNL	neural cell adhesi
634	74	4.5	1159	2	S62562	probable nuclear p
635	74	4.5	1164	2	B71429	phytochrome D - Ar
636	74	4.5	1390	2	T14004	trfA protein - sli
637	74	4.5	1694	2	H64106	IgA-specific metal
638	74	4.5	1828	2	A40115	microtubule-associ
639	74	4.5	1938	1	MWKW1	myosin heavy chain
640	74	4.5	2414	2	A54277	transcription adap
641	73.5	4.4	168	2	A31196	prespore-specific
642	73.5	4.4	182	2	T30078	hypothetical prote
643	73.5	4.4	253	2	T32879	hypothetical prote
644	73.5	4.4	263	2	T38003	hypothetical ser-t
645	73.5	4.4	292	2	S24169	mucin - rat
646	73.5	4.4	305	2	S44661	ZK353.4 protein -
647	73.5	4.4	335	2	AE3000	cell division prot
648	73.5	4.4	335	2	D98283	hypothetical prote
649	73.5	4.4	345	2	D91201	type III secretion
650	73.5	4.4	345	2	H86047	escU [imported] -
651	73.5	4.4	358	2	AD2378	hypothetical prote
652	73.5	4.4	371	2	S20075	promastigote surfa
653	73.5	4.4	376	2	T48245	hypothetical prote
654	73.5	4.4	381	2	E69862	hypothetical prote
655	73.5	4.4	397	2	G69287	hypothetical prote
656	73.5	4.4	405	2	A60534	P2B/LAMP-1 precurs
657	73.5	4.4	445	2	A54852	potassium rectifie
658	73.5	4.4	447	2	A39321	mucin - rat (fragm
659	73.5	4.4	457	2	T20884	hypothetical prote
660	73.5	4.4	458	2	T31631	hypothetical prote
661	73.5	4.4	459	2	I48854	gene murine tumour
662	73.5	4.4	476	2	B44997	merozoite surface
663	73.5	4.4	484	1	A24994	cellulose 1,4-beta
664	73.5	4.4	511	1	VGBE1K	glycoprotein C - h
665	73.5	4.4	540	2	H98086	chaperonin GroEL [
666	73.5	4.4	540	2	G95222	chaperonin, 60 kDa
667	73.5	4.4	542	2	T19952	hypothetical prote
668	73.5	4.4	550	1	VGIHD6	E2 glycoprotein pr
669	73.5	4.4	555	2	T26413	hypothetical prote
670	73.5	4.4	556	2	C87609	sensor histidine k
671	73.5	4.4	569	2	A46462	T cell activation
672	73.5	4.4	601	2	H90270	hypothetical prote
673	73.5	4.4	603	2	T39866	hypothetical prote
674	73.5	4.4	626	2	AB1328	probable peptidogl
675	73.5	4.4	654	2	T33044	hypothetical prote
676	73.5	4.4	696	2	G81262	probable integral
677	73.5	4.4	708	2	F87245	penicillin-bonding
678	73.5	4.4	713	2	T44447	neuregulin-3 [impo
679	73.5	4.4	756	2	JC5886	signaling mediator
680	73.5	4.4	799	2	H71255	probable cell divi
681	73.5	4.4	819	2	B95136	conserved domain p
682	73.5	4.4	901	2	A44825	phosphoprotein, sy
683	73.5	4.4	905	2	T02205	Lu-ECAM-1 protein
684	73.5	4.4	990	2	H88733	protein F32E10.3 [
685	73.5	4.4	1004	2	T38074	hypothetical prote
686	73.5	4.4	1139	1	E64234	cytadherence-acces

687	73.5	4.4	1291	2	T22382	hypothetical prote
688	73.5	4.4	2232	2	T34434	hypothetical prote
689	73.5	4.4	4385	2	T29042	hypothetical prote
690	73	4.4	188	2	C96593	unknown protein, 9
691	73	4.4	198	2	E71837	protein-export mem
692	73	4.4	213	2	S43949	histone H1 - mouse
693	73	4.4	260	2	I50109	gastrulation prote
694	73	4.4	288	2	JQ2365	polyprotein - Bean
695	73	4.4	315	1	HNVZVV	hemagglutinin prec
696	73	4.4	316	2	G86333	hypothetical prote
697	73	4.4	327	2	S20074	promastigote surfa
698	73	4.4	359	2	S42787	serine/threonine-r
699	73	4.4	369	2	E84291	iron (III) ABC tra
700	73	4.4	422	2	A55417	synaptotagmin II -
701	73	4.4	428	1	Q4ECAD	damX protein (aroB
702	73	4.4	441	2	A43555	GAP-43-related pro
703	73	4.4	448	2	G88639	protein C34H4.2 [i
704	73	4.4	461	2	T51044	related to spore c
705	73	4.4	469	2	E64456	hypothetical prote
706	73	4.4	482	2	A44997	merozoite surface
707	73	4.4	486	2	S66097	cell-cycle protein
708	73	4.4	486	2	A89927	elastin binding pr
709	73	4.4	492	1	CHBOA3	gamma-aminobutyric
710	73	4.4	496	2	E90181	hypothetical prote
711	73	4.4	509	1	A37259	membrane glycoprot
712	73	4.4	550	2	C75557	hypothetical prote
713	73	4.4	558	2	A98199	translocated intim
714	73	4.4	558	2	E86045	probable transloca
715	73	4.4	600	2	E72027	phosphoenolpyruvat
716	73	4.4	600	2	A86597	phosphoenolpyruvat
717	73	4.4	669	2	A46511	envelope protein -
718	73	4.4	688	2	A43491	env polyprotein -
719	73	4.4	720	2	T51007	hypothetical prote
720	73	4.4	728	2	T20561	hypothetical prote
721	73	4.4	781	2	T49472	hormone-sensitive
722	73	4.4	814	2	T33140	hypothetical prote
723	73	4.4	880	2	S44833	F54H12.5 protein -
724	73	4.4	918	2	A36337	membrane glycoprot
725	73	4.4	932	1	VGBEBC	glycoprotein gI pr
726	73	4.4	958	2	T10679	hypothetical prote
727	73	4.4	1055	2	H90023	hypothetical prote
728	73	4.4	1071	2	T22327	hypothetical prote
729	73	4.4	1256	1	A43829	muramidase-release
730	73	4.4	1320	2	JC5630	TCOF1 protein - mo
731	73	4.4	1345	2	S46817	hypothetical prote
732	73	4.4	1702	2	A41859	IgA-specific metal
733	73	4.4	1993	2	AF1450	probable peptidogl
734	73	4.4	2179	1	GNNYH4	genome polyprotein
735	73	4.4	2285	2	T12796	probable transglyc
736	73	4.4	2416	2	T13825	adenomatous polypo
737	73	4.4	2468	2	A83412	hypothetical prote
738	73	4.4	2722	2	T20532	hypothetical prote
739	72.5	4.4	263	2	I51225	snail1 protein - z
740	72.5	4.4	303	2	S40973	hypothetical prote
741	72.5	4.4	314	2	B95034	dihydropteroate sy
742	72.5	4.4	321	2	T26153	hypothetical prote
743	72.5	4.4	328	2	S35336	transcription fact
744	72.5	4.4	340	2	C90894	probable LACI-type
745	72.5	4.4	340	2	F85723	probable LACI-type
746	72.5	4.4	340	2	G64905	sugar-binding prot
747	72.5	4.4	382	2	T27058	hypothetical prote
748	72.5	4.4	391	2	T35470	probable integral
749	72.5	4.4	406	2	T23934	hypothetical prote
750	72.5	4.4	415	2	T32490	hypothetical prote
751	72.5	4.4	463	1	A36479	milk fat globule m
752	72.5	4.4	487	2	S40820	probable permease
753	72.5	4.4	498	1	VGXPLM	surface glycoprote
754	72.5	4.4	499	2	AI2449	hypothetical prote
755	72.5	4.4	507	2	S05542	hypothetical prote
756	72.5	4.4	511	2	T35194	transcription init
757	72.5	4.4	560	2	T32661	hypothetical prote
758	72.5	4.4	580	2	B38418	jockey protein 1 -
759	72.5	4.4	610	2	S35049	mucin JER57 - huma
760	72.5	4.4	642	2	T39607	fork head protein
761	72.5	4.4	648	2	PC4395	mucin 3 - human (f
762	72.5	4.4	657	2	A82415	conserved hypothet
763	72.5	4.4	663	2	T18631	hypothetical prote
764	72.5	4.4	710	2	A99486	ABC transporter, b
765	72.5	4.4	728	2	F72693	probable phosphoes
766	72.5	4.4	729	2	G96559	hypothetical prote
767	72.5	4.4	743	2	D86888	penicillin-binding
768	72.5	4.4	765	1	T44946	transducer protein
769	72.5	4.4	896	2	S36326	clathrin assembly
770	72.5	4.4	907	1	QQBE21	membrane antigen g
771	72.5	4.4	915	2	S36327	clathrin assembly
772	72.5	4.4	944	2	C70839	probable mmpL3 pro
773	72.5	4.4	982	2	A53253	microtubule-associ
774	72.5	4.4	1016	1	JS0428	NAD ADP-ribosyltra
775	72.5	4.4	1036	2	S73601	protein P200 - Myc
776	72.5	4.4	1116	2	S77213	DNA-directed DNA p
777	72.5	4.4	1148	2	T09073	splicing factor Si
778	72.5	4.4	1152	2	A33183	microtubule-associ
779	72.5	4.4	1180	2	E86719	hypothetical prote
780	72.5	4.4	1199	2	A40670	nuclear envelope p
781	72.5	4.4	1219	2	T14578	nucleoporin Nup153
782	72.5	4.4	1222	2	T22490	hypothetical prote
783	72.5	4.4	1309	1	BVBYD9	RAD9 protein - yea
784	72.5	4.4	1312	2	E95006	beta-N-acetylhexos
785	72.5	4.4	1555	2	T18688	hypothetical prote
786	72.5	4.4	1635	2	T14075	chitinase (EC 3.2.
787	72.5	4.4	1847	2	T18308	probable vitelloge
788	72.5	4.4	1973	2	G89608	protein B0272.5 [i
789	72.5	4.4	1973	2	T18686	hypothetical prote
790	72.5	4.4	2305	2	B89608	protein C23F12.1 [
791	72.5	4.4	2305	2	T15571	hypothetical prote
792	72.5	4.4	2314	1	A46151	protein-tyrosine-p
793	72.5	4.4	2897	2	B48666	cell proliferation
794	72.5	4.4	3069	2	H70656	fatty-acid synthas
795	72.5	4.4	3256	2	A48666	cell proliferation
796	72	4.3	139	2	G98226	hypothetical prote
797	72	4.3	139	2	AI3059	hypothetical prote
798	72	4.3	159	2	F72758	hypothetical prote
799	72	4.3	197	2	T33525	hypothetical prote
800	72	4.3	199	2	JE0351	OX40 ligand protei
801	72	4.3	236	2	T03041	hypothetical prote
802	72	4.3	246	2	PC4397	mucin 3 T10 - huma
803	72	4.3	282	2	B37994	RF2 protein - saim
804	72	4.3	317	1	GEHUS	bone sialoprotein
805	72	4.3	322	2	G69946	phage-related prot
806	72	4.3	324	2	S36646	integrin-associate
807	72	4.3	330	2	T49644	hypothetical prote
808	72	4.3	334	2	T19637	hypothetical prote
809	72	4.3	425	1	FOMVGC	gag polyprotein -
810	72	4.3	428	2	D86003	hypothetical prote
811	72	4.3	428	2	F91157	probable membrane
812	72	4.3	460	2	A84154	amino acid transpo
813	72	4.3	508	2	A33378	fasciclin III prec
814	72	4.3	509	2	A96563	probable protein k
815	72	4.3	544	2	S07144	neurofilament trip
816	72	4.3	548	1	QFPGL	neurofilament trip
817	72	4.3	576	2	T38293	hypothetical serin
818	72	4.3	587	2	S38634	chaperonin, mitoch
819	72	4.3	592	2	D70863	hypothetical prote
820	72	4.3	622	2	A90570	lipoprotein [impor
821	72	4.3	674	2	S74506	ribonuclease E - S
822	72	4.3	677	2	T00369	hypothetical prote
823	72	4.3	736	2	T41259	hypothetical prote
824	72	4.3	770	1	S30293	transcription fact
825	72	4.3	817	2	T21336	hypothetical prote
826	72	4.3	855	2	D98004	histidine Motif-Co
827	72	4.3	876	2	T49801	hypothetical prote
828	72	4.3	884	2	T20405	hypothetical prote
829	72	4.3	958	2	T26258	hypothetical prote
830	72	4.3	1034	2	S49947	SMT4 protein - yea
831	72	4.3	1038	2	AG2187	hypothetical prote
832	72	4.3	1146	2	S46837	hypothetical prote

833	72	4.3	1176	2	T49482	hypothetical prote
834	72	4.3	1196	2	H85061	hypothetical prote
835	72	4.3	1203	2	T17415	mycelial surface a
836	72	4.3	1388	2	A57655	tim (timeless) pro
837	72	4.3	1489	2	T31108	cyst germination s
838	72	4.3	1547	2	T28657	blackjack protein,
839	72	4.3	1570	2	T18272	1-phosphatidylinos
840	72	4.3	1778	2	T50074	probable nucleopor
841	72	4.3	1829	2	T24583	hypothetical prote
842	72	4.3	2441	2	S39161	CREB-binding prote
843	72	4.3	2578	2	A56922	transcription fact
844	72	4.3	2971	2	T08026	hypothetical prote
845	71.5	4.3	141	2	A38196	non-structural hyp
846	71.5	4.3	146	2	S52800	hypothetical prote
847	71.5	4.3	162	2	C84948	NADH2 dehydrogenas
848	71.5	4.3	164	2	A26490	histone H1, macron
849	71.5	4.3	178	2	JQ1547	stripe disease-spe
850	71.5	4.3	231	2	F84311	hypothetical prote
851	71.5	4.3	263	2	S01360	salivary glue prot
852	71.5	4.3	313	2	JQ1862	31R protein - vari
853	71.5	4.3	313	2	T28598	hypothetical prote
854	71.5	4.3	313	2	A34677	secretory pathway
855	71.5	4.3	363	2	T25278	hypothetical prote
856	71.5	4.3	372	2	F43674	US7 protein - huma
857	71.5	4.3	373	2	S43455	hypothetical prote
858	71.5	4.3	381	2	S65212	hypothetical prote
859	71.5	4.3	385	2	T38113	hypothetical serin
860	71.5	4.3	392	2	T49471	mucin (muc3) relat
861	71.5	4.3	393	2	T49578	hypothetical prote
862	71.5	4.3	395	2	I52842	CD43 Lp-3 antigen
863	71.5	4.3	395	2	A43545	leukosialin CD43 p
864	71.5	4.3	408	2	A46712	glycoprotein IIa -
865	71.5	4.3	414	2	B84600	hypothetical prote
866	71.5	4.3	423	2	T22865	hypothetical prote
867	71.5	4.3	442	1	S11712	transcription init
868	71.5	4.3	443	1	D64584	heat shock protein
869	71.5	4.3	466	2	AI0957	chromosomal replic
870	71.5	4.3	482	2	T48397	S-receptor kinase-
871	71.5	4.3	503	2	G75262	hypothetical prote
872	71.5	4.3	507	2	T50398	hypothetical serin
873	71.5	4.3	540	1	A55145	thiamine-phosphate
874	71.5	4.3	584	2	T19565	hypothetical prote
875	71.5	4.3	631	2	I52257	episialin - mouse
876	71.5	4.3	661	1	VCMVCB	env polyprotein -
877	71.5	4.3	665	2	E81444	probable methyl-ac
878	71.5	4.3	675	2	T47378	probable transposa
879	71.5	4.3	755	2	T20950	hypothetical prote
880	71.5	4.3	760	1	S07896	transcription fact
881	71.5	4.3	882	2	T01168	hypothetical prote
882	71.5	4.3	1043	2	T23875	hypothetical prote
883	71.5	4.3	1121	2	T02764	myosin-I binding p
884	71.5	4.3	1156	2	T43326	germline RNA helic
885	71.5	4.3	1172	2	T32759	hypothetical prote
886	71.5	4.3	1234	2	T31623	hypothetical prote
887	71.5	4.3	1260	2	A87046	hypothetical prote
888	71.5	4.3	1297	2	T30274	proteoliaisin - se
889	71.5	4.3	1459	2	T32271	hypothetical prote
890	71.5	4.3	1557	2	D41214	protein-tyrosine-p
891	71.5	4.3	1566	2	T20058	hypothetical prote
892	71.5	4.3	1630	2	C41214	protein-tyrosine-p
893	71	4.3	98	2	S53367	mucin 5AC (clone M
894	71	4.3	135	2	T49996	AtAGP4 - Arabidops
895	71	4.3	168	2	JN0073	glycophorin A - mo
896	71	4.3	177	2	G75285	hypothetical prote
897	71	4.3	213	2	A86228	hypothetical prote
898	71	4.3	240	2	T33698	hypothetical prote
899	71	4.3	242	2	T27226	hypothetical prote
900	71	4.3	304	2	T15922	hypothetical prote
901	71	4.3	310	2	T20535	hypothetical prote
902	71	4.3	329	2	T43012	conserved hypothet
903	71	4.3	343	2	S75435	hypothetical prote
904	71	4.3	349	2	T05857	hypothetical prote
905	71	4.3	360	2	T33835	hypothetical prote
906	71	4.3	370	2	S49008	fork head protein
907	71	4.3	378	2	S00842	leukosialin precur
908	71	4.3	379	1	S71571	alcohol dehydrogen
909	71	4.3	394	2	T21752	hypothetical prote
910	71	4.3	410	1	S68153	cellulase (EC 3.2.
911	71	4.3	415	2	A35560	lysosomal membrane
912	71	4.3	433	2	S19996	hypothetical prote
913	71	4.3	455	2	A87913	protein B0205.10 [
914	71	4.3	462	2	T32751	hypothetical prote
915	71	4.3	474	1	TVRTC4	Ca2+/calmodulin-de
916	71	4.3	496	2	T30976	hypothetical prote
917	71	4.3	500	1	S60929	probable aldehyde
918	71	4.3	502	2	I52637	Ca2+/calmodulin-de
919	71	4.3	530	2	S62439	hypothetical serin
920	71	4.3	534	2	G97703	hypothetical prote
921	71	4.3	622	2	T15467	hypothetical prote
922	71	4.3	626	1	NBHUIA	platelet glycoprot
923	71	4.3	665	1	VCMVVR	env polyprotein pr
924	71	4.3	669	2	T08827	hypothetical prote
925	71	4.3	670	2	T13739	probable hormone r
926	71	4.3	711	2	T48335	receptor like prot
927	71	4.3	719	2	T27977	lin-15A protein -
928	71	4.3	738	2	I40719	isocitrate dehydro
929	71	4.3	751	2	T21967	hypothetical prote
930	71	4.3	767	1	JU0474	glucan 1,4-alpha-g
931	71	4.3	778	1	ALBYG	glucan 1,4-alpha-g
932	71	4.3	784	2	AH2560	hypothetical prote
933	71	4.3	785	2	S54016	SOK2 protein - yea
934	71	4.3	791	2	T39924	hypothetical prote
935	71	4.3	814	1	KXBY	kexin (EC 3.4.21.6
936	71	4.3	880	2	D89756	protein T23E7.2b [
937	71	4.3	968	2	T00353	hypothetical prote
938	71	4.3	977	2	H84469	hypothetical prote
939	71	4.3	982	2	T19171	hypothetical prote
940	71	4.3	1032	2	T18293	guanylate kinase-i
941	71	4.3	1200	1	SNPSO	ice nucleation pro
942	71	4.3	1204	2	C75015	probable pyrolysin
943	71	4.3	1244	2	T19615	hypothetical prote
944	71	4.3	1256	2	G97902	alpha-amylase (EC
945	71	4.3	1302	2	T23236	hypothetical prote
946	71	4.3	1326	2	H89134	protein F25G6.9 [i
947	71	4.3	1367	2	T33819	hypothetical prote
948	71	4.3	1533	2	T00344	hypothetical prote
949	71	4.3	1583	2	S59644	sister chromatid c
950	71	4.3	1751	2	A45604	major blood-stage
951	71	4.3	1819	2	T32008	hypothetical prote
952	71	4.3	1842	2	T43409	probable fatty-aci
953	71	4.3	1842	2	T38781	fatty acid synthas
954	71	4.3	2035	2	A40718	host cell factor C
955	71	4.3	2090	2	S26058	probable transform
956	71	4.3	2848	2	T32550	hypothetical prote
957	71	4.3	2957	2	T33152	hypothetical prote
958	71	4.3	5035	1	I46646	ryanodine receptor
959	70.5	4.3	118	2	S49913	cryptogein - Phyto
960	70.5	4.3	128	2	A35690	mucin 3 (clone SIB
961	70.5	4.3	146	1	ERAD32	early E3 16K glyco
962	70.5	4.3	172	2	F49247	merozoite surface
963	70.5	4.3	174	2	E49247	merozoite surface
964	70.5	4.3	193	2	G90125	hypothetical prote
965	70.5	4.3	204	2	S67295	probable membrane
966	70.5	4.3	209	2	C89850	conserved hypothet
967	70.5	4.3	211	2	C71482	probable endonucle
968	70.5	4.3	212	2	F86545	hypothetical prote
969	70.5	4.3	212	2	F72077	hypothetical prote
970	70.5	4.3	236	2	PC4396	mucin 3 T9 - human
971	70.5	4.3	255	2	I46606	MHC SLA-DQ alpha c
972	70.5	4.3	264	2	T09377	hypothetical prote
973	70.5	4.3	284	2	T28018	hypothetical prote
974	70.5	4.3	288	2	T41112	hypothetical prote
975	70.5	4.3	308	2	T29756	hypothetical prote
976	70.5	4.3	312	2	T25994	hypothetical prote
977	70.5	4.3	314	2	B97905	dihydropteroate sy
978	70.5	4.3	316	1	A43661	dihydropteroate sy

979	70.5	4.3	321	2	T19259	hypothetical prote
980	70.5	4.3	330	2	S28102	rlx protein - Stap
981	70.5	4.3	350	2	AI0139	UTP-hexose-1-phosp
982	70.5	4.3	380	1	D34285	ubiquinol-cytochro
983	70.5	4.3	382	2	A28067	lysosomal membrane
984	70.5	4.3	385	2	F70591	probable kefB prot
985	70.5	4.3	393	2	S62335	I71-7 protein - fr
986	70.5	4.3	402	2	E86185	hypothetical prote
987	70.5	4.3	403	1	S35541	transcription fact
988	70.5	4.3	427	2	C88883	protein JC8.10 [im
989	70.5	4.3	431	1	JC2002	transcription fact
990	70.5	4.3	431	2	T11911	NADH2 dehydrogenas
991	70.5	4.3	433	2	S37790	probable serine/th
992	70.5	4.3	445	2	T23199	hypothetical prote
993	70.5	4.3	462	2	A48933	gamma-aminobutyric
994	70.5	4.3	465	2	H82345	mannose-1-phosphat
995	70.5	4.3	491	2	T52398	hypothetical prote
996	70.5	4.3	522	2	S41819	nucleoporin p62 -
997	70.5	4.3	526	2	A34896	adenylate cyclase-
998	70.5	4.3	526	2	C84552	hypothetical prote
999	70.5	4.3	562	2	A85042	hypothetical prote
1000	70.5	4.3	608	2	A46312	gag polyprotein -
1001	70.5	4.3	616	2	T29234	hypothetical prote
1002	70.5	4.3	629	2	AE1525	probable peptidogl
1003	70.5	4.3	649	2	T24505	hypothetical prote
1004	70.5	4.3	675	2	D85065	receptor protein k
1005	70.5	4.3	716	2	T26998	hypothetical prote
1006	70.5	4.3	809	2	T18970	hypothetical prote
1007	70.5	4.3	814	2	F59430	GTPase regulator a
1008	70.5	4.3	839	2	I50590	class I INCENP pro
1009	70.5	4.3	846	2	T38840	hypothetical trp-a
1010	70.5	4.3	874	2	B86322	F6A14.8 protein -
1011	70.5	4.3	877	2	I50591	class II INCENP pr
1012	70.5	4.3	893	2	T18271	hypothetical prote
1013	70.5	4.3	899	2	C84765	hypothetical prote
1014	70.5	4.3	910	1	S73361	dnaJ homolog prote
1015	70.5	4.3	942	2	S53963	MCS1 protein - yea
1016	70.5	4.3	979	2	A35913	regulatory factor
1017	70.5	4.3	999	1	IJHUG3	desmoglein 3 precu
1018	70.5	4.3	1015	2	JC6552	DNA topoisomerase
1019	70.5	4.3	1028	2	E85089	probable transposo
1020	70.5	4.3	1032	2	G89427	protein T08D2.3 [i
1021	70.5	4.3	1052	2	C64221	hypothetical 114K
1022	70.5	4.3	1106	2	T31742	hypothetical prote
1023	70.5	4.3	1115	2	A47541	protein kinase IRE
1024	70.5	4.3	1123	2	T18270	hypothetical prote
1025	70.5	4.3	1131	2	T15787	hypothetical prote
1026	70.5	4.3	1221	2	AI0193	ribonuclease E (EC
1027	70.5	4.3	1520	2	T44231	hypothetical prote
1028	70.5	4.3	1603	2	S17983	gene posterior sex
1029	70.5	4.3	1742	2	T17120	cellulase (EC 3.2.
1030	70.5	4.3	1872	2	T00339	hypothetical prote
1031	70.5	4.3	2271	2	F90073	hypothetical prote
1032	70.5	4.3	2717	2	A34203	DNA-binding protei
1033	70.5	4.3	3054	1	GNBVEV	genome polyprotein
1034	70	4.2	147	2	JC7938	type II antifreeze
1035	70	4.2	148	2	T32622	hypothetical prote
1036	70	4.2	150	2	T52587	probable arabinoga
1037	70	4.2	150	2	T48611	agp6 protein - Ara
1038	70	4.2	209	2	AB2218	hypothetical prote
1039	70	4.2	210	2	JC7830	cytokine-inducible
1040	70	4.2	214	2	A46629	mucin 6, gastric (
1041	70	4.2	221	2	T47592	hypothetical prote
1042	70	4.2	234	2	G64858	probable membrane
1043	70	4.2	239	2	B83709	hypothetical prote
1044	70	4.2	256	2	AC2283	hypothetical prote
1045	70	4.2	298	2	C55223	minor tail protein
1046	70	4.2	310	2	T26267	hypothetical prote
1047	70	4.2	311	2	H96002	probable sugar kin
1048	70	4.2	321	2	T42750	hypothetical prote
1049	70	4.2	329	2	S38082	pathogenesis-relat
1050	70	4.2	333	2	G98297	ribose ABC transpo
1051	70	4.2	333	2	AH2985	ABC transporter, m
1052	70	4.2	350	2	S22456	hydroxyproline-ric
1053	70	4.2	350	2	AH3043	dehydrogenase Atu3
1054	70	4.2	350	2	D98242	lipopolysaccharide
1055	70	4.2	355	2	B26883	neural cell adhesi
1056	70	4.2	357	2	E72245	hydrolase, ama/hip
1057	70	4.2	358	2	A88082	protein T05A8.7 [i
1058	70	4.2	360	2	T08673	hypothetical prote
1059	70	4.2	409	2	T18726	hypothetical prote
1060	70	4.2	424	2	I51210	synaptotagmin p65
1061	70	4.2	425	2	T18723	hypothetical prote
1062	70	4.2	426	2	T04985	probable transamin
1063	70	4.2	445	2	S45713	potassium channel
1064	70	4.2	446	2	S66268	inward rectifier p
1065	70	4.2	455	2	AE0181	hypothetical prote
1066	70	4.2	456	2	T38221	hypothetical serin
1067	70	4.2	458	2	T26630	hypothetical prote
1068	70	4.2	461	2	T38698	nocl protein - fis
1069	70	4.2	462	2	T19830	hypothetical prote
1070	70	4.2	487	2	AI1505	hypothetical cell
1071	70	4.2	497	2	T51195	hypothetical prote
1072	70	4.2	529	2	S18453	variant surface gl
1073	70	4.2	542	2	B47022	chitinase (EC 3.2.
1074	70	4.2	584	2	JC7809	sulfakinin recepto
1075	70	4.2	589	2	AI0684	hypothetical prote
1076	70	4.2	599	2	G71481	probable phosphoen
1077	70	4.2	609	2	S62518	hypothetical prote
1078	70	4.2	611	2	T22456	hypothetical prote
1079	70	4.2	613	2	B90294	hypothetical prote
1080	70	4.2	617	2	T15408	hypothetical prote
1081	70	4.2	625	2	S34035	hypothetical prote
1082	70	4.2	651	2	S18874	nucleolin - Africa
1083	70	4.2	653	2	E86787	hypothetical prote
1084	70	4.2	662	2	T50464	glucose-regulated
1085	70	4.2	697	2	E96752	hypothetical prote
1086	70	4.2	706	2	S33761	transferrin precur
1087	70	4.2	714	2	T22454	hypothetical prote
1088	70	4.2	753	2	T24869	hypothetical prote
1089	70	4.2	768	2	E86417	unknown protein, 5
1090	70	4.2	770	2	T51024	related to C2H2 zi
1091	70	4.2	822	2	T51049	related to nucleol
1092	70	4.2	823	2	F90914	hypothetical prote
1093	70	4.2	835	2	JC6140	cell surface-assoc
1094	70	4.2	937	2	A56517	nucleoporin Nup98
1095	70	4.2	971	2	T19431	hypothetical prote
1096	70	4.2	971	2	F88448	protein C45G9.10 [
1097	70	4.2	1004	2	A55142	myosin-light-chain
1098	70	4.2	1186	2	T19050	hypothetical prote
1099	70	4.2	1213	2	A41724	limb deformity (ld
1100	70	4.2	1274	2	JN0015	trp protein - frui
1101	70	4.2	1275	2	JU0092	trp protein - frui
1102	70	4.2	1415	2	T08945	hypothetical prote
1103	70	4.2	1420	1	A44361	amiloride-sensitiv
1104	70	4.2	1589	2	C44766	defective chorion-
1105	70	4.2	1784	2	T10532	gag-pol polyprotei
1106	70	4.2	1868	2	S48938	hypothetical prote
1107	70	4.2	2440	2	S39162	transcription coac
1108	70	4.2	3163	1	JQ1895	genome polyprotein
1109	69.5	4.2	120	1	W4WL42	E4 protein - human
1110	69.5	4.2	124	2	E84613	hypothetical prote
1111	69.5	4.2	146	2	S52810	hypothetical prote
1112	69.5	4.2	171	2	H86413	hypothetical prote
1113	69.5	4.2	202	2	AB2378	hypothetical prote
1114	69.5	4.2	217	2	S01358	salivary glue prot
1115	69.5	4.2	219	2	B72291	hypothetical prote
1116	69.5	4.2	266	2	H55590	hypothetical prote
1117	69.5	4.2	271	2	B96773	hypothetical prote
1118	69.5	4.2	299	2	G70784	probable mmpS3 pro
1119	69.5	4.2	313	2	H36854	hemagglutinin - va
1120	69.5	4.2	316	2	S58719	probable membrane
1121	69.5	4.2	326	2	I48351	fos-related antige
1122	69.5	4.2	338	2	F69437	hypothetical prote
1123	69.5	4.2	338	2	S28004	probable cell surf
1124	69.5	4.2	364	2	T32589	hypothetical prote

1125	69.5	4.2	372	1	QQBE88	glycoprotein I pre
1126	69.5	4.2	372	2	T06745	hypothetical prote
1127	69.5	4.2	400	2	T32705	hypothetical prote
1128	69.5	4.2	417	2	AD0200	isocitrate dehydro
1129	69.5	4.2	423	2	T24383	hypothetical prote
1130	69.5	4.2	425	2	T24111	hypothetical prote
1131	69.5	4.2	427	2	T38526	ubiquitin regulato
1132	69.5	4.2	441	2	C75076	heme biosynthesis
1133	69.5	4.2	450	2	C90608	hypothetical prote
1134	69.5	4.2	458	2	F86433	protein T17H7.5 [i
1135	69.5	4.2	503	1	VMUT1B	variant surface gl
1136	69.5	4.2	514	2	A44100	cell adhesion mole
1137	69.5	4.2	514	2	A31643	cell adhesion 80K
1138	69.5	4.2	519	2	S69989	unspecific monooxy
1139	69.5	4.2	520	2	S14600	E2 glycoprotein pr
1140	69.5	4.2	532	2	G70986	probable coA ligas
1141	69.5	4.2	537	2	B97013	and cellulose-bind
1142	69.5	4.2	538	2	AG2902	conserved hypothet
1143	69.5	4.2	550	2	H97677	hypothetical prote
1144	69.5	4.2	551	2	G95176	conserved hypothet
1145	69.5	4.2	552	2	T25593	hypothetical prote
1146	69.5	4.2	568	2	A34891	Ig heavy chain pre
1147	69.5	4.2	574	2	A86365	probable auxin tra
1148	69.5	4.2	593	2	S55189	hypothetical prote
1149	69.5	4.2	593	2	T26865	hypothetical prote
1150	69.5	4.2	610	2	S59394	protein kinase RCK
1151	69.5	4.2	611	2	A54086	calnexin-t - mouse
1152	69.5	4.2	629	2	S20516	dnaK-type molecula
1153	69.5	4.2	640	2	T25367	hypothetical prote
1154	69.5	4.2	645	2	S41372	dnaK-type molecula
1155	69.5	4.2	646	2	T19206	hypothetical prote
1156	69.5	4.2	658	2	JC8011	G protein-coupled
1157	69.5	4.2	675	2	T03744	myoD protein inhib
1158	69.5	4.2	719	2	T47727	hypothetical prote
1159	69.5	4.2	736	2	T19366	hypothetical prote
1160	69.5	4.2	782	2	A82940	hypothetical prote
1161	69.5	4.2	816	2	A49151	fibroblast growth
1162	69.5	4.2	833	2	AF2089	hypothetical prote
1163	69.5	4.2	844	2	B64678	NADH2 dehydrogenas
1164	69.5	4.2	850	1	MMHUE4	erythrocyte membra
1165	69.5	4.2	852	2	T46091	hypothetical prote
1166	69.5	4.2	862	2	T46289	hypothetical prote
1167	69.5	4.2	871	2	S47518	cadherin - African
1168	69.5	4.2	942	2	T19553	hypothetical prote
1169	69.5	4.2	993	2	AE1905	outer membrane sec
1170	69.5	4.2	1051	2	JC4091	glycoprotein A - P
1171	69.5	4.2	1087	1	QFMSH	neurofilament trip
1172	69.5	4.2	1132	2	T43483	translation initia
1173	69.5	4.2	1460	2	S48457	nucleoporin RAT7 -
1174	69.5	4.2	1502	2	S45429	probable membrane
1175	69.5	4.2	1522	2	S48904	probable purine nu
1176	69.5	4.2	1870	2	D88486	protein F20H11.2 [
1177	69.5	4.2	1875	2	S38173	myosin-like protei
1178	69.5	4.2	1957	2	A45627	myosin heavy chain
1179	69.5	4.2	2894	2	C64474	hypothetical prote
1180	69.5	4.2	4199	2	S76412	hypothetical prote
1181	69	4.2	171	2	T31478	hypothetical prote
1182	69	4.2	234	2	T35448	hypothetical prote
1183	69	4.2	255	2	T22429	hypothetical prote
1184	69	4.2	258	2	S23106	priA protein - shi
1185	69	4.2	284	2	T06241	histone H1 (clone
1186	69	4.2	299	2	S44554	citrate transport
1187	69	4.2	303	2	S29185	sodium channel pro
1188	69	4.2	339	2	S08981	malate dehydrogena
1189	69	4.2	339	2	F97121	probable membrane-
1190	69	4.2	343	2	G86709	hypothetical prote
1191	69	4.2	344	1	RWRTC2	T-cell surface gly
1192	69	4.2	356	2	S73315	protoporphyrin IX
1193	69	4.2	371	1	FOMVCS	gag polyprotein -
1194	69	4.2	382	2	S71669	finger protein MIG
1195	69	4.2	387	2	T15462	hypothetical prote
1196	69	4.2	396	2	T26987	hypothetical prote
1197	69	4.2	400	1	A39822	leukosialin precur
1198	69	4.2	416	2	T34279	hypothetical prote
1199	69	4.2	423	2	T44258	transducer protein
1200	69	4.2	424	1	VGBEE9	glycoprotein gp63
1201	69	4.2	427	2	E83711	hypothetical prote
1202	69	4.2	431	2	G86277	F14L17.11 protein
1203	69	4.2	443	2	T14916	mitosis-specific c
1204	69	4.2	467	2	T26195	hypothetical prote
1205	69	4.2	483	2	G86902	dextransucrase (EC
1206	69	4.2	486	2	D64474	hypothetical prote
1207	69	4.2	490	1	C57150	NADP-reducing hydr
1208	69	4.2	495	2	T38959	hypothetical prote
1209	69	4.2	511	2	I50114	early growth respo
1210	69	4.2	513	2	S50915	SIN3 protein-bindi
1211	69	4.2	525	2	A35596	nuclear pore glyco
1212	69	4.2	538	2	S60645	NADH2 dehydrogenas
1213	69	4.2	555	2	B41492	58K antigen - Rick
1214	69	4.2	556	2	S06838	gamma-aminobutyric
1215	69	4.2	556	2	S51892	probable membrane
1216	69	4.2	583	2	T18999	hypothetical prote
1217	69	4.2	610	1	I46001	C4b-binding protei
1218	69	4.2	611	2	A53418	calmegin precursor
1219	69	4.2	647	2	B34457	204 protein - mous
1220	69	4.2	650	2	S22835	alpha-agglutinin -
1221	69	4.2	651	2	T21175	hypothetical prote
1222	69	4.2	652	2	S50210	surface layer prot
1223	69	4.2	658	2	T41309	hypothetical threo
1224	69	4.2	670	2	F84540	hypothetical prote
1225	69	4.2	677	2	S54561	RNA14 protein - ye
1226	69	4.2	725	2	E96592	hypothetical prote
1227	69	4.2	739	2	H72364	aspartokinase II -
1228	69	4.2	790	2	T34293	hypothetical prote
1229	69	4.2	793	1	KXRTF	furin (EC 3.4.21.7
1230	69	4.2	814	2	T49207	receptor kinase-li
1231	69	4.2	825	2	S26706	transcription fact
1232	69	4.2	836	2	T21631	hypothetical prote
1233	69	4.2	854	1	QRHYLD	LDL receptor precu
1234	69	4.2	871	2	T28706	hypothetical prote
1235	69	4.2	879	1	QRRTLD	LDL receptor precu
1236	69	4.2	903	1	VGBEK1	glycoprotein B pre
1237	69	4.2	988	2	A40628	probable transposa
1238	69	4.2	995	2	T27327	hypothetical prote
1239	69	4.2	1007	2	JC8066	138K protein - Tet
1240	69	4.2	1157	2	A55152	PAS1 protein - yea
1241	69	4.2	1203	2	T04294	hypothetical prote
1242	69	4.2	1204	2	F81158	exodeoxyribonuclea
1243	69	4.2	1215	2	S60904	hypothetical prote
1244	69	4.2	1360	2	T34302	cell polarity prot
1245	69	4.2	1385	2	T13415	hypothetical prote
1246	69	4.2	1455	1	A48925	mannose receptor p
1247	69	4.2	1624	2	T25592	hypothetical prote
1248	69	4.2	1633	2	T01879	hypothetical prote
1249	69	4.2	1680	2	T41628	probable transcrip
1250	69	4.2	1758	2	S57015	probable purine nu
1251	69	4.2	1804	2	H96597	hypothetical prote
1252	69	4.2	1819	2	D97033	uncharacterized pr
1253	69	4.2	1963	1	MWKW	myosin heavy chain
1254	69	4.2	2067	2	A42854	probable spindle p
1255	69	4.2	2329	2	S44625	C50C3.6 protein -
1256	69	4.2	2361	2	T25752	hypothetical prote
1257	69	4.2	2464	1	QRMSP1	microtubule-associ
1258	68.5	4.1	168	2	S52994	arabinogalactan-li
1259	68.5	4.1	189	1	ERAD75	early E3 20.6K gly
1260	68.5	4.1	189	2	JX0235	core protein MGC-2
1261	68.5	4.1	204	2	S51232	gibberellin-respon
1262	68.5	4.1	218	2	AH1837	hypothetical prote
1263	68.5	4.1	246	2	S47805	hypothetical 27.4K
1264	68.5	4.1	246	2	D91186	probable outer mem
1265	68.5	4.1	246	2	C86033	probable outer mem
1266	68.5	4.1	257	2	C84890	hypothetical prote
1267	68.5	4.1	261	2	D84262	hypothetical prote
1268	68.5	4.1	280	2	AE2031	gamma-tocopherol m
1269	68.5	4.1	287	2	S45662	histone H1 - tomat
1270	68.5	4.1	287	2	D95406	hypothetical prote

1271	68.5	4.1	288	2	T22846	hypothetical prote
1272	68.5	4.1	318	2	T20063	hypothetical prote
1273	68.5	4.1	345	2	T12344	NADH2 dehydrogenas
1274	68.5	4.1	349	2	T42965	glycoprotein - ate
1275	68.5	4.1	359	2	G70814	probable far prote
1276	68.5	4.1	378	2	T35403	probable polypreny
1277	68.5	4.1	385	2	H97239	polyferredoxin [im
1278	68.5	4.1	385	2	JC7783	RAD 23B protein -
1279	68.5	4.1	394	2	G84206	hypothetical prote
1280	68.5	4.1	408	1	QRHUBE	beta-3-adrenergic
1281	68.5	4.1	412	1	AJMSRS	argininosuccinate
1282	68.5	4.1	412	1	AJRTRS	argininosuccinate
1283	68.5	4.1	413	2	T04520	hypothetical prote
1284	68.5	4.1	414	1	QRHUB3	beta-3-adrenergic
1285	68.5	4.1	414	2	G64091	cell division prot
1286	68.5	4.1	420	2	A88962	protein F59A7.1 [i
1287	68.5	4.1	421	2	S09595	synaptotagmin P65
1288	68.5	4.1	426	2	A35641	5-aminoimidazole r
1289	68.5	4.1	435	2	C86340	protein F2D10.28 [
1290	68.5	4.1	435	2	T25350	hypothetical prote
1291	68.5	4.1	443	2	F71929	heat shock protein
1292	68.5	4.1	458	2	AC0121	probable exported
1293	68.5	4.1	498	1	VGXPLA	surface glycoprote
1294	68.5	4.1	502	2	T21935	hypothetical prote
1295	68.5	4.1	509	2	T48459	cytochrome P450-li
1296	68.5	4.1	514	1	A47692	fumarate hydratase
1297	68.5	4.1	527	2	T26732	hypothetical prote
1298	68.5	4.1	535	2	B84443	hypothetical prote
1299	68.5	4.1	536	2	AG1482	hypothetical prote
1300	68.5	4.1	553	2	A49364	59 protein, brain
1301	68.5	4.1	573	2	H96744	probable cytosolic
1302	68.5	4.1	588	2	JC8021	chitinase (EC 3.2.
1303	68.5	4.1	592	2	T32402	hypothetical prote
1304	68.5	4.1	594	2	S51412	hypothetical prote
1305	68.5	4.1	630	2	A39344	tumor-associated m
1306	68.5	4.1	637	2	T20981	hypothetical prote
1307	68.5	4.1	647	2	S26386	transcription fact
1308	68.5	4.1	659	2	T40383	hypothetical prote
1309	68.5	4.1	668	1	F64370	ferrous iron trans
1310	68.5	4.1	670	2	S22293	zinc finger protei
1311	68.5	4.1	696	2	G71829	probable outer mem
1312	68.5	4.1	697	2	A86402	protein T22C5.17 [
1313	68.5	4.1	699	2	T09483	Cys-rich protein R
1314	68.5	4.1	721	2	E70766	hypothetical prote
1315	68.5	4.1	725	2	T01268	leucine-rich repea
1316	68.5	4.1	737	2	AG2156	hypothetical prote
1317	68.5	4.1	751	2	AC2098	hypothetical prote
1318	68.5	4.1	763	2	S55616	glycoprotein H - e
1319	68.5	4.1	770	2	G88445	protein C26E6.2 [i
1320	68.5	4.1	795	2	T20609	hypothetical prote
1321	68.5	4.1	798	2	T50514	hypothetical prote
1322	68.5	4.1	825	1	GLHQ	beta-glucosidase (
1323	68.5	4.1	846	2	S52418	GTP-binding regula
1324	68.5	4.1	853	2	H70939	probable nirB prot
1325	68.5	4.1	865	2	AC1966	hypothetical prote
1326	68.5	4.1	914	2	T25220	hypothetical prote
1327	68.5	4.1	915	2	T33030	hypothetical prote
1328	68.5	4.1	925	2	T00781	hypothetical prote
1329	68.5	4.1	952	2	T18837	hypothetical prote
1330	68.5	4.1	1043	2	T13172	gag-like protein p
1331	68.5	4.1	1278	2	A71609	probable secreted
1332	68.5	4.1	1285	2	H85041	hypothetical prote
1333	68.5	4.1	1311	2	A56390	mannosyl-glycoprot
1334	68.5	4.1	1435	2	S69632	regulatory protein
1335	68.5	4.1	1438	2	A48216	neurexin III-alpha
1336	68.5	4.1	1444	1	A30588	140K adhesin precu
1337	68.5	4.1	1541	2	S46686	hypothetical prote
1338	68.5	4.1	1791	2	T24089	hypothetical prote
1339	68.5	4.1	2114	2	E96505	hypothetical prote
1340	68.5	4.1	2292	1	GNNYEB	genome polyprotein
1341	68.5	4.1	2292	1	GNNYED	genome polyprotein
1342	68.5	4.1	2292	2	S55401	capsid polyprotein
1343	68	4.1	62	2	S53366	mucin 5AC (clone M
1344	68	4.1	208	1	HSRT1T	histone H1t - rat
1345	68	4.1	211	2	H72608	hypothetical prote
1346	68	4.1	228	2	T33579	hypothetical prote
1347	68	4.1	245	2	D81977	hypothetical prote
1348	68	4.1	246	2	H90833	major tail protein
1349	68	4.1	256	2	B85691	probable tail comp
1350	68	4.1	268	2	T32740	hypothetical prote
1351	68	4.1	288	2	T21790	hypothetical prote
1352	68	4.1	295	2	S50316	CIN5 protein - yea
1353	68	4.1	301	2	H70644	hypothetical prote
1354	68	4.1	304	2	G89790	hypothetical prote
1355	68	4.1	333	2	T15367	hypothetical prote
1356	68	4.1	339	2	AH0050	probable periplasm
1357	68	4.1	360	2	S69063	probable membrane
1358	68	4.1	372	2	T45628	glycerophosphodies
1359	68	4.1	378	2	S61992	SLG1 protein - yea
1360	68	4.1	380	1	S51826	alcohol dehydrogen
1361	68	4.1	384	2	H64161	hypothetical prote
1362	68	4.1	387	2	A56275	1,3-propanediol de
1363	68	4.1	388	2	T43019	probable DNA-bindi
1364	68	4.1	402	2	T20595	hypothetical prote
1365	68	4.1	416	2	T19149	hypothetical prote
1366	68	4.1	420	2	T42616	envelope protein -
1367	68	4.1	422	1	BMHU1Y	synaptotagmin I -
1368	68	4.1	423	2	T14531	S-locus-specific g
1369	68	4.1	423	2	H84257	Htr13 transducer [
1370	68	4.1	426	2	I48379	gene hb protein -
1371	68	4.1	427	2	JH0413	synaptotagmin o-p6
1372	68	4.1	452	2	T46147	zinc finger protei
1373	68	4.1	461	2	D96647	hypothetical prote
1374	68	4.1	461	2	T39862	hypothetical prote
1375	68	4.1	479	2	A84588	probable tyrosine
1376	68	4.1	487	1	S07061	glutamate receptor
1377	68	4.1	493	2	D86652	IMP dehydrogenase
1378	68	4.1	500	2	AI1913	apolipoprotein N-a
1379	68	4.1	503	2	T51782	hypothetical prote
1380	68	4.1	514	2	S18449	variant surface gl
1381	68	4.1	515	2	B84406	TRK potassium upta
1382	68	4.1	516	2	A31270	radial spoke prote
1383	68	4.1	537	1	FOMVM7	gag polyprotein -
1384	68	4.1	543	2	A38093	transformation-sen
1385	68	4.1	550	2	T06379	SAR DNA-binding pr
1386	68	4.1	562	2	B41035	chitinase (EC 3.2.
1387	68	4.1	562	2	S50371	chitinase (EC 3.2.
1388	68	4.1	573	2	S50661	hypothetical prote
1389	68	4.1	576	2	S75958	hypothetical prote
1390	68	4.1	581	2	T22455	hypothetical prote
1391	68	4.1	590	2	S66956	hypothetical prote
1392	68	4.1	599	1	A54906	afamin precursor -
1393	68	4.1	600	2	S56744	mucin (clone pGM7-
1394	68	4.1	610	2	T22909	hypothetical prote
1395	68	4.1	621	1	YRNC	monophenol monooxy
1396	68	4.1	623	2	T28051	hypothetical prote
1397	68	4.1	630	2	S77346	hypothetical prote
1398	68	4.1	632	2	T48616	hypothetical prote
1399	68	4.1	638	2	S36723	FUN36 protein - ye
1400	68	4.1	645	2	T16078	hypothetical prote
1401	68	4.1	647	2	T39141	hypothetical prote
1402	68	4.1	648	2	T04837	probable serine/th
1403	68	4.1	655	1	A55726	RNA-binding protei
1404	68	4.1	659	2	H81431	methyl-accepting c
1405	68	4.1	659	2	A98085	hypothetical prote
1406	68	4.1	662	2	B81251	probable methyl-ac
1407	68	4.1	668	2	B86831	hypothetical prote
1408	68	4.1	669	2	B70186	translation elonga
1409	68	4.1	686	2	S66693	hypothetical prote
1410	68	4.1	695	2	I51652	dsRNA-binding prot
1411	68	4.1	698	1	JX0202	long-chain-fatty-a
1412	68	4.1	709	2	S51793	dibasic processing
1413	68	4.1	730	2	A75486	hypothetical prote
1414	68	4.1	733	2	T01875	probable long-chai
1415	68	4.1	752	2	T34355	hypothetical prote
1416	68	4.1	761	2	T03719	probable thyroid r

1417	68	4.1	784	2	C82679	cell division prot
1418	68	4.1	786	2	A55501	cyclin F - human
1419	68	4.1	790	1	FOMVHZ	gag-kit polyprotei
1420	68	4.1	793	2	S65240	probable membrane
1421	68	4.1	833	2	G75621	arylesterase/monox
1422	68	4.1	849	2	T20422	hypothetical prote
1423	68	4.1	859	2	S66827	aluminium resistan
1424	68	4.1	864	2	A43954	glutamate receptor
1425	68	4.1	869	2	S35792	glutamate receptor
1426	68	4.1	899	1	GNMVMM	pol polyprotein -
1427	68	4.1	903	2	T00074	hypothetical prote
1428	68	4.1	908	2	S19098	glutamate receptor
1429	68	4.1	923	2	A86334	T20H2.17 protein -
1430	68	4.1	971	2	T10678	hypothetical prote
1431	68	4.1	974	2	S34189	starch phosphoryla
1432	68	4.1	991	2	S43891	dna exoribonucleas
1433	68	4.1	1010	2	T16616	hypothetical prote
1434	68	4.1	1018	2	T18249	conserved hypothet
1435	68	4.1	1052	2	T14343	zinc finger RNA bi
1436	68	4.1	1072	2	A37127	microtubule-associ
1437	68	4.1	1117	2	S63399	probable membrane
1438	68	4.1	1153	2	T21386	hypothetical prote
1439	68	4.1	1173	2	S48877	Ca2+-transporting
1440	68	4.1	1196	2	S35994	DNA repair protein
1441	68	4.1	1203	2	T51029	related to pathway
1442	68	4.1	1230	2	T22458	hypothetical prote
1443	68	4.1	1260	2	S60896	agglutinin-like pr
1444	68	4.1	1275	2	T33369	hypothetical prote
1445	68	4.1	1279	2	T13613	hypothetical prote
1446	68	4.1	1280	2	T00365	hypothetical prote
1447	68	4.1	1338	2	T40993	protein kinase cek
1448	68	4.1	1371	2	T29019	hypothetical prote
1449	68	4.1	1429	2	T13720	gene expanded prot
1450	68	4.1	1440	1	SYHUQT	multifunctional am
1451	68	4.1	1541	2	A37023	IgA-specific metal
1452	68	4.1	1545	2	B41859	IgA-specific metal
1453	68	4.1	1578	2	I48216	neurexin III-alpha
1454	68	4.1	1711	2	T31337	1,4-beta-glucanase
1455	68	4.1	1772	2	A45532	major merozoite su
1456	68	4.1	1968	1	S05697	myosin heavy chain
1457	68	4.1	2228	2	T14029	variant-specific s
1458	68	4.1	2810	2	T22298	hypothetical prote
1459	68	4.1	3191	2	T22945	hypothetical prote
1460	68	4.1	3712	2	S18253	laminin alpha-1 ch
1461	67.5	4.1	117	2	AB0028	50S ribosomal prot
1462	67.5	4.1	127	2	T30102	hypothetical prote
1463	67.5	4.1	137	2	F95239	conserved domain p
1464	67.5	4.1	137	2	H98103	hypothetical prote
1465	67.5	4.1	159	2	T31598	hypothetical prote
1466	67.5	4.1	180	2	T31974	hypothetical prote
1467	67.5	4.1	191	2	S38117	hypothetical prote
1468	67.5	4.1	210	2	B88082	protein T05A8.6 [i
1469	67.5	4.1	232	1	WMADC2	early E1A 25K prot
1470	67.5	4.1	235	2	T02598	probable replicati
1471	67.5	4.1	238	2	T07921	probable starch sy
1472	67.5	4.1	240	2	H69932	hypothetical prote
1473	67.5	4.1	248	2	PQ0769	glycoprotein G - b
1474	67.5	4.1	252	2	AG1423	hypothetical prote
1475	67.5	4.1	256	2	H36857	B26R protein - var
1476	67.5	4.1	297	2	S55063	conserved hypothet
1477	67.5	4.1	306	2	AE1156	hypothetical prote
1478	67.5	4.1	311	2	T40921	hypothetical prote
1479	67.5	4.1	326	2	S15749	transforming prote
1480	67.5	4.1	327	2	D90530	hypothetical prote
1481	67.5	4.1	345	2	E88103	protein W10G11.5 [
1482	67.5	4.1	345	2	S73729	MG307 homolog H08_
1483	67.5	4.1	346	2	T46916	hypothetical prote
1484	67.5	4.1	348	2	C88088	protein B0454.9 [i
1485	67.5	4.1	348	2	T40623	probable polyA-bin
1486	67.5	4.1	355	2	T15526	hypothetical prote
1487	67.5	4.1	358	2	T01296	leucine-rich repea
1488	67.5	4.1	364	1	OOHUR	opsin, red-sensiti
1489	67.5	4.1	369	2	AG1950	hypothetical prote
1490	67.5	4.1	376	2	D72647	hypothetical prote
1491	67.5	4.1	383	2	E96972	riboflavin biosynt
1492	67.5	4.1	391	2	A44063	paired box transcr
1493	67.5	4.1	399	2	T42242	hypothetical 44.2K
1494	67.5	4.1	410	2	C84638	probable WRKY-type
1495	67.5	4.1	426	2	AI1920	ABC transporter AT
1496	67.5	4.1	467	2	B86225	protein T12M4.6 [i
1497	67.5	4.1	476	2	T27051	hypothetical prote
1498	67.5	4.1	482	2	AI2094	hypothetical prote
1499	67.5	4.1	487	2	T49424	hypothetical prote
1500	67.5	4.1	493	2	A34130	gamma-aminobutyric

ALIGNMENTS

RESULT 1
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CA
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <ZHO>
A;Cross-references: UNIPROT:P15379; UNIPARC:UPI000002A5F4; GB:M30655; NID:g200332; PIDN
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 13.9%; Score 229.5; DB 2; Length 363;
Best Local Similarity 24.9%; Pred. No. 7.7e-11;
Matches 89; Conservative 57; Mismatches 148; Indels 63; Gaps 14;

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Qy         15 WTTR---LLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGK 71
              | |      |:| ||  ::: : |:||  |:  | |      :: ||| : |:    :|
Db          6 WHTAWGLCLLQLSLAHQQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTM 65

Qy         72 DQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNS 131
              ||:: ||   |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:
Db         66 DQMKLALSKGFETCRYGFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCFNA 124

Qy        132 SDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT---- 182
              |      |     |:   : |:     |   :  | | ||    | |    | |
Db        125 SAPPEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDD 179

Qy        183 ----------TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFK--- 227
                       :||      | :|  :      : |   ||::| : :   ::: : :
Db        180 DVSSGSTIEKSTPEGYILHTYLPTEQPTGDQDDSPFIRSTLATRDRDSSKDSRGSSRTVT 239

Qy        228 --NEAAGFGG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFP 267
                :| ||                   :|  |::|| |     |  | |     :
Db        240 HGSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAVNS 293

Qy        268 FTNKNQQKEMI---ETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 321
                 |:|:::       |:: | :: |  | ||  :     :| ||:|  :|: |:
Db        294 RRRCGQKKKLVINGGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 349
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RESULT 2
A30901
lymphocyte adhesion receptor precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 21-Jul-2000
C;Accession: A33935; A30901
R;Idzerda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John,
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion rece
A;Reference number: A33935; MUID:89282830; PMID:2471974

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A;Accession: A33935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <IDZ>
A;Cross-references: UNIPARC:UPI000012736C; GB:M22452; NID:g176576; PID:g176577
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD44; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antig
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>
F;21-270/Domain: extracellular #status predicted <EXT>
F;271-290/Domain: transmembrane #status predicted <TMM>
F;291-362/Domain: intracellular #status predicted <CYT>
F;25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             13.4%;  Score 222.5;  DB 2;  Length 362;
  Best Local Similarity   25.5%;  Pred. No. 2.8e-10;
  Matches   92;  Conservative   43;  Mismatches  127;  Indels   99;  Gaps   16;

Qy         20 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 79
              ||| ||   :: : ::||  ||  | |     :: ||| : |:    :|    |:| ||
Db         14 LVQLSL--AQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS 71

Qy         80 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 139
                ||||  ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPGEDC 129

Qy        140 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP------APT---------- 182
                 |:   : |      |   :  | | |     | | |      :||
Db        130 -----TSVTDLPNAFDGPITITIVNRDGTRYVKKGEYRTNPEDINPSSPTDDDVSSGSSS 184

Qy        183 ----------------TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAF 226
                           |:|| |                    | ||:  |   :: ||
Db        185 ERSSTLGGYIFYNHFSTSPPIPDEDG---------------PWITDSTDRTPATRDQGAF 229

Qy        227 K----------NEAAGF------GG------------VPTALLVLALLFFGAAAGLGFCY 258
                      :|:||       ||            :|  |::|| |     |  |  |
Db        230 DPSGGSHTTHGSESAGHSHGSREGGANTTSGPLRTPQIPEWLIILASL-LALALILAVC- 287

Qy        259 VKRYVKAFPPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----NPEESKSPS 311
                 :          |:|:::       |:: |::  |  | ||  :     | | |::|
Db        288 ----IAVNSRRRCGQKKKLVINNGNGAVEDRKSSGLN-GEASKSQEMVHLVNKESSETPD 342

Qy        312 K 312
              :
Db        343 Q 343


RESULT 3
A34424
CD44 membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
A;Reference number: A34424; MUID:90046829; PMID:2682651
A;Accession: A34424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <NOT>
A;Cross-references: UNIPARC:UPI00000E88CD; GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:
R;Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antige
A;Reference number: A34907; MUID:90094420; PMID:2403559
A;Accession: A34907
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 8-195,'G',197-365 <WOL>
A;Cross-references: UNIPARC:UPI000016CFB0; GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

  Query Match             13.4%;  Score 222.5;  DB 2;  Length 365;
  Best Local Similarity   24.5%;  Pred. No. 2.8e-10;
  Matches   88;  Conservative   56;  Mismatches  150;  Indels   65;  Gaps   14;

Qy         15 WTTR---LLVQGSLR--AEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLA 69
                | |     |:| ||    ::: : |:||  |:  | |      :: ||| : |:    :|
Db          6 WHTAWGLCLLQLSLAHPHQQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLP 65

Qy         70 GKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCY 129
                ||:: ||   |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:
Db         66 TMDQMKLALSKGFETCRYGFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCF 124

Qy        130 NSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST---------- 177
                |:|      |     |:   : |:     |   :  | | ||    | |
Db        125 NASAPPEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNII 179

Qy        178 ----IPAPTTTPPAPAS----TSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFK- 227
                     |    | |    | :|  :      : |   ||::| : :   ::: : :
Db        180 DDDVSSGSTIEKSTPESYILHTYLPTEQPTGDQDDSFFIRSTLATRDRDSSKDSRGSSRT 239

Qy        228 ----NEAAGFGG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKA 265
                   :| ||                   :|  |::|| |     |  |  |     :
Db        240 VTHGSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAV 293

Qy        266 FPFTNKNQQKEMI---ETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 321
                  |:|:::       |:: | :: |  | ||  :     :| ||:|  :|: |:
Db        294 NSRRRCGQKKKLVINGGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 351


RESULT 4
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.; Matzku, S.
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinom
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: UNIPROT:P26051; UNIPARC:UPI000012736D; GB:M61874; NID:g576534; PIDN:
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: UNIPARC:UPI0000179A9B; GB:M61875
C;Keywords: cell adhesion

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  Matches   84;  Conservative   40;  Mismatches  165;  Indels   38;  Gaps   11;

Qy         15 WTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQV 74
                |    |:| ||  ::: : ::||  |:  | |      :: ||| : |     :|    |:
Db         10 WGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQM 69

Qy         75 ETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDT 134
                | ||:  |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|
Db         70 ELALRKGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAP 128

Qy        135 WTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------- 182
                   |      |:   : |:     |   :  | | ||    | |    | |
Db        129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVS 183

Qy        183 -------TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFKNEAAGF 233
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                 :||      | :|  :      : |   ||::|  | |:|       |   :
Db        184 SGSTIEKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATIATTPWVSAHTKQNQERTQW 243

Qy        234 GGV---PTALLVLALLFFGAAAGLGFCYVKRYVK--AFPFTNKNQQKEMIETKVVKEEKA 288
              :   |  ||                 : : : :    || |   | |  ||
Db        244 NPIHSNPEVLLQTTTRMTDIDRNSTSAHGENWTQEPQPPFNNHEYQDEE-ETPHATSTTW 302

Qy        289 NDSNPNEESKKTDK-----NPEESKSP 310
                | |   |   | |     |  : |:|
Db        303 ADPNSTTEEAATQKEKWFENEWQGKNP 329


RESULT 5
A35616
T-cell surface glycoprotein CD44 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A35616
R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A;Title: CD44 is the principal cell surface receptor for hyaluronate.
A;Reference number: A35616; MUID:90304889; PMID:1694723
A;Accession: A35616
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-362 <ARU>
A;Cross-references: UNIPROT:P20944; UNIPARC:UPI0000179518
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein

  Query Match             13.1%;  Score 217.5;  DB 2;  Length 362;
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  Matches   88;  Conservative   46;  Mismatches  149;  Indels   63;  Gaps   12;

Qy         24 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFE 83
              ||  |:: : ::||  |:  | |     :: ||| : |:    :|   ||:  ||   ||
Db         18 SLAHEQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVMALSKGFE 77

Qy         84 TCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI 143
              || ||:: :| ||| || ||  |  | || |     |  :  ||:|:|      |
Db         78 TCRYGFI-EGHVVIPRIQPNAICAANHTGVYILTSNTS-HYDTYCFNASAPLEEDC---- 131

Qy        144 ITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPTTTPPAPAS-------- 190
               |:   : |:     |   :  | | ||    | |    | |  ||    :|
Db        132 -TSVTDLPNSFEGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNTTDDDVSSGSSSEKST 190

Qy        191 -------TSIPRRKKLICVTEVFMETSTMSTE--------------------TEPFVEN 222
                    | :|         : :   |||:|                       |    |
Db        191 SGGYVFHTYLPTIHSTADQDDPYFIGSTMATRDQDSSMDPRGNSLTVTDGSKLTGHSSGN 250

Qy        223 KAAFKNEAAGFG---GVPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 279
              : :  |  :  |    :|  |:||| |    |  |  |     :         |:|:::
Db        251 QDSGANTTSRPGRKPQIPEWLIVLASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 304

Qy        280 TKVVKEEKANDSNPNEESKKTDKNPE----ESKSPSKTTVRCLEAE 321
                  |  |  |:| : :  |: |     :| ||:|  : : |:
Db        305 NS--GNGKVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQFMTAD 348


RESULT 6
A53286
cell-surface glycoprotein CD44 precursor - bovine
N;Alternate names: CD44 protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53286; S22123
R;Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A;Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A;Reference number: A53286; MUID:92017904; PMID:1922105
A;Accession: A53286
A;Molecule type: mRNA
A;Residues: 1-366 <BOS>
A;Cross-references: UNIPROT:Q29423; UNIPARC:UPI0000127366; EMBL:X62881; NID:g186; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F;274-294/Domain: transmembrane #status predicted <TMM>
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match             12.6%;  Score 208.5;  DB 2;  Length 366;
  Best Local Similarity   23.8%;  Pred. No. 3.7e-09;
  Matches   81;  Conservative   44;  Mismatches  142;  Indels   73;  Gaps   11;

Qy         20 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 79
              ||| ||   :: : ::||  |:  | |     :: ||| : |:    :|    |:| |
Db         14 LVQLSL--AQIDLNITCRYAGVFHVEKNGRYSISKTEAADLCKAFNSTLPTMAQMEAARN 71

Qy         80 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 139
               |||| ||:: :| ||| || ||  |  | || |     | |:   |:|:|      |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTICFNASAPPGEDC 129

Qy        140 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP--------APTTTPPAPAS 190
                  |:   : |       |   :  | | |:    | | |        :|:: |    |
Db        130 -----TSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSVVSPSSPPDDEMS 184

Qy        191 TSIPRRKKLICVTEVF----------------------METSTMSTETEPFVENKAAFK 227
              :  |  :      :|                      :|    :  :|   :
Db        185 SGSPSERSTSGGYSIFHTHLPTVHPSRPRRPWSQRAENTSDTRDYGSSHDPSGRSYTTHA 244

Qy        228 NEAAGFGG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFT 269
              :|:||                   :|  |::|| |     |  |  |     :
Db        245 SESAGHSSGSEEHGANTTSGPMRKPQIPEWLIILASL-LALALILAVC-----IAVNSRR 298

Qy        270 NKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKS 309
                |:|:::          | :   || | :  | | |||
Db        299 RCGQKKKLVIN--------NGNGTMEERKPSGLNGEASKS 330


RESULT 7
JH0417
cell adhesion molecule CD44 - human
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 31-Dec-2004
C;Accession: JH0417; A32376; G02251; A32377
R;Harn, H.J.; Isola, N.; Cooper, D.L.
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991
A;Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte c
A;Reference number: JH0417; MUID:91337049; PMID:1840487
A;Accession: JH0417
A;Molecule type: mRNA
A;Residues: 1-361 <HAR>
A;Cross-references: UNIPROT:Q92493; UNIPARC:UPI000016A68F; GB:M59040; NID:g180129; PIDN
A;Experimental source: reticulocyte
A;Note: the authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA
R;Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.
Cell 56, 1057-1062, 1989
A;Title: A lymphocyte molecule implicated in lymph node homing is a member of the carti
A;Reference number: A32376; MUID:89168434; PMID:2466575
A;Accession: A32376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238,'E',240-361 <STA>
A;Cross-references: UNIPARC:UPI0000143A5B; GB:M24915; NID:g180196; PIDN:AAA35674.1; PID
R;Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.
submitted to the EMBL Data Library, November 1995
A;Reference number: H00921
A;Accession: G02251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-25,'M',27-108,'S',110-361 <BOS>
A;Cross-references: UNIPARC:UPI000016A285; EMBL:U40373; NID:g1101785; PID:g1101786
R;Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.;
Cell 56, 1063-1072, 1989
```

```
A;Title: A human lymphocyte homing receptor, the hermes antigen, is related to cartilage
A;Reference number: A32377; MUID:89168435; PMID:2466576
A;Accession: A32377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108,'S',110-293,'S' <GOL>
A;Cross-references: UNIPARC:UPI0000070BED; GB:M25078; NID:g186660; PIDN:AAA36138.1; PID:
C;Keywords: alternative splicing; cell adhesion; surface antigen; transmembrane protein
F;269-285/Domain: transmembrane #status predicted <TMM>

  Query Match            12.4%;  Score 205;  DB 2;  Length 361;
  Best Local Similarity   24.4%;  Pred. No. 7e-09;
  Matches   83;  Conservative   46;  Mismatches  145;  Indels   66;  Gaps   14;

Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 144
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDC----- 129

Qy        145 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA---PTTTPPAPASTSIPRRKKLI 200
              |:   : |      |   :  | | |     | | |    |:       |:     :
Db        130 TSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSST 189

Qy        201 CVTEVPMETSTM-------------STETEPFVENKAAFK----------NEAAGF---- 233
                :|   ||:              ||:  |   ::  |           :|: |
Db        190 SGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATRDQDTFHPSGGSHTTHGSESDGHSHGS 249

Qy        234 --GG------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 279
                ||            :|  |::|| |    |  |  |     :          |:|:::
Db        250 QEGGANTTSGPIRTPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 303

Qy        280 TK---VVKEEKANDSNPNEESKKTDK----NPEESKSPSK 312
                |:: | :  |  | ||  :     | | |::| :
Db        304 NSGNGAVEDRKPSGLN-GEASKSQEMVHLVNKESSETPDQ 342


RESULT 8
S45305
CD44 antigen precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S45305
R;Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.
Biochim. Biophys. Acta 1218, 112-114, 1994
A;Title: Molecular cloning of the canine CD44 antigen cDNA.
A;Reference number: S45305; MUID:94250687; PMID:7514890
A;Accession: S45305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <MIL>
A;Cross-references: UNIPROT:Q28284; UNIPARC:UPI0000127367; EMBL:Z27115; NID:g473226; PID
C;Superfamily: human cell adhesion protein CD44

  Query Match            12.2%;  Score 202.5;  DB 2;  Length 351;
  Best Local Similarity   23.4%;  Pred. No. 1.1e-08;
  Matches   84;  Conservative   49;  Mismatches  145;  Indels   81;  Gaps   15;

Qy         15 WTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQV 74
              |   ||    |   :: : ::||  |:  | |     :: | | : |:    :|    |:
Db          3 WGLCLL---RLSLAQIDLNITCRYAGVFHVEKNGRYSISRTAAADLCKAFNSTLPTMAQM 59

Qy         75 ETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDT 134
              | ||   |||| ||:: :| ||| || ||  |  |  || |  :  : |:  ||:|:|
Db         60 ERALSVGFETCRYGFI-EGHVVIPRIQPNAICAANHTGVYI-LISNTSQYDTYCFNASAP 117

Qy        135 WTNSCIPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA---PTTTPPAPAS 190
                |     |:   : |     |   :  | | ||    | | |    |:       |
Db        118 PEEDC-----TSVTHLPNAFDGPITITIVNRDGTRYSQKGEYRTNPEDINPSNPTDDDVS 172

Qy        191 TSIPRRKKLICVTEVF-----------METSTMSTETE-------------PFVENKAA 225
                :     :       :|             ::| :|: ::              |   :
Db        173 SGSSSERSTSAGYNIFHTHLPTAYPTEDQDSSRVSSNSDHTPITKDHDSSVHPSERSHTT 232

Qy        226 FKNEAAGF------GG------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFP 267
                :|:||       ||            :|  |::|| |    |  |  |
Db        233 HGSESAGHSSGSQEGGANTTSGPMRKPQIPEWLIILASL-LALALILAVCIA-------- 283

Qy        268 FTNKNQQKEMIETKVVKEEKAN----DSNP---NEESKKTDK-----NPEESKSPSKTT 314
                  | ::   : | :      |    | |   | |: |: :     | | |::| : |
Db        284 ---VNSRRRCGQKKKLVINNGNGAVGDRKPSGINGEASKSQEMVHLVNKEPSETPDQYT 339


RESULT 9
A47195
lymphocyte homing receptor isoform CD44 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47195
R;Screaton, G.R.; Bell, M.V.; Jackson, D.G.; Cornelis, F.B.; Gerth, U.; Bell, J.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 12160-12164, 1992
A;Title: Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals at
A;Reference number: A47195; MUID:93101687; PMID:1465456
A;Accession: A47195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-742 <SCR>
A;Cross-references: UNIPROT:Q9UJ36; UNIPARC:UPI000017C297
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120739,
, NCBIN:120764, NCBIN:120766, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:120776, NCE

  Query Match            12.2%;  Score 202;  DB 2;  Length 742;
  Best Local Similarity   26.0%;  Pred. No. 3e-08;
  Matches   61;  Conservative   30;  Mismatches   84;  Indels   60;  Gaps    7;

Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 ----------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 170
                                           || |   :|  :  ::  ::|   :   |
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        171 VASPYSTI-PAPTTTPP--------APASTSIPRRKKLICVTEVFMETSTMSTET 216
                :   :||: | |     |          ||:|                | ||  :|||
Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATT-------------LMSTSATATET 234


RESULT 10
JH0518
lymphocyte homing receptor CD44, splice form CD44R1 - human
N;Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface
N;Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing recept
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R;Dougherty, G.J.; Lansdorp, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A;Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 lym
A;Reference number: JH0518; MUID:91277598; PMID:2056274
A;Accession: JH0518
A;Molecule type: mRNA
A;Residues: 1-426 <DOU>
A;Cross-references: UNIPROT:Q9UCB0; UNIPARC:UPI0000179519
A;Experimental source: lymphocytes, cell line KG1a
A;Accession: JH0519
A;Molecule type: mRNA
A;Residues: 1-223,288-426 <DO2>
A;Cross-references: UNIPARC:UPI000017951A
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A;Experimental source: lymphocyte, cell line KG1a
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta,
Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal e
A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
A;Molecule type: DNA
A;Residues: 223-357 <COO>
A;Cross-references: UNIPARC:UPI000017951B
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat
A;Reference number: A39209; MUID:91177958; PMID:2007624
A;Accession: A39209
A;Molecule type: mRNA
A;Residues: 184-376 <BRO>
A;Cross-references: UNIPARC:UPI000016A690; GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:g
R;Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by ins
A;Reference number: A42402; MUID:92165834; PMID:1537855
A;Accession: A42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-223,288-359 <JAC>
A;Cross-references: UNIPARC:UPI000017951C
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
A;Note: variant B
A;Accession: C42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-320 <JA2>
A;Cross-references: UNIPARC:UPI000017951D
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
A;Note: variant D
R;Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy
A;Reference number: A53029; MUID:94149816; PMID:7508992
A;Accession: A53029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76,'X',78-89 <SHE>
A;Cross-references: UNIPARC:UPI000006D03F
C;Genetics:
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 35/1; 65/1; 133/1
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycc
F;1-426/Product: lymphocyte homing receptor CD44, splice form CD44R1 #status predicted <
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 12.0%; Score 199.5; DB 2; Length 426;
Best Local Similarity 22.2%; Pred. No. 2.4e-08;
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;

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Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 -----------------------------PEIITTKDPIFNTQTATQTTE-------FI 163
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        164 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 201
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        202 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAGFGGVP------TALLVLALL 246
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLL----- 308

Qy        247 FFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKV-----VKEEKANDSNPN-EESKKT 300
Db        309 ------------EGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSG 355

Qy        301 DKNPEESKSPSKTT 314
Db        356 DQDTFHPSGGSHTT 369
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RESULT 11
S13530
CD44E protein, epithelial - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S13530
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with
A;Reference number: S13530; MUID:91122041; PMID:1991450
A;Accession: S13530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-493 <STA>
A;Cross-references: UNIPARC:UPI0000159271; EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PI
C;Keywords: transmembrane protein

Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 2.9e-08;
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;

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Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 -----------------------------PEIITTKDPIFNTQTATQTTE-------FI 163
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        164 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 201
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        202 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAG 232
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTG 293
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RESULT 12
I77371
CD44R5 - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I77371
R;Tanabe, K.K.; Nishi, T.; Saya, H.
Mol. Carcinog. 7, 212-220, 1993
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44
A;Reference number: I57483; MUID:93356912; PMID:8352881
A;Accession: I77371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-395 <RES>
A;Cross-references: UNIPARC:UPI000016B3F6; GB:S66400; NID:g435697; PIDN:AAB27919.1; PID
C;Genetics:

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A;Gene: GDB:CD44
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 257/1
C;Superfamily: human cell adhesion protein CD44

  Query Match            11.9%;  Score 198;  DB 2;  Length 395;
  Best Local Similarity  23.0%;  Pred. No. 2.9e-08;
  Matches   85;  Conservative   49;  Mismatches  145;  Indels   90;  Gaps   14;

Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 ------------------------------PEIITTKDPIFNTQTATQTTEFIVSDS--- 167
                                           || |   :|  :  ::  ::|   :
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        168 --TYSVASPY----------STIPAPTTTPPAPASTSI-PRRKKLICVTEVFMETSTMST 214
                |:|   |           ||   | |   :  ||:: |       : |    |  :|
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        215 ET------EPFVENKAAFKNEAAGF------GG------------VPTALLVLALLFFGA 250
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Db        255 TTRDQDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASL-LAL 313

Qy        251 AAGLGFCYVKRYVKAFPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----N 303
              | | |     :          |:|:::       |:: | :  |  | ||  :    |
Db        314 ALILAVC-----IAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLN-GEASKSQEMVHLVN 367

Qy        304 PEESKSPSK 312
              | |::| :
Db        368 KESSETPDQ 376


RESULT 13
I37369
epican - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: I37369; S24631
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.
J. Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is
A;Reference number: I37369; PMID:1281868
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Accession: I37369
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-699 <RES>
A;Cross-references: UNIPARC:UPI000016A89D; EMBL:X66733; NID:g31190; PID:g31191

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Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
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Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 ------------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 170
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Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        171 VASPYSTI-PAPTTTPP--APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENK 223
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Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATS---------TSSNTISAGWEPNEENE 240


RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butcl
Immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <TA2>
A;Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NID:g1059; PIDN:
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

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Qy         25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 84
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:: ||   |||
Db         17 LSLAQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMQKALNIGFET 76

Qy         85 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
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Db         77 CRIGFI-EGHVVIPPIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        141 -------PEIIT----------------TKDPIFNTQTATQTTEFIVSDSTYSVASPYST 177
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Db        135 LPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSTPADDDVSSGSSSERSTSGGYSI 194

Qy        178 IPA--PTTTP------------PAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENK 223
                 ||| |             |    |:  |       |    |||  || ::   |
Db        195 FHTHLPTTRPTQDQSSPWVSDSPEKTPTTKDRASGGRAQTTHGSETSGHSTGSQ---EGG 251

Qy        224 AAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETK-- 281
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Db        252 ASTTSGPIRRPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKKKLVINNGN 305

Qy        282 -VVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 321
               | : ||:  |  | |:  :     :|  |:|  : : |:
Db        306 GAVDDRKASGLN-GEASRSQEMVHLVNKESSETQDQFMTAD 345


RESULT 15
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2109 <LIX>
A;Cross-references: UNIPROT:P07898; UNIPARC:UPI000013177F; GB:L21913; NID:g416133; PIDN:
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
A;Accession: S39796
A;Molecule type: mRNA
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A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,'A'
A;Cross-references: UNIPARC:UPI0000173C73; GB:M88101
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.
A;Reference number: S27356; MUID:93111968; PMID:1339285
A;Accession: S27356
A;Molecule type: mRNA
A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1549,'T'
A;Cross-references: UNIPARC:UPI0000173C74; UNIPARC:UPI0000173C75; EMBL:M88101
R;Sai, S.; Tanaka, T.; Kosher, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A;Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly
A;Reference number: A25442; MUID:86259736; PMID:3460082
A;Accession: A25442
A;Molecule type: mRNA
A;Residues: 1693-1795,'G',1797-1855,1894-2109 <SAI>
A;Cross-references: UNIPARC:UPI00001712F6; GB:M13993; NID:g211654; PIDN:AAA48720.1; PID:
A;Experimental source: sternal cartilage
R;Tanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A;Reference number: A32002; MUID:89008500; PMID:3170613
A;Accession: A32002
A;Molecule type: DNA
A;Residues: 1893-1987,'S',1989-2022 <TAN>
A;Cross-references: UNIPARC:UPI0000173C76
A;Note: the authors translated the codon TCC for residue 1787 as Phe
R;Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s
A;Reference number: I50216; MUID:90307744; PMID:1694853
A;Accession: I50216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PA',1044-1559 <KRU>
A;Cross-references: UNIPARC:UPI00001712FB; GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:
R;Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an
A;Reference number: A37072; MUID:90307743; PMID:2365711
A;Accession: A37072
A;Molecule type: protein
A;Residues: 998-1015,'X',1017-1019,'X',1021-1023 <KR2>
A;Cross-references: UNIPARC:UPI0000173C77
A;Note: amino end of 86K core peptide CS-A
A;Accession: B37072
A;Molecule type: protein
A;Residues: 1247-1250,'D',1252-1272,'X',1274-1275 <KR3>
A;Cross-references: UNIPARC:UPI0000173C78
A;Note: amino end of 75K core peptide CS-B
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: alternative splicing
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2109/Product: aggrecan #status predicted <MAT>
F;44-131/Domain: immunoglobulin homology <IMM>
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-346/Domain: link protein repeat homology <LNK2>
F;537-614/Domain: link protein repeat homology <LNK3>
F;635-716/Domain: link protein repeat homology <LNK4>
F;1859-1890/Domain: EGF homology <EGF>
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F;2024-2080/Domain: complement factor H repeat homology <FHD>

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Db        258 EKFTFQEAFDKCHSLGARLATTGELYLAWKDGMDMCSAGWLADRSVRYPISRARPN--CG 315

Qy        108 KNGVGV-LIWKVPV--------SRQFAAYCYNSSDTWTNSCIP-----EIITTKDPIFNT 153
              | |||  ::  |         | :: | ||:  |    : :|     |: |     |
Db        316 GNLVGVRTVYLNPANQTGYPHPSSRYDAICYSGDD--FEALVPGLFTDEVGTELGSAFTI 373

Qy        154 QTATQT----------TEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRRKKLICVT 203
              || |||           ||   ::  |:|:        | |    | | :|     :  |
Db        374 QTVTQTEVELPLPRNVTE---EEARGSIATLEPMEITATATELYEAFTVLPD----LFAT 426

Qy        204 EVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVKRYV 263
              | :||::       |  ||    : |  |   ||          |          |
Db        427 SVTVETAS------PREEN--VTREEITGIWAVPEE-----------------VTTSV 459

Qy        264 KAFPFTNKNQQKEMIETKVVKEEKANDSNPNEES 297
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Db        460 SGTAFTT-----GMAEVSSVEEAIAVTATPGLES 488

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Job time : 49.4292 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:04 ; Search time 22.783 Seconds
(without alignments)
1168.483 Million cell updates/sec

Title: US-10-063-510-6
Perfect score: 1657
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1657	100.0	322	2	US-09-907-794A-201	Sequence 201, App
3	1657	100.0	322	2	US-09-905-125A-201	Sequence 201, App
4	1657	100.0	322	2	US-09-902-775A-201	Sequence 201, App
5	1657	100.0	322	2	US-09-906-700-201	Sequence 201, App
6	1657	100.0	322	2	US-09-903-603A-201	Sequence 201, App
7	1657	100.0	322	2	US-09-904-920A-201	Sequence 201, App
8	1657	100.0	322	2	US-09-909-064-201	Sequence 201, App
9	1657	100.0	322	2	US-09-905-381A-201	Sequence 201, App
10	1657	100.0	322	2	US-09-906-618-201	Sequence 201, App
11	1657	100.0	322	2	US-09-906-646-201	Sequence 201, App
12	1657	100.0	322	2	US-09-904-462-201	Sequence 201, App
13	1657	100.0	322	2	US-09-902-736A-201	Sequence 201, App
14	1657	100.0	322	2	US-09-906-722A-201	Sequence 201, App
15	1657	100.0	344	2	US-09-949-016-7765	Sequence 7765, Ap
16	1651	99.6	322	1	US-08-892-880-2	Sequence 2, Appli
17	1103	66.6	318	2	US-09-724-864-60	Sequence 60, Appl
18	231.5	14.0	363	1	US-07-946-497-7	Sequence 7, Appli
19	231.5	14.0	363	1	US-08-483-322-7	Sequence 7, Appli
20	231.5	14.0	363	1	US-08-478-882-7	Sequence 7, Appli
21	224.5	13.5	339	1	US-08-892-880-3	Sequence 3, Appli
22	222.5	13.4	362	6	5504194-2	Patent No. 5504194
23	222	13.4	503	1	US-07-946-497-2	Sequence 2, Appli
24	222	13.4	503	1	US-08-483-322-2	Sequence 2, Appli
25	222	13.4	503	1	US-08-478-882-2	Sequence 2, Appli
26	207	12.5	361	1	US-07-946-497-6	Sequence 6, Appli
27	207	12.5	361	1	US-08-483-322-6	Sequence 6, Appli
28	207	12.5	361	1	US-08-478-882-6	Sequence 6, Appli
29	205	12.4	361	2	US-09-949-016-5968	Sequence 5968, Ap
30	175	10.6	295	2	US-09-949-016-9143	Sequence 9143, Ap
31	161	9.7	90	1	US-08-242-097-3	Sequence 3, Appli
32	161	9.7	90	2	US-09-206-695-3	Sequence 3, Appli
33	161	9.7	90	2	US-09-799-118-3	Sequence 3, Appli
34	150	9.1	510	2	US-10-104-047-2580	Sequence 2580, Ap
35	145	8.8	259	2	US-09-949-016-10954	Sequence 10954, A
36	145	8.8	277	1	US-08-024-868-2	Sequence 2, Appli
37	145	8.8	277	1	US-08-242-097-2	Sequence 2, Appli
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40	145	8.8	277	2	US-09-799-118-2	Sequence 2, Appli
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42	144	8.7	275	2	US-09-466-778-12	Sequence 12, Appl
43	131.5	7.9	883	2	US-10-195-970-3	Sequence 3, Appli
44	131	7.9	649	2	US-10-188-495-63	Sequence 63, Appl
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46	130.5	7.9	883	2	US-10-195-970-6	Sequence 6, Appli
47	130.5	7.9	883	2	US-10-188-495-72	Sequence 72, Appl
48	130.5	7.9	2316	2	US-09-949-002-314	Sequence 314, App
49	130.5	7.9	2415	2	US-09-949-002-398	Sequence 398, App
50	129.5	7.8	457	2	US-09-466-778-5	Sequence 5, Appli
51	129.5	7.8	2157	2	US-09-466-778-2	Sequence 2, Appli
52	128.5	7.8	912	4	PCT-US95-03747-2	Sequence 2, Appli
53	126.5	7.6	457	2	US-09-774-639-108	Sequence 108, App
54	124.5	7.5	482	2	US-10-104-047-3794	Sequence 3794, Ap
55	121.5	7.3	360	2	US-09-907-794A-213	Sequence 213, App
56	121.5	7.3	360	2	US-09-905-125A-213	Sequence 213, App
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59	121.5	7.3	360	2	US-09-903-603A-213	Sequence 213, App
60	121.5	7.3	360	2	US-09-904-920A-213	Sequence 213, App
61	121.5	7.3	360	2	US-09-909-064-213	Sequence 213, App
62	121.5	7.3	360	2	US-09-905-381A-213	Sequence 213, App
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71	114.5	6.9	1257	1	US-08-340-428B-49	Sequence 49, Appl
72	113.5	6.8	97	1	US-08-242-097-5	Sequence 5, Appli
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75	111	6.7	328	1	US-08-225-477B-5	Sequence 5, Appli
76	111	6.7	328	4	PCT-US95-04353-5	Sequence 5, Appli
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78	109	6.6	353	2	US-09-466-778-11	Sequence 11, Appl
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80	107	6.5	355	2	US-09-466-778-9	Sequence 9, Appli
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88	103	6.2	432	2	US-09-248-796A-18913	Sequence 18913, A
89	102.5	6.2	326	1	US-08-225-477B-6	Sequence 6, Appli
90	102.5	6.2	326	4	PCT-US95-04353-6	Sequence 6, Appli
91	101.5	6.1	590	2	US-09-520-781-12	Sequence 12, Appl
92	101.5	6.1	590	2	US-09-957-187-12	Sequence 12, Appl
93	101.5	6.1	590	2	US-09-991-053-12	Sequence 12, Appl
94	100	6.0	333	1	US-08-225-477B-4	Sequence 4, Appli
95	100	6.0	333	4	PCT-US95-04353-4	Sequence 4, Appli
96	100	6.0	378	1	US-08-225-477B-9	Sequence 9, Appli
97	100	6.0	378	4	PCT-US95-04353-9	Sequence 9, Appli
98	99	6.0	260	2	US-09-638-203-3	Sequence 3, Appli
99	98.5	5.9	2870	2	US-09-479-467A-15	Sequence 15, Appl
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101	98.5	5.9	3178	2	US-09-479-467A-4	Sequence 4, Appli
102	98.5	5.9	3178	2	US-09-655-160-4	Sequence 4, Appli
103	96.5	5.8	477	2	US-09-248-796A-21985	Sequence 21985, A
104	95.5	5.8	376	2	US-09-487-558B-206	Sequence 206, App
105	93	5.6	629	2	US-09-241-581B-6	Sequence 6, Appli
106	93	5.6	629	2	US-08-265-428-6	Sequence 6, Appli
107	93	5.6	629	4	PCT-US95-07721-6	Sequence 6, Appli
108	92.5	5.6	300	2	US-09-254-465A-10	Sequence 10, Appl
109	92.5	5.6	300	2	US-09-397-243D-12	Sequence 12, Appl
110	92.5	5.6	300	2	US-09-953-499-10	Sequence 10, Appl
111	92.5	5.6	523	2	US-09-248-796A-17555	Sequence 17555, A
112	92	5.6	201	2	US-09-270-767-32397	Sequence 32397, A
113	92	5.6	201	2	US-09-270-767-47614	Sequence 47614, A
114	92	5.6	966	2	US-09-487-558B-372	Sequence 372, App
115	91.5	5.5	639	2	US-09-823-240A-5	Sequence 5, Appli
116	90.5	5.5	601	2	US-09-248-796A-24733	Sequence 24733, A
117	90	5.4	545	2	US-09-248-796A-24484	Sequence 24484, A
118	90	5.4	827	2	US-09-248-796A-17307	Sequence 17307, A
119	90	5.4	1367	2	US-09-487-558B-108	Sequence 108, App
120	89	5.4	353	1	US-08-073-807A-17	Sequence 17, Appl
121	89	5.4	380	1	US-08-073-807A-18	Sequence 18, Appl
122	89	5.4	416	1	US-08-073-807A-2	Sequence 2, Appli
123	89	5.4	416	2	US-09-311-784A-26	Sequence 26, Appl
124	89	5.4	471	2	US-09-949-016-9525	Sequence 9525, Ap
125	88.5	5.3	265	2	US-09-248-796A-21903	Sequence 21903, A
126	88.5	5.3	451	2	US-09-252-991A-17201	Sequence 17201, A
127	88	5.3	261	2	US-09-248-796A-14279	Sequence 14279, A
128	88	5.3	685	2	US-09-248-796A-20197	Sequence 20197, A
129	87.5	5.3	334	2	US-09-248-796A-24627	Sequence 24627, A
130	87.5	5.3	536	2	US-09-292-225-21	Sequence 21, Appl
131	87.5	5.3	555	2	US-09-292-225-15	Sequence 15, Appl
132	87.5	5.3	555	2	US-09-292-225-18	Sequence 18, Appl
133	87.5	5.3	717	2	US-10-104-047-3100	Sequence 3100, Ap
134	87.5	5.3	795	2	US-09-270-767-43662	Sequence 43662, A
135	87.5	5.3	1085	1	US-08-485-588-5	Sequence 5, Appli
136	87.5	5.3	1085	1	US-08-484-565-5	Sequence 5, Appli
137	87.5	5.3	1085	1	US-08-480-751-5	Sequence 5, Appli
138	87.5	5.3	1085	1	US-08-943-986-5	Sequence 5, Appli
139	87.5	5.3	1085	2	US-08-353-784-5	Sequence 5, Appli
140	87.5	5.3	1085	2	US-08-484-719B-5	Sequence 5, Appli
141	87.5	5.3	1085	2	US-08-484-159-5	Sequence 5, Appli
142	87	5.3	288	2	US-09-216-393B-341	Sequence 341, App
143	87	5.3	288	2	US-09-216-393B-344	Sequence 344, App
144	87	5.3	631	2	US-09-620-412C-325	Sequence 325, App
145	87	5.3	631	2	US-09-598-419-325	Sequence 325, App
146	87	5.3	664	2	US-10-197-220-168	Sequence 168, App
147	87	5.3	849	1	US-08-405-392-18	Sequence 18, Appl
148	87	5.3	849	2	US-08-487-691-18	Sequence 18, Appl
149	87	5.3	849	2	US-08-189-738A-19	Sequence 19, Appl
150	87	5.3	862	1	US-08-325-267A-4	Sequence 4, Appli
151	87	5.3	894	2	US-08-362-525-22	Sequence 22, Appl
152	87	5.3	894	2	US-08-971-692-15	Sequence 15, Appl
153	87	5.3	905	1	US-08-405-392-2	Sequence 2, Appli
154	87	5.3	905	2	US-08-487-691-2	Sequence 2, Appli
155	87	5.3	905	2	US-08-666-221B-4	Sequence 4, Appli
156	87	5.3	905	2	US-08-189-738A-2	Sequence 2, Appli
157	87	5.3	1016	2	US-10-197-220-95	Sequence 95, Appl
158	87	5.3	1537	1	US-08-325-267A-2	Sequence 2, Appli
159	87	5.3	1537	2	US-09-487-558B-104	Sequence 104, App
160	86.5	5.2	410	1	US-08-073-807A-16	Sequence 16, Appl
161	86.5	5.2	503	2	US-09-487-558B-424	Sequence 424, App
162	86.5	5.2	788	2	US-09-294-663-3	Sequence 3, Appli
163	86.5	5.2	807	2	US-09-294-663-4	Sequence 4, Appli
164	86.5	5.2	2781	2	US-09-698-295-10	Sequence 10, Appl
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166	86	5.2	750	2	US-09-165-239A-4	Sequence 4, Appli
167	86	5.2	786	2	US-09-103-429A-3	Sequence 3, Appli
168	86	5.2	805	2	US-09-103-429A-4	Sequence 4, Appli
169	86	5.2	905	2	US-08-666-221B-10	Sequence 10, Appl
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171	85.5	5.2	531	2	US-09-270-767-32631	Sequence 32631, A
172	85.5	5.2	531	2	US-09-270-767-47848	Sequence 47848, A
173	85.5	5.2	781	2	US-09-949-016-6959	Sequence 6959, Ap
174	85	5.1	318	2	US-09-902-540-10266	Sequence 10266, A
175	84.5	5.1	270	2	US-09-248-796A-14475	Sequence 14475, A
176	84.5	5.1	507	2	US-09-949-016-8889	Sequence 8889, Ap
177	84.5	5.1	507	2	US-09-949-016-8897	Sequence 8897, Ap
178	84.5	5.1	1011	2	US-08-836-325-2	Sequence 2, Appli
179	84.5	5.1	1011	2	US-09-457-571-2	Sequence 2, Appli
180	84.5	5.1	1984	2	US-08-836-325-10	Sequence 10, Appl
181	84.5	5.1	1984	2	US-09-457-571-10	Sequence 10, Appl
182	84.5	5.1	1989	2	US-08-836-325-12	Sequence 12, Appl
183	84.5	5.1	1989	2	US-09-457-571-12	Sequence 12, Appl
184	84	5.1	216	2	US-08-928-361B-8	Sequence 8, Appli
185	84	5.1	216	2	US-08-928-361B-27	Sequence 27, Appl
186	84	5.1	216	2	US-09-588-995A-8	Sequence 8, Appli
187	84	5.1	920	1	US-07-718-575-10	Sequence 10, Appl
188	84	5.1	920	1	US-08-481-206-10	Sequence 10, Appl
189	84	5.1	920	1	US-08-486-269A-10	Sequence 10, Appl
190	84	5.1	1075	2	US-09-487-558B-110	Sequence 110, App
191	84	5.1	1721	2	US-08-700-651-5	Sequence 5, Appli
192	84	5.1	1721	2	US-08-928-361B-6	Sequence 6, Appli
193	84	5.1	1721	2	US-09-588-995A-6	Sequence 6, Appli
194	84	5.1	1837	2	US-08-928-361B-5	Sequence 5, Appli
195	84	5.1	1837	2	US-09-588-995A-5	Sequence 5, Appli
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197	83.5	5.0	393	2	US-09-377-557-14	Sequence 14, Appl
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199	83.5	5.0	879	1	US-08-220-151-2	Sequence 2, Appli
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202	83.5	5.0	879	1	US-08-413-118-3	Sequence 3, Appli
203	83.5	5.0	879	1	US-08-413-118-106	Sequence 106, App
204	83.5	5.0	879	2	US-08-473-446-2	Sequence 2, Appli
205	83.5	5.0	879	2	US-08-473-446-3	Sequence 3, Appli
206	83.5	5.0	879	2	US-08-473-446-106	Sequence 106, App
207	83.5	5.0	5179	2	US-09-538-092-1258	Sequence 1258, Ap
208	83	5.0	147	2	US-09-230-637-43	Sequence 43, Appl
209	83	5.0	175	2	US-09-270-767-33553	Sequence 33553, A
210	83	5.0	175	2	US-09-270-767-48770	Sequence 48770, A
211	83	5.0	205	2	US-09-248-796A-21984	Sequence 21984, A
212	83	5.0	351	2	US-09-248-796A-23675	Sequence 23675, A
213	83	5.0	409	2	US-09-538-092-1214	Sequence 1214, Ap
214	83	5.0	409	2	US-09-949-016-6281	Sequence 6281, Ap
215	83	5.0	454	2	US-09-949-016-11120	Sequence 11120, A
216	83	5.0	605	2	US-09-487-558B-428	Sequence 428, App
217	83	5.0	736	2	US-09-457-040B-26	Sequence 26, Appl
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219	82.5	5.0	203	2	US-09-270-767-50257	Sequence 50257, A
220	82.5	5.0	219	2	US-09-134-001C-5651	Sequence 5651, Ap
221	82.5	5.0	400	2	US-10-300-819B-2	Sequence 2, Appli
222	82.5	5.0	447	2	US-09-252-991A-28081	Sequence 28081, A
223	82.5	5.0	591	2	US-09-270-767-32687	Sequence 32687, A
224	82.5	5.0	591	2	US-09-270-767-47904	Sequence 47904, A
225	82.5	5.0	790	2	US-09-949-016-7017	Sequence 7017, Ap
226	82.5	5.0	790	2	US-09-949-016-8169	Sequence 8169, Ap
227	82.5	5.0	790	2	US-09-949-016-8170	Sequence 8170, Ap
228	82.5	5.0	866	1	US-08-405-392-17	Sequence 17, Appl
229	82.5	5.0	866	2	US-08-487-691-17	Sequence 17, Appl
230	82	4.9	208	2	US-09-991-181-416	Sequence 416, App
231	82	4.9	208	2	US-09-990-444-416	Sequence 416, App
232	82	4.9	208	2	US-09-832-129-36	Sequence 36, Appl
233	82	4.9	208	2	US-09-997-333-416	Sequence 416, App
234	82	4.9	208	2	US-09-992-598-416	Sequence 416, App
235	82	4.9	455	2	US-09-949-016-10519	Sequence 10519, A
236	82	4.9	455	2	US-09-949-016-10520	Sequence 10520, A
237	82	4.9	455	2	US-09-949-016-10760	Sequence 10760, A
238	82	4.9	455	2	US-09-949-016-10761	Sequence 10761, A
239	82	4.9	508	2	US-09-248-796A-18191	Sequence 18191, A
240	82	4.9	525	2	US-09-248-796A-19001	Sequence 19001, A
241	82	4.9	529	2	US-09-248-796A-20186	Sequence 20186, A
242	82	4.9	538	2	US-09-248-796A-20842	Sequence 20842, A
243	82	4.9	553	1	US-08-651-572-2	Sequence 2, Appli
244	82	4.9	553	2	US-09-066-544-2	Sequence 2, Appli
245	82	4.9	553	2	US-08-951-086-2	Sequence 2, Appli
246	82	4.9	553	2	US-09-430-669-2	Sequence 2, Appli

247	82	4.9	715	2	US-09-215-221-25	Sequence 25, Appl
248	82	4.9	1026	2	US-09-248-796A-16128	Sequence 16128, A
249	82	4.9	1083	2	US-09-538-092-812	Sequence 812, App
250	81.5	4.9	522	2	US-09-248-796A-14121	Sequence 14121, A
251	81.5	4.9	586	1	US-08-630-822A-70	Sequence 70, Appl
252	81.5	4.9	586	1	US-09-005-069-70	Sequence 70, Appl
253	81.5	4.9	586	2	US-09-171-156A-30	Sequence 30, Appl
254	81.5	4.9	586	2	US-09-004-730A-30	Sequence 30, Appl
255	81.5	4.9	586	2	US-08-981-799A-30	Sequence 30, Appl
256	81.5	4.9	687	1	US-08-540-804-4	Sequence 4, Appli
257	81.5	4.9	687	1	US-08-218-265-4	Sequence 4, Appli
258	81.5	4.9	687	2	US-08-521-872-4	Sequence 4, Appli
259	81.5	4.9	687	2	US-08-590-399-4	Sequence 4, Appli
260	81.5	4.9	1445	1	US-08-015-986A-2	Sequence 2, Appli
261	81.5	4.9	1445	1	US-08-446-363-2	Sequence 2, Appli
262	81	4.9	49	1	US-08-340-428B-23	Sequence 23, Appl
263	81	4.9	49	4	PCT-US93-07306-23	Sequence 23, Appl
264	81	4.9	289	2	US-09-466-778-8	Sequence 8, Appli
265	81	4.9	413	2	US-08-669-408B-10	Sequence 10, Appl
266	81	4.9	531	2	US-09-248-796A-15560	Sequence 15560, A
267	81	4.9	855	1	US-08-816-693A-2	Sequence 2, Appli
268	81	4.9	855	2	US-08-885-291-2	Sequence 2, Appli
269	81	4.9	855	2	US-09-496-672-2	Sequence 2, Appli
270	81	4.9	855	2	US-09-618-425-11	Sequence 11, Appl
271	81	4.9	883	2	US-09-248-796A-18931	Sequence 18931, A
272	81	4.9	1169	2	US-09-487-558B-106	Sequence 106, App
273	81	4.9	1322	2	US-09-487-558B-114	Sequence 114, App
274	80.5	4.9	334	2	US-09-197-970B-7	Sequence 7, Appli
275	80.5	4.9	478	2	US-09-345-473E-51	Sequence 51, Appl
276	80.5	4.9	478	2	US-09-862-027-51	Sequence 51, Appl
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279	80.5	4.9	595	1	US-08-232-087A-2	Sequence 2, Appli
280	80.5	4.9	595	2	US-09-006-353A-9	Sequence 9, Appli
281	80.5	4.9	595	2	US-09-573-986-9	Sequence 9, Appli
282	80.5	4.9	595	2	US-09-949-016-6048	Sequence 6048, Ap
283	80.5	4.9	624	2	US-09-877-730-24	Sequence 24, Appl
284	80.5	4.9	642	2	US-09-949-016-8043	Sequence 8043, Ap
285	80.5	4.9	673	2	US-09-949-016-7388	Sequence 7388, Ap
286	80.5	4.9	712	2	US-09-877-730-22	Sequence 22, Appl
287	80.5	4.9	793	2	US-09-877-730-28	Sequence 28, Appl
288	80.5	4.9	991	2	US-09-877-730-12	Sequence 12, Appl
289	80.5	4.9	1069	2	US-09-877-730-2	Sequence 2, Appli
290	80.5	4.9	1072	2	US-09-877-730-18	Sequence 18, Appl
291	80.5	4.9	1150	2	US-09-877-730-8	Sequence 8, Appli
292	80	4.8	52	1	US-08-225-477B-10	Sequence 10, Appl
293	80	4.8	52	4	PCT-US95-04353-10	Sequence 10, Appl
294	80	4.8	95	2	US-09-252-991A-28504	Sequence 28504, A
295	80	4.8	251	2	US-09-248-796A-23216	Sequence 23216, A
296	80	4.8	257	2	US-09-902-540-15102	Sequence 15102, A
297	80	4.8	372	2	US-09-248-796A-19896	Sequence 19896, A
298	80	4.8	404	2	US-09-270-767-41751	Sequence 41751, A
299	80	4.8	423	2	US-09-270-767-44448	Sequence 44448, A
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301	80	4.8	451	4	PCT-US95-09941-2	Sequence 2, Appli
302	80	4.8	468	1	US-08-959-011-3	Sequence 3, Appli
303	80	4.8	823	2	US-09-248-796A-16699	Sequence 16699, A
304	80	4.8	893	2	US-08-189-738A-18	Sequence 18, Appl
305	79.5	4.8	153	2	US-09-252-991A-17880	Sequence 17880, A
306	79.5	4.8	154	2	US-09-270-767-40476	Sequence 40476, A
307	79.5	4.8	154	2	US-09-270-767-55692	Sequence 55692, A
308	79.5	4.8	324	2	US-09-489-039A-8593	Sequence 8593, Ap
309	79.5	4.8	374	2	US-09-248-796A-17283	Sequence 17283, A
310	79.5	4.8	439	2	US-10-360-101-226	Sequence 226, App
311	79.5	4.8	461	1	US-08-385-229-2	Sequence 2, Appli
312	79.5	4.8	461	1	US-08-650-000-2	Sequence 2, Appli
313	79.5	4.8	461	2	US-09-042-785A-7	Sequence 7, Appli
314	79.5	4.8	461	2	US-08-477-347-3	Sequence 3, Appli
315	79.5	4.8	461	2	US-09-006-353A-4	Sequence 4, Appli
316	79.5	4.8	461	2	US-08-476-862-2	Sequence 2, Appli
317	79.5	4.8	461	2	US-09-573-986-4	Sequence 4, Appli
318	79.5	4.8	461	2	US-08-406-824A-2	Sequence 2, Appli
319	79.5	4.8	461	2	US-09-800-909-2	Sequence 2, Appli
320	79.5	4.8	461	2	US-09-758-124-2	Sequence 2, Appli
321	79.5	4.8	461	2	US-09-800-908-3	Sequence 3, Appli
322	79.5	4.8	461	2	US-09-896-096A-17	Sequence 17, Appl
323	79.5	4.8	461	2	US-09-949-016-6019	Sequence 6019, Ap
324	79.5	4.8	461	2	US-10-046-433-6	Sequence 6, Appli
325	79.5	4.8	461	6	5395760-2	Patent No. 5395760
326	79.5	4.8	491	2	US-09-949-016-7840	Sequence 7840, Ap
327	79.5	4.8	515	2	US-09-198-452A-1094	Sequence 1094, Ap
328	79.5	4.8	515	2	US-09-438-185A-1021	Sequence 1021, Ap
329	79.5	4.8	559	2	US-09-543-681A-7241	Sequence 7241, Ap
330	79.5	4.8	601	2	US-09-270-767-45496	Sequence 45496, A
331	79.5	4.8	756	1	US-08-434-730-16	Sequence 16, Appl
332	79.5	4.8	985	2	US-09-993-777-6	Sequence 6, Appli
333	79.5	4.8	985	2	US-09-993-777-66	Sequence 66, Appl
334	79.5	4.8	985	4	PCT-US96-03916-6	Sequence 6, Appli
335	79.5	4.8	985	4	PCT-US96-03916-66	Sequence 66, Appl
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337	79.5	4.8	1123	2	US-09-262-537-4	Sequence 4, Appli
338	79.5	4.8	1177	2	US-09-262-537-2	Sequence 2, Appli
339	79.5	4.8	1403	2	US-09-262-537-6	Sequence 6, Appli
340	79	4.8	175	2	US-08-700-651-12	Sequence 12, Appl
341	79	4.8	175	2	US-08-928-361B-17	Sequence 17, Appl
342	79	4.8	175	2	US-09-588-995A-17	Sequence 17, Appl
343	79	4.8	217	2	US-09-949-016-11174	Sequence 11174, A
344	79	4.8	334	2	US-09-107-532A-6336	Sequence 6336, Ap
345	79	4.8	374	2	US-09-489-847-166	Sequence 166, App
346	79	4.8	382	2	US-09-907-794A-137	Sequence 137, App
347	79	4.8	382	2	US-09-905-125A-137	Sequence 137, App
348	79	4.8	382	2	US-09-902-775A-137	Sequence 137, App
349	79	4.8	382	2	US-09-906-700-137	Sequence 137, App
350	79	4.8	382	2	US-09-903-603A-137	Sequence 137, App
351	79	4.8	382	2	US-09-904-920A-137	Sequence 137, App
352	79	4.8	382	2	US-09-909-064-137	Sequence 137, App
353	79	4.8	382	2	US-09-905-381A-137	Sequence 137, App
354	79	4.8	382	2	US-09-906-618-137	Sequence 137, App
355	79	4.8	382	2	US-09-906-646-137	Sequence 137, App
356	79	4.8	382	2	US-09-904-462-137	Sequence 137, App
357	79	4.8	382	2	US-09-902-736A-137	Sequence 137, App
358	79	4.8	382	2	US-09-906-722A-137	Sequence 137, App
359	79	4.8	398	2	US-09-248-796A-21599	Sequence 21599, A
360	79	4.8	638	2	US-09-248-796A-18739	Sequence 18739, A
361	79	4.8	1312	2	US-09-345-882-29	Sequence 29, Appl
362	79	4.8	1312	2	US-10-071-179-29	Sequence 29, Appl
363	79	4.8	1848	2	US-08-296-791-6	Sequence 6, Appli
364	79	4.8	1848	2	US-09-839-996-6	Sequence 6, Appli
365	79	4.8	1848	2	US-10-080-505-6	Sequence 6, Appli
366	79	4.8	1848	2	US-10-645-655-6	Sequence 6, Appli
367	79	4.8	1848	4	PCT-US95-10661A-6	Sequence 6, Appli
368	79	4.8	3969	2	US-08-061-376-5	Sequence 5, Appli
369	78.5	4.7	130	2	US-08-700-651-9	Sequence 9, Appli
370	78.5	4.7	130	2	US-08-928-361B-14	Sequence 14, Appl
371	78.5	4.7	130	2	US-09-588-995A-14	Sequence 14, Appl
372	78.5	4.7	322	2	US-09-248-796A-23680	Sequence 23680, A
373	78.5	4.7	360	2	US-09-489-039A-9383	Sequence 9383, Ap
374	78.5	4.7	431	2	US-09-949-016-8402	Sequence 8402, Ap
375	78.5	4.7	542	2	US-09-538-092-289	Sequence 289, App
376	78.5	4.7	595	1	US-08-225-989-2	Sequence 2, Appli
377	78.5	4.7	595	1	US-08-570-923-2	Sequence 2, Appli
378	78.5	4.7	595	1	US-08-580-014-2	Sequence 2, Appli
379	78.5	4.7	595	2	US-09-079-785-2	Sequence 2, Appli
380	78.5	4.7	595	2	US-09-921-667-6	Sequence 6, Appli
381	78.5	4.7	595	2	US-09-628-126-2	Sequence 2, Appli
382	78.5	4.7	653	2	US-09-520-781-10	Sequence 10, Appl
383	78.5	4.7	653	2	US-09-957-187-10	Sequence 10, Appl
384	78.5	4.7	653	2	US-09-991-053-10	Sequence 10, Appl
385	78.5	4.7	3224	1	US-08-705-660-34	Sequence 34, Appl
386	78.5	4.7	3224	2	US-08-989-045-34	Sequence 34, Appl
387	78.5	4.7	3224	2	US-09-538-092-1161	Sequence 1161, Ap
388	78.5	4.7	3224	2	US-09-315-355A-34	Sequence 34, Appl
389	78	4.7	280	2	US-09-907-794A-325	Sequence 325, App
390	78	4.7	280	2	US-09-905-125A-325	Sequence 325, App
391	78	4.7	280	2	US-09-902-775A-325	Sequence 325, App
392	78	4.7	280	2	US-09-906-700-325	Sequence 325, App

393	78	4.7	280	2	US-09-903-603A-325	Sequence 325, App
394	78	4.7	280	2	US-09-904-920A-325	Sequence 325, App
395	78	4.7	280	2	US-09-806-536A-1	Sequence 1, Appli
396	78	4.7	280	2	US-09-909-064-325	Sequence 325, App
397	78	4.7	280	2	US-09-905-381A-325	Sequence 325, App
398	78	4.7	280	2	US-09-906-618-325	Sequence 325, App
399	78	4.7	280	2	US-09-906-646-325	Sequence 325, App
400	78	4.7	280	2	US-09-904-462-325	Sequence 325, App
401	78	4.7	280	2	US-09-902-736A-325	Sequence 325, App
402	78	4.7	280	2	US-09-906-722A-325	Sequence 325, App
403	78	4.7	300	2	US-09-248-796A-16245	Sequence 16245, A
404	78	4.7	398	2	US-09-248-796A-14978	Sequence 14978, A
405	78	4.7	494	2	US-09-248-796A-16546	Sequence 16546, A
406	78	4.7	564	2	US-10-069-540A-2	Sequence 2, Appli
407	78	4.7	609	2	US-09-198-452A-579	Sequence 579, App
408	78	4.7	1006	2	US-09-949-016-7897	Sequence 7897, Ap
409	78	4.7	1442	1	US-08-015-986A-3	Sequence 3, Appli
410	78	4.7	1442	1	US-08-446-363-3	Sequence 3, Appli
411	78	4.7	1744	2	US-09-438-185A-542	Sequence 542, App
412	78	4.7	2176	2	US-09-949-016-9923	Sequence 9923, Ap
413	77.5	4.7	497	2	US-09-377-557-10	Sequence 10, Appl
414	77.5	4.7	514	2	US-08-738-168B-15	Sequence 15, Appl
415	77.5	4.7	1262	2	US-09-107-433-5067	Sequence 5067, Ap
416	77.5	4.7	1475	2	US-09-538-092-1160	Sequence 1160, Ap
417	77.5	4.7	3969	2	US-09-538-092-1262	Sequence 1262, Ap
418	77	4.6	162	2	US-09-068-140A-2	Sequence 2, Appli
419	77	4.6	173	2	US-09-068-140A-13	Sequence 13, Appl
420	77	4.6	249	2	US-08-700-651-15	Sequence 15, Appl
421	77	4.6	249	2	US-08-928-361B-20	Sequence 20, Appl
422	77	4.6	249	2	US-09-588-995A-20	Sequence 20, Appl
423	77	4.6	714	2	US-09-949-016-7038	Sequence 7038, Ap
424	77	4.6	908	2	US-09-949-016-7580	Sequence 7580, Ap
425	77	4.6	1140	2	US-09-538-092-647	Sequence 647, App
426	77	4.6	1401	2	US-09-127-670-6	Sequence 6, Appli
427	77	4.6	2123	2	US-08-968-685A-10	Sequence 10, Appl
428	76.5	4.6	134	2	US-09-248-796A-27317	Sequence 27317, A
429	76.5	4.6	240	1	US-08-114-555A-8	Sequence 8, Appli
430	76.5	4.6	240	2	US-08-559-397A-14	Sequence 14, Appl
431	76.5	4.6	303	2	US-09-248-796A-14269	Sequence 14269, A
432	76.5	4.6	334	2	US-10-012-231A-41	Sequence 41, Appl
433	76.5	4.6	334	2	US-10-015-389A-41	Sequence 41, Appl
434	76.5	4.6	334	2	US-10-006-768A-41	Sequence 41, Appl
435	76.5	4.6	334	2	US-10-015-671A-41	Sequence 41, Appl
436	76.5	4.6	334	2	US-10-015-393A-41	Sequence 41, Appl
437	76.5	4.6	334	2	US-10-011-833A-41	Sequence 41, Appl
438	76.5	4.6	334	2	US-10-006-041A-41	Sequence 41, Appl
439	76.5	4.6	334	2	US-10-012-064A-41	Sequence 41, Appl
440	76.5	4.6	348	2	US-09-216-295-16	Sequence 16, Appl
441	76.5	4.6	348	2	US-09-632-570-16	Sequence 16, Appl
442	76.5	4.6	348	2	US-09-632-575-46	Sequence 46, Appl
443	76.5	4.6	382	1	US-08-415-818-7	Sequence 7, Appli
444	76.5	4.6	382	1	US-08-894-236-7	Sequence 7, Appli
445	76.5	4.6	382	1	US-08-555-268A-14	Sequence 14, Appl
446	76.5	4.6	382	2	US-09-430-775-36	Sequence 36, Appl
447	76.5	4.6	382	4	PCT-US96-01444-7	Sequence 7, Appli
448	76.5	4.6	397	2	US-09-198-452A-201	Sequence 201, App
449	76.5	4.6	397	2	US-09-438-185A-188	Sequence 188, App
450	76.5	4.6	452	2	US-09-248-796A-16219	Sequence 16219, A
451	76.5	4.6	484	1	US-08-127-499A-26	Sequence 26, Appl
452	76.5	4.6	484	1	US-08-482-847-26	Sequence 26, Appl
453	76.5	4.6	653	2	US-09-991-181-229	Sequence 229, App
454	76.5	4.6	653	2	US-09-990-444-229	Sequence 229, App
455	76.5	4.6	653	2	US-09-997-333-229	Sequence 229, App
456	76.5	4.6	653	2	US-09-992-598-229	Sequence 229, App
457	76.5	4.6	901	2	US-09-248-796A-14747	Sequence 14747, A
458	76.5	4.6	1013	2	US-08-860-886-2	Sequence 2, Appli
459	76.5	4.6	1307	2	US-10-104-047-2438	Sequence 2438, Ap
460	76.5	4.6	5037	2	US-09-424-783-4	Sequence 4, Appli
461	76	4.6	154	2	US-09-270-767-61124	Sequence 61124, A
462	76	4.6	299	2	US-09-270-767-44350	Sequence 44350, A
463	76	4.6	321	2	US-09-248-796A-20146	Sequence 20146, A
464	76	4.6	345	2	US-09-543-681A-6150	Sequence 6150, Ap
465	76	4.6	380	2	US-09-134-001C-4558	Sequence 4558, Ap
466	76	4.6	386	2	US-09-328-352-4722	Sequence 4722, Ap
467	76	4.6	402	2	US-09-270-767-45612	Sequence 45612, A
468	76	4.6	482	2	US-09-991-181-513	Sequence 513, App
469	76	4.6	482	2	US-09-990-444-513	Sequence 513, App
470	76	4.6	482	2	US-09-997-333-513	Sequence 513, App
471	76	4.6	482	2	US-09-992-598-513	Sequence 513, App
472	76	4.6	509	2	US-09-907-794A-315	Sequence 315, App
473	76	4.6	509	2	US-09-905-125A-315	Sequence 315, App
474	76	4.6	509	2	US-09-902-775A-315	Sequence 315, App
475	76	4.6	509	2	US-09-906-700-315	Sequence 315, App
476	76	4.6	509	2	US-09-903-603A-315	Sequence 315, App
477	76	4.6	509	2	US-09-904-920A-315	Sequence 315, App
478	76	4.6	509	2	US-09-909-064-315	Sequence 315, App
479	76	4.6	509	2	US-09-905-381A-315	Sequence 315, App
480	76	4.6	509	2	US-09-906-618-315	Sequence 315, App
481	76	4.6	509	2	US-09-906-646-315	Sequence 315, App
482	76	4.6	509	2	US-09-904-462-315	Sequence 315, App
483	76	4.6	509	2	US-09-902-736A-315	Sequence 315, App
484	76	4.6	509	2	US-09-906-722A-315	Sequence 315, App
485	76	4.6	563	2	US-09-949-016-10405	Sequence 10405, A
486	76	4.6	687	1	US-08-232-538-6	Sequence 6, Appli
487	76	4.6	687	1	US-08-786-164-6	Sequence 6, Appli
488	76	4.6	687	2	US-09-427-353-2	Sequence 2, Appli
489	76	4.6	758	1	US-08-874-678-1	Sequence 1, Appli
490	76	4.6	758	2	US-08-643-839-1	Sequence 1, Appli
491	76	4.6	758	2	US-09-051-363-24	Sequence 24, Appl
492	76	4.6	758	2	US-09-348-886-1	Sequence 1, Appli
493	76	4.6	758	2	US-10-105-901A-1	Sequence 1, Appli
494	76	4.6	780	1	US-08-232-538-14	Sequence 14, Appl
495	76	4.6	780	1	US-08-786-164-14	Sequence 14, Appl
496	76	4.6	985	2	US-09-248-796A-16090	Sequence 16090, A
497	76	4.6	1014	2	US-09-078-347A-3	Sequence 3, Appli
498	76	4.6	1014	2	US-09-596-248D-25	Sequence 25, Appl
499	76	4.6	1014	2	US-09-296-662-35	Sequence 35, Appl
500	76	4.6	1063	2	US-09-596-248D-47	Sequence 47, Appl
501	76	4.6	1338	2	US-08-750-141A-3	Sequence 3, Appli
502	76	4.6	1338	2	US-09-119-014D-6	Sequence 6, Appli
503	76	4.6	1401	2	US-08-781-891-206	Sequence 206, App
504	76	4.6	1401	2	US-09-618-166-206	Sequence 206, App
505	76	4.6	1426	2	US-09-136-574A-43	Sequence 43, Appl
506	76	4.6	1645	2	US-09-976-594-769	Sequence 769, App
507	75.5	4.6	258	2	US-08-961-083-90	Sequence 90, Appl
508	75.5	4.6	258	2	US-09-536-784-90	Sequence 90, Appl
509	75.5	4.6	258	2	US-09-765-271-90	Sequence 90, Appl
510	75.5	4.6	258	2	US-09-765-272A-90	Sequence 90, Appl
511	75.5	4.6	348	1	US-08-035-392-2	Sequence 2, Appli
512	75.5	4.6	348	1	US-08-504-511A-2	Sequence 2, Appli
513	75.5	4.6	430	1	US-08-035-392-4	Sequence 4, Appli
514	75.5	4.6	430	1	US-08-504-511A-4	Sequence 4, Appli
515	75.5	4.6	451	2	US-09-134-001C-4461	Sequence 4461, Ap
516	75.5	4.6	453	2	US-09-230-225B-4	Sequence 4, Appli
517	75.5	4.6	510	2	US-09-270-767-43633	Sequence 43633, A
518	75.5	4.6	511	1	US-08-220-151-17	Sequence 17, Appl
519	75.5	4.6	511	1	US-08-413-118-17	Sequence 17, Appl
520	75.5	4.6	511	2	US-08-473-446-17	Sequence 17, Appl
521	75.5	4.6	565	2	US-08-961-083-218	Sequence 218, App
522	75.5	4.6	565	2	US-09-536-784-218	Sequence 218, App
523	75.5	4.6	565	2	US-09-765-271-218	Sequence 218, App
524	75.5	4.6	565	2	US-09-765-272A-218	Sequence 218, App
525	75.5	4.6	639	2	US-09-949-016-6812	Sequence 6812, Ap
526	75.5	4.6	641	2	US-10-164-595-46	Sequence 46, Appl
527	75.5	4.6	652	2	US-09-949-016-7323	Sequence 7323, Ap
528	75	4.5	210	2	US-09-270-767-32951	Sequence 32951, A
529	75	4.5	210	2	US-09-270-767-48168	Sequence 48168, A
530	75	4.5	424	1	US-08-419-414-2	Sequence 2, Appli
531	75	4.5	425	2	US-09-748-537-14	Sequence 14, Appl
532	75	4.5	554	1	US-08-524-051-2	Sequence 2, Appli
533	75	4.5	554	2	US-09-052-778-16	Sequence 16, Appl
534	75	4.5	557	2	US-09-248-796A-26892	Sequence 26892, A
535	75	4.5	904	2	US-09-198-484-2	Sequence 2, Appli
536	75	4.5	941	2	US-07-757-022B-14	Sequence 14, Appl
537	75	4.5	1022	2	US-07-757-022B-84	Sequence 84, Appl
538	75	4.5	1038	2	US-07-757-022B-74	Sequence 74, Appl

539	75	4.5	1049	2	US-07-757-022B-58	Sequence 58, Appl
540	75	4.5	1140	2	US-07-757-022B-104	Sequence 104, App
541	75	4.5	1151	1	US-08-286-889-37	Sequence 37, Appl
542	75	4.5	1151	1	US-08-485-618-37	Sequence 37, Appl
543	75	4.5	1151	1	US-08-362-652-37	Sequence 37, Appl
544	75	4.5	1151	1	US-08-605-672-37	Sequence 37, Appl
545	75	4.5	1151	1	US-08-482-293A-37	Sequence 37, Appl
546	75	4.5	1151	1	US-08-943-363-37	Sequence 37, Appl
547	75	4.5	1151	2	US-09-193-043-37	Sequence 37, Appl
548	75	4.5	1151	2	US-09-688-307A-37	Sequence 37, Appl
549	75	4.5	1151	2	US-09-350-259-37	Sequence 37, Appl
550	75	4.5	1161	2	US-09-193-043-55	Sequence 55, Appl
551	75	4.5	1161	2	US-09-688-307A-55	Sequence 55, Appl
552	75	4.5	1161	2	US-09-350-259-55	Sequence 55, Appl
553	75	4.5	1162	1	US-08-728-323A-2	Sequence 2, Appli
554	75	4.5	1162	2	US-09-298-568-2	Sequence 2, Appli
555	75	4.5	1162	2	US-09-410-399-2	Sequence 2, Appli
556	75	4.5	1162	2	US-09-894-273-2	Sequence 2, Appli
557	75	4.5	1270	2	US-07-757-022B-44	Sequence 44, Appl
558	75	4.5	1311	2	US-07-757-022B-42	Sequence 42, Appl
559	75	4.5	1313	2	US-07-757-022B-142	Sequence 142, App
560	75	4.5	1314	2	US-07-757-022B-50	Sequence 50, Appl
561	75	4.5	1320	2	US-07-757-022B-46	Sequence 46, Appl
562	75	4.5	1320	2	US-07-757-022B-60	Sequence 60, Appl
563	75	4.5	1320	2	US-10-164-595-58	Sequence 58, Appl
564	75	4.5	1354	2	US-07-757-022B-48	Sequence 48, Appl
565	75	4.5	1361	2	US-07-757-022B-40	Sequence 40, Appl
566	75	4.5	1363	2	US-07-757-022B-52	Sequence 52, Appl
567	75	4.5	1404	2	US-07-757-022B-2	Sequence 2, Appli
568	75	4.5	1404	2	US-07-757-022B-62	Sequence 62, Appl
569	75	4.5	1404	2	US-10-164-595-78	Sequence 78, Appl
570	75	4.5	1404	2	US-09-298-970A-1	Sequence 1, Appli
571	75	4.5	1404	2	US-09-897-188-1	Sequence 1, Appli
572	75	4.5	1411	2	US-09-949-016-10827	Sequence 10827, A
573	74.5	4.5	109	2	US-09-107-532A-4999	Sequence 4999, Ap
574	74.5	4.5	145	2	US-08-808-599A-41	Sequence 41, Appl
575	74.5	4.5	186	2	US-09-252-991A-20433	Sequence 20433, A
576	74.5	4.5	216	2	US-09-248-796A-25076	Sequence 25076, A
577	74.5	4.5	270	2	US-09-134-000C-3553	Sequence 3553, Ap
578	74.5	4.5	312	2	US-09-248-796A-20143	Sequence 20143, A
579	74.5	4.5	333	2	US-09-107-532A-6475	Sequence 6475, Ap
580	74.5	4.5	386	2	US-09-270-767-44120	Sequence 44120, A
581	74.5	4.5	429	2	US-09-949-016-8183	Sequence 8183, Ap
582	74.5	4.5	429	2	US-09-949-016-8184	Sequence 8184, Ap
583	74.5	4.5	478	1	US-08-456-670B-40	Sequence 40, Appl
584	74.5	4.5	478	2	US-09-372-036-40	Sequence 40, Appl
585	74.5	4.5	530	2	US-09-912-935-38	Sequence 38, Appl
586	74.5	4.5	564	2	US-09-949-016-6898	Sequence 6898, Ap
587	74.5	4.5	565	2	US-09-949-016-6902	Sequence 6902, Ap
588	74.5	4.5	587	2	US-09-815-923-4	Sequence 4, Appli
589	74.5	4.5	639	2	US-09-248-796A-20583	Sequence 20583, A
590	74.5	4.5	758	2	US-09-949-016-8288	Sequence 8288, Ap
591	74.5	4.5	794	2	US-09-252-991A-28569	Sequence 28569, A
592	74.5	4.5	998	1	US-08-449-645A-20	Sequence 20, Appl
593	74.5	4.5	998	1	US-08-702-367A-20	Sequence 20, Appl
594	74.5	4.5	998	4	PCT-US95-04681-20	Sequence 20, Appl
595	74.5	4.5	1638	2	US-09-071-035-258	Sequence 258, App
596	74.5	4.5	1638	2	US-09-071-035-262	Sequence 262, App
597	74.5	4.5	1638	2	US-09-071-035-266	Sequence 266, App
598	74.5	4.5	1638	2	US-10-206-576-258	Sequence 258, App
599	74.5	4.5	1638	2	US-10-206-576-262	Sequence 262, App
600	74.5	4.5	1638	2	US-10-206-576-266	Sequence 266, App
601	74.5	4.5	1747	2	US-09-134-000C-5999	Sequence 5999, Ap
602	74	4.5	197	2	US-09-513-999C-7852	Sequence 7852, Ap
603	74	4.5	257	2	US-09-567-458A-2	Sequence 2, Appli
604	74	4.5	279	2	US-09-248-796A-16859	Sequence 16859, A
605	74	4.5	299	2	US-09-107-433-3811	Sequence 3811, Ap
606	74	4.5	323	2	US-09-270-767-44688	Sequence 44688, A
607	74	4.5	339	1	US-08-433-854-4	Sequence 4, Appli
608	74	4.5	339	1	US-08-174-745A-4	Sequence 4, Appli
609	74	4.5	339	1	US-08-195-947-4	Sequence 4, Appli
610	74	4.5	339	1	US-08-433-885-4	Sequence 4, Appli
611	74	4.5	339	1	US-08-433-908B-4	Sequence 4, Appli
612	74	4.5	339	2	US-08-410-614-4	Sequence 4, Appli
613	74	4.5	370	2	US-09-270-767-37418	Sequence 37418, A
614	74	4.5	370	2	US-09-270-767-52635	Sequence 52635, A
615	74	4.5	395	2	US-09-949-016-9564	Sequence 9564, Ap
616	74	4.5	422	2	US-09-949-016-8251	Sequence 8251, Ap
617	74	4.5	428	2	US-09-134-000C-6457	Sequence 6457, Ap
618	74	4.5	472	2	US-09-625-188-6	Sequence 6, Appli
619	74	4.5	493	2	US-09-248-796A-17819	Sequence 17819, A
620	74	4.5	681	2	US-08-760-615-4	Sequence 4, Appli
621	74	4.5	681	2	US-09-336-910A-2	Sequence 2, Appli
622	74	4.5	778	2	US-09-248-796A-16358	Sequence 16358, A
623	74	4.5	910	2	US-09-270-767-42083	Sequence 42083, A
624	74	4.5	1021	2	US-09-902-540-16773	Sequence 16773, A
625	74	4.5	1693	2	US-08-840-316-1	Sequence 1, Appli
626	74	4.5	1693	2	US-08-809-523-1	Sequence 1, Appli
627	74	4.5	1693	2	US-08-471-971-1	Sequence 1, Appli
628	74	4.5	1693	2	US-09-402-776-1	Sequence 1, Appli
629	74	4.5	1693	2	US-08-470-246-1	Sequence 1, Appli
630	74	4.5	1693	2	US-08-316-765-1	Sequence 1, Appli
631	74	4.5	1693	2	US-09-724-475-1	Sequence 1, Appli
632	74	4.5	1693	4	PCT-US93-08849A-1	Sequence 1, Appli
633	74	4.5	1693	4	PCT-US93-08849-1	Sequence 1, Appli
634	74	4.5	1729	2	US-09-134-000C-5675	Sequence 5675, Ap
635	74	4.5	2414	1	US-08-227-536-2	Sequence 2, Appli
636	74	4.5	2414	2	US-09-538-092-1289	Sequence 1289, Ap
637	74	4.5	2414	4	PCT-US95-04682-2	Sequence 2, Appli
638	73.5	4.4	124	2	US-08-700-651-11	Sequence 11, Appl
639	73.5	4.4	124	2	US-08-928-361B-16	Sequence 16, Appl
640	73.5	4.4	124	2	US-09-588-995A-16	Sequence 16, Appl
641	73.5	4.4	128	2	US-08-700-651-7	Sequence 7, Appli
642	73.5	4.4	128	2	US-08-928-361B-12	Sequence 12, Appl
643	73.5	4.4	128	2	US-09-588-995A-12	Sequence 12, Appl
644	73.5	4.4	130	2	US-08-700-651-8	Sequence 8, Appli
645	73.5	4.4	130	2	US-08-928-361B-13	Sequence 13, Appl
646	73.5	4.4	130	2	US-09-588-995A-13	Sequence 13, Appl
647	73.5	4.4	138	2	US-08-700-651-10	Sequence 10, Appl
648	73.5	4.4	138	2	US-08-928-361B-15	Sequence 15, Appl
649	73.5	4.4	138	2	US-09-588-995A-15	Sequence 15, Appl
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655	73.5	4.4	397	2	US-08-649-006A-4	Sequence 4, Appli
656	73.5	4.4	397	2	US-09-771-023-4	Sequence 4, Appli
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659	73.5	4.4	499	2	US-09-431-367B-2	Sequence 2, Appli
660	73.5	4.4	540	2	US-09-583-110-3685	Sequence 3685, Ap
661	73.5	4.4	570	2	US-09-565-501A-104	Sequence 104, App
662	73.5	4.4	570	2	US-09-639-206A-104	Sequence 104, App
663	73.5	4.4	570	2	US-09-874-923-104	Sequence 104, App
664	73.5	4.4	638	1	US-08-463-262A-11	Sequence 11, Appl
665	73.5	4.4	638	1	US-08-463-989-11	Sequence 11, Appl
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667	73.5	4.4	638	2	US-09-003-570-11	Sequence 11, Appl
668	73.5	4.4	638	2	US-09-864-541A-11	Sequence 11, Appl
669	73.5	4.4	641	2	US-09-613-303-51	Sequence 51, Appl
670	73.5	4.4	641	2	US-10-267-311-51	Sequence 51, Appl
671	73.5	4.4	646	2	US-09-902-540-12044	Sequence 12044, A
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673	73.5	4.4	712	2	US-09-949-016-10600	Sequence 10600, A
674	73.5	4.4	713	2	US-08-899-437-2	Sequence 2, Appli
675	73.5	4.4	713	2	US-09-126-121-2	Sequence 2, Appli
676	73.5	4.4	763	2	US-08-961-083-66	Sequence 66, Appl
677	73.5	4.4	763	2	US-09-536-784-66	Sequence 66, Appl
678	73.5	4.4	763	2	US-09-765-271-66	Sequence 66, Appl
679	73.5	4.4	763	2	US-09-765-272A-66	Sequence 66, Appl
680	73.5	4.4	780	2	US-09-248-796A-16702	Sequence 16702, A
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682	73.5	4.4	795	2	US-10-055-412B-11	Sequence 11, Appl
683	73.5	4.4	819	2	US-09-468-656A-10	Sequence 10, Appl
684	73.5	4.4	821	2	US-09-193-562D-12	Sequence 12, Appl

685	73.5	4.4	821	2	US-10-055-412B-12	Sequence 12, Appl
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694	73.5	4.4	1876	2	US-09-839-479-70	Sequence 70, Appl
695	73.5	4.4	1878	2	US-09-418-710-13	Sequence 13, Appl
696	73.5	4.4	1878	2	US-09-839-479-13	Sequence 13, Appl
697	73	4.4	155	2	US-09-252-991A-22634	Sequence 22634, A
698	73	4.4	162	2	US-08-700-651-13	Sequence 13, Appl
699	73	4.4	326	2	US-09-248-796A-19891	Sequence 19891, A
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701	73	4.4	332	2	US-10-282-162-10	Sequence 10, Appl
702	73	4.4	340	2	US-09-248-796A-24600	Sequence 24600, A
703	73	4.4	380	2	US-09-270-767-43987	Sequence 43987, A
704	73	4.4	428	2	US-09-489-039A-10901	Sequence 10901, A
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706	73	4.4	488	2	US-09-069-781B-5	Sequence 5, Appli
707	73	4.4	488	2	US-09-137-132-5	Sequence 5, Appli
708	73	4.4	488	2	US-08-864-564A-5	Sequence 5, Appli
709	73	4.4	488	2	US-09-094-410-5	Sequence 5, Appli
710	73	4.4	488	2	US-08-708-123D-5	Sequence 5, Appli
711	73	4.4	488	2	US-08-583-153A-5	Sequence 5, Appli
712	73	4.4	488	2	US-08-638-524B-5	Sequence 5, Appli
713	73	4.4	497	2	US-08-956-171E-5234	Sequence 5234, Ap
714	73	4.4	497	2	US-08-781-986A-5234	Sequence 5234, Ap
715	73	4.4	502	2	US-09-248-796A-15481	Sequence 15481, A
716	73	4.4	579	2	US-09-198-452A-918	Sequence 918, App
717	73	4.4	606	2	US-09-438-185A-853	Sequence 853, App
718	73	4.4	645	2	US-09-270-767-42233	Sequence 42233, A
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724	73	4.4	708	1	US-09-058-263-2	Sequence 2, Appli
725	73	4.4	708	1	US-09-059-099-2	Sequence 2, Appli
726	73	4.4	708	2	US-09-058-264-2	Sequence 2, Appli
727	73	4.4	708	2	US-09-455-962-2	Sequence 2, Appli
728	73	4.4	708	4	PCT-US95-06530-2	Sequence 2, Appli
729	73	4.4	830	2	US-09-107-433-4309	Sequence 4309, Ap
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737	73	4.4	918	2	US-09-949-002-333	Sequence 333, App
738	73	4.4	933	1	US-08-682-847-2	Sequence 2, Appli
739	73	4.4	937	2	US-09-949-002-536	Sequence 536, App
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741	73	4.4	951	2	US-10-282-162-9	Sequence 9, Appli
742	73	4.4	1158	2	US-09-313-942-26	Sequence 26, Appl
743	73	4.4	1158	2	US-10-282-162-26	Sequence 26, Appl
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747	73	4.4	1702	2	US-09-839-996-5	Sequence 5, Appli
748	73	4.4	1702	2	US-10-080-505-5	Sequence 5, Appli
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753	73	4.4	2736	2	US-09-252-991A-30227	Sequence 30227, A
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755	72.5	4.4	150	2	US-09-588-995A-18	Sequence 18, Appl
756	72.5	4.4	167	2	US-08-956-171E-5216	Sequence 5216, Ap
757	72.5	4.4	167	2	US-08-781-986A-5216	Sequence 5216, Ap
758	72.5	4.4	185	2	US-09-248-796A-18311	Sequence 18311, A
759	72.5	4.4	204	2	US-09-902-540-14080	Sequence 14080, A
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761	72.5	4.4	206	2	US-09-438-185A-822	Sequence 822, App
762	72.5	4.4	293	2	US-09-496-320-5	Sequence 5, Appli
763	72.5	4.4	315	2	US-09-328-352-5948	Sequence 5948, Ap
764	72.5	4.4	328	2	US-09-489-039A-12803	Sequence 12803, A
765	72.5	4.4	340	2	US-09-492-709A-262	Sequence 262, App
766	72.5	4.4	368	2	US-09-248-796A-19000	Sequence 19000, A
767	72.5	4.4	378	2	US-09-248-796A-18526	Sequence 18526, A
768	72.5	4.4	445	2	US-09-710-279-1294	Sequence 1294, Ap
769	72.5	4.4	462	6	5171671-2	Patent No. 5171671
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771	72.5	4.4	494	2	US-09-902-540-9960	Sequence 9960, Ap
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773	72.5	4.4	608	2	US-09-949-016-11148	Sequence 11148, A
774	72.5	4.4	608	2	US-09-949-016-11149	Sequence 11149, A
775	72.5	4.4	608	2	US-09-949-016-11150	Sequence 11150, A
776	72.5	4.4	608	2	US-09-949-016-11151	Sequence 11151, A
777	72.5	4.4	652	2	US-09-310-463-4	Sequence 4, Appli
778	72.5	4.4	652	2	US-08-842-248A-4	Sequence 4, Appli
779	72.5	4.4	678	2	US-09-991-181-179	Sequence 179, App
780	72.5	4.4	678	2	US-09-990-444-179	Sequence 179, App
781	72.5	4.4	678	2	US-09-997-333-179	Sequence 179, App
782	72.5	4.4	678	2	US-09-992-598-179	Sequence 179, App
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784	72.5	4.4	707	2	US-10-101-464A-80	Sequence 80, Appl
785	72.5	4.4	719	2	US-09-949-016-7766	Sequence 7766, Ap
786	72.5	4.4	743	2	US-10-104-047-2340	Sequence 2340, Ap
787	72.5	4.4	798	2	US-09-270-767-42988	Sequence 42988, A
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792	72.5	4.4	878	2	US-09-724-418A-2	Sequence 2, Appli
793	72.5	4.4	907	2	US-08-783-774-2	Sequence 2, Appli
794	72.5	4.4	907	2	US-09-328-599A-1	Sequence 1, Appli
795	72.5	4.4	907	4	PCT-US95-04611A-19	Sequence 19, Appl
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797	72.5	4.4	1306	2	US-09-134-000C-6670	Sequence 6670, Ap
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801	72.5	4.4	2308	2	US-10-000-954-2	Sequence 2, Appli
802	72.5	4.4	2314	2	US-09-816-703A-2	Sequence 2, Appli
803	72.5	4.4	3069	2	US-09-712-363-246	Sequence 246, App
804	72.5	4.4	3256	2	US-09-919-172-98	Sequence 98, Appl
805	72.5	4.4	3256	2	US-09-976-594-22	Sequence 22, Appl
806	72.5	4.4	3256	2	US-09-919-039-21	Sequence 21, Appl
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808	72	4.3	295	2	US-09-270-767-45025	Sequence 45025, A
809	72	4.3	303	2	US-09-270-767-57613	Sequence 57613, A
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812	72	4.3	327	2	US-09-270-767-42324	Sequence 42324, A
813	72	4.3	342	2	US-09-949-016-10365	Sequence 10365, A
814	72	4.3	372	2	US-09-489-039A-13193	Sequence 13193, A
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818	72	4.3	457	2	US-09-949-016-7211	Sequence 7211, Ap
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821	72	4.3	559	2	US-09-545-814-14	Sequence 14, Appl
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823	72	4.3	583	2	US-09-545-814-5	Sequence 5, Appli
824	72	4.3	599	1	US-08-910-551B-2	Sequence 2, Appli
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827	72	4.3	785	2	US-08-895-590-3	Sequence 3, Appli
828	72	4.3	785	2	US-09-539-879A-3	Sequence 3, Appli
829	72	4.3	801	1	US-08-725-012-2	Sequence 2, Appli
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833	72	4.3	903	2	US-10-055-412B-46	Sequence 46, Appl
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841	72	4.3	2441	2	US-08-961-739-2	Sequence 2, Appli
842	72	4.3	2441	2	US-09-514-247A-8	Sequence 8, Appli
843	72	4.3	2441	2	US-09-686-316-2	Sequence 2, Appli
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846	71.5	4.3	218	2	US-09-605-703B-2490	Sequence 2490, Ap
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848	71.5	4.3	232	2	US-09-746-311B-366	Sequence 366, App
849	71.5	4.3	240	2	US-09-107-532A-4430	Sequence 4430, Ap
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852	71.5	4.3	386	2	US-09-248-796A-18312	Sequence 18312, A
853	71.5	4.3	442	1	US-08-363-255-4	Sequence 4, Appli
854	71.5	4.3	442	1	US-08-363-255-11	Sequence 11, Appl
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856	71.5	4.3	442	2	US-09-401-415-6	Sequence 6, Appli
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858	71.5	4.3	650	2	US-09-134-000C-5177	Sequence 5177, Ap
859	71.5	4.3	732	2	US-09-134-000C-6359	Sequence 6359, Ap
860	71.5	4.3	920	2	US-09-538-092-1197	Sequence 1197, Ap
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866	71	4.3	169	2	US-09-252-991A-32019	Sequence 32019, A
867	71	4.3	188	2	US-09-248-796A-14699	Sequence 14699, A
868	71	4.3	189	2	US-09-270-767-39457	Sequence 39457, A
869	71	4.3	189	2	US-09-270-767-54674	Sequence 54674, A
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871	71	4.3	230	2	US-09-248-796A-22910	Sequence 22910, A
872	71	4.3	239	2	US-09-248-796A-16743	Sequence 16743, A
873	71	4.3	251	2	US-09-248-796A-20695	Sequence 20695, A
874	71	4.3	272	2	US-09-248-796A-14774	Sequence 14774, A
875	71	4.3	316	2	US-09-504-358-10	Sequence 10, Appl
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877	71	4.3	316	2	US-10-230-562-10	Sequence 10, Appl
878	71	4.3	385	2	US-09-248-796A-23097	Sequence 23097, A
879	71	4.3	401	6	5252556-1	Patent No. 5252556
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881	71	4.3	554	2	US-09-599-360B-78	Sequence 78, Appl
882	71	4.3	610	1	US-07-821-717B-6	Sequence 6, Appli
883	71	4.3	610	1	US-08-119-262B-6	Sequence 6, Appli
884	71	4.3	610	1	US-08-135-929A-11	Sequence 11, Appl
885	71	4.3	610	1	US-08-234-265A-11	Sequence 11, Appl
886	71	4.3	630	2	US-09-485-529-8	Sequence 8, Appli
887	71	4.3	633	2	US-09-248-796A-20407	Sequence 20407, A
888	71	4.3	646	2	US-09-248-796A-16701	Sequence 16701, A
889	71	4.3	785	2	US-09-487-558B-348	Sequence 348, App
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891	71	4.3	1011	2	US-09-602-362E-27	Sequence 27, Appl
892	71	4.3	1239	2	US-10-076-622-577	Sequence 577, App
893	71	4.3	1374	2	US-09-771-161A-267	Sequence 267, App
894	71	4.3	1835	2	US-08-836-325-15	Sequence 15, Appl
895	71	4.3	1835	2	US-09-457-571-15	Sequence 15, Appl
896	71	4.3	1841	2	US-09-477-962-99	Sequence 99, Appl
897	71	4.3	1938	2	US-09-949-016-6609	Sequence 6609, Ap
898	71	4.3	2035	1	US-08-046-585-5	Sequence 5, Appli
899	71	4.3	2035	1	US-08-393-703-5	Sequence 5, Appli
900	71	4.3	2035	4	PCT-US93-11721-5	Sequence 5, Appli
901	71	4.3	2045	2	US-09-949-016-10491	Sequence 10491, A
902	71	4.3	2090	2	US-09-538-092-1081	Sequence 1081, Ap
903	71	4.3	2120	2	US-09-949-016-9768	Sequence 9768, Ap
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905	70.5	4.3	157	2	US-09-270-767-53317	Sequence 53317, A
906	70.5	4.3	173	2	US-09-107-532A-4115	Sequence 4115, Ap
907	70.5	4.3	198	2	US-09-489-039A-9988	Sequence 9988, Ap
908	70.5	4.3	213	2	US-09-244-805-11	Sequence 11, Appl
909	70.5	4.3	213	2	US-09-538-092-1255	Sequence 1255, Ap
910	70.5	4.3	220	2	US-09-198-452A-461	Sequence 461, App
911	70.5	4.3	220	2	US-09-438-185A-442	Sequence 442, App
912	70.5	4.3	232	2	US-09-333-809-214	Sequence 214, App
913	70.5	4.3	232	2	US-09-333-809-215	Sequence 215, App
914	70.5	4.3	232	2	US-09-333-809-216	Sequence 216, App
915	70.5	4.3	232	2	US-09-746-311B-363	Sequence 363, App
916	70.5	4.3	232	2	US-09-746-311B-364	Sequence 364, App
917	70.5	4.3	232	2	US-09-746-311B-365	Sequence 365, App
918	70.5	4.3	237	2	US-09-248-796A-22928	Sequence 22928, A
919	70.5	4.3	244	2	US-09-107-532A-4536	Sequence 4536, Ap
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923	70.5	4.3	292	2	US-08-852-020-6	Sequence 6, Appli
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926	70.5	4.3	401	2	US-09-949-016-7956	Sequence 7956, Ap
927	70.5	4.3	432	2	US-09-134-000C-3498	Sequence 3498, Ap
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935	70.5	4.3	574	2	US-09-248-796A-16162	Sequence 16162, A
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937	70.5	4.3	676	2	US-09-003-574-34	Sequence 34, Appl
938	70.5	4.3	676	2	US-09-003-570-34	Sequence 34, Appl
939	70.5	4.3	676	2	US-09-864-541A-34	Sequence 34, Appl
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941	70.5	4.3	942	2	US-09-538-092-602	Sequence 602, App
942	70.5	4.3	979	2	US-09-538-092-990	Sequence 990, App
943	70.5	4.3	1014	2	US-09-949-016-8229	Sequence 8229, Ap
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998	69.5	4.2	298	2	US-09-852-797-76	Sequence 76, Appl
999	69.5	4.2	298	2	US-09-853-161-76	Sequence 76, Appl
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1019	69.5	4.2	339	1	US-08-938-534-18	Sequence 18, Appl
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1062	69	4.2	509	2	US-09-292-225-38	Sequence 38, Appl
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1065	69	4.2	556	2	US-09-487-558B-426	Sequence 426, App
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1087	69	4.2	988	2	US-09-357-375-19	Sequence 19, Appl
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1104	68.5	4.1	391	2	US-09-200-090-4	Sequence 4, Appli
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1145	68	4.1	183	2	US-09-270-767-51047	Sequence 51047, A
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1173	68	4.1	527	2	US-09-320-774-9	Sequence 9, Appli
1174	68	4.1	527	2	US-09-940-244-144	Sequence 144, App
1175	68	4.1	527	2	US-09-381-212-144	Sequence 144, App
1176	68	4.1	527	2	US-09-713-601A-144	Sequence 144, App
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1407	67	4.0	503	4	PCT-US94-10080-10	Sequence 10, Appl
1408	67	4.0	514	2	US-09-712-363-154	Sequence 154, App
1409	67	4.0	541	2	US-09-248-796A-25057	Sequence 25057, A
1410	67	4.0	543	2	US-09-949-016-8822	Sequence 8822, Ap
1411	67	4.0	570	2	US-08-826-246-2	Sequence 2, Appli
1412	67	4.0	570	2	US-08-944-495-2	Sequence 2, Appli
1413	67	4.0	570	2	US-09-126-640-7	Sequence 7, Appli
1414	67	4.0	570	2	US-08-925-588-2	Sequence 2, Appli

1415	67	4.0	570	2	US-09-288-292A-7	Sequence 7, Appli
1416	67	4.0	570	2	US-09-372-044-2	Sequence 2, Appli
1417	67	4.0	570	2	US-08-825-486-2	Sequence 2, Appli
1418	67	4.0	570	2	US-08-826-248-2	Sequence 2, Appli
1419	67	4.0	598	2	US-09-538-092-1083	Sequence 1083, Ap
1420	67	4.0	623	2	US-09-485-529-7	Sequence 7, Appli
1421	67	4.0	645	2	US-10-104-047-3227	Sequence 3227, Ap
1422	67	4.0	661	1	US-08-232-538-12	Sequence 12, Appl
1423	67	4.0	661	1	US-08-786-164-12	Sequence 12, Appl
1424	67	4.0	668	2	US-09-134-000C-5289	Sequence 5289, Ap
1425	67	4.0	688	2	US-09-477-962-96	Sequence 96, Appl
1426	67	4.0	784	2	US-09-538-092-1254	Sequence 1254, Ap
1427	67	4.0	786	2	US-09-949-016-10170	Sequence 10170, A
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1429	67	4.0	886	2	US-09-784-316-4	Sequence 4, Appli
1430	67	4.0	886	2	US-10-229-124-4	Sequence 4, Appli
1431	67	4.0	908	1	US-07-903-456-2	Sequence 2, Appli
1432	67	4.0	908	2	US-08-666-221B-6	Sequence 6, Appli
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1434	67	4.0	908	2	US-08-666-221B-14	Sequence 14, Appl
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1436	67	4.0	908	2	US-09-949-016-7025	Sequence 7025, Ap
1437	67	4.0	915	2	US-09-949-016-9697	Sequence 9697, Ap
1438	67	4.0	976	1	US-08-449-645A-18	Sequence 18, Appl
1439	67	4.0	976	1	US-08-702-367A-18	Sequence 18, Appl
1440	67	4.0	976	2	US-09-949-016-6499	Sequence 6499, Ap
1441	67	4.0	976	4	PCT-US95-04681-18	Sequence 18, Appl
1442	67	4.0	1013	2	US-09-949-016-7991	Sequence 7991, Ap
1443	67	4.0	1124	2	US-09-605-703B-2576	Sequence 2576, Ap
1444	67	4.0	1132	2	US-09-528-784A-87	Sequence 87, Appl
1445	67	4.0	1132	2	US-09-569-098A-87	Sequence 87, Appl
1446	67	4.0	1231	2	US-09-071-035-420	Sequence 420, App
1447	67	4.0	1231	2	US-10-206-576-420	Sequence 420, App
1448	67	4.0	1265	2	US-09-071-035-418	Sequence 418, App
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1464	66.5	4.0	91	2	US-09-588-995A-19	Sequence 19, Appl
1465	66.5	4.0	154	2	US-09-252-991A-32034	Sequence 32034, A
1466	66.5	4.0	173	2	US-09-328-352-5235	Sequence 5235, Ap
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1471	66.5	4.0	206	2	US-09-417-264-6	Sequence 6, Appli
1472	66.5	4.0	235	2	US-09-247-155-126	Sequence 126, App
1473	66.5	4.0	235	2	US-09-903-190-126	Sequence 126, App
1474	66.5	4.0	236	2	US-09-148-545-202	Sequence 202, App
1475	66.5	4.0	236	2	US-09-621-011-202	Sequence 202, App
1476	66.5	4.0	239	2	US-09-248-796A-21096	Sequence 21096, A
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1479	66.5	4.0	249	2	US-09-514-422-6	Sequence 6, Appli
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1483	66.5	4.0	305	2	US-09-134-001C-5038	Sequence 5038, Ap
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1488	66.5	4.0	331	2	US-08-808-720-5	Sequence 5, Appli
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1492	66.5	4.0	376	2	US-09-270-767-42614	Sequence 42614, A
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1494	66.5	4.0	381	2	US-09-270-767-53582	Sequence 53582, A
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1496	66.5	4.0	407	1	US-08-776-585-3	Sequence 3, Appli
1497	66.5	4.0	408	1	US-08-351-473B-3	Sequence 3, Appli
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1499	66.5	4.0	436	2	US-09-248-796A-17505	Sequence 17505, A
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ALIGNMENTS

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RESULT 1
US-09-232-160-21
; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
;  APPLICANT: Steve Daniel
;  APPLICANT: James Gilmore
;  APPLICANT: Susan G. Stuart
;  APPLICANT: Laura Stuve
;  TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
;  TITLE OF INVENTION: PROLIFERATION
;  FILE REFERENCE: PA-0003 US
;  CURRENT APPLICATION NUMBER: US/09/232,160
;  CURRENT FILING DATE: 1999-01-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PERL Program
; SEQ ID NO 21
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 3044710
US-09-232-160-21

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
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Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 2
US-09-907-794A-201
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; Sequence 201, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322
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RESULT 3
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; Sequence 201, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
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;  PRIOR APPLICATION NUMBER: US 60/146,222
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;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
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;  PRIOR APPLICATION NUMBER: PCT/US99/28313
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;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-905-125A-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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RESULT 4
US-09-902-775A-201
; Sequence 201, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-775A-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
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  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              |||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 5
US-09-906-700-201
; Sequence 201, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,700
;  CURRENT FILING DATE:  2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-700-201

  Query Match             100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
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Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
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Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 6
US-09-903-603A-201
; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-903-603A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
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Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
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Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
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Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
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Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322
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RESULT 7
US-09-904-920A-201
; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15

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;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-904-920A-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
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Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 8
US-09-909-064-201
; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,064
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
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;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-909-064-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
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Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              ||||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 9
US-09-905-381A-201
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,381A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-905-381A-201

  Query Match             100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              ||||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 10
US-09-906-618-201
; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
```

```
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,618
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-618-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPPTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPPTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              ||||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 11
US-09-906-646-201
; Sequence 201, Application US/09906646
; Patent No. 6852848
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,646
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-646-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
              ||||||||||||||||||||||
Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 12
US-09-904-462-201
; Sequence 201, Application US/09904462
; Patent No. 6878807
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,462
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-462-201

  Query Match           100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120

Qy        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 180

Qy        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 240

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
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Db        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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Db        301 DKNPEESKSPSKTTVRCLEAEV 322


RESULT 13
US-09-902-736A-201
; Sequence 201, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,736A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-736A-201

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  Best Local Similarity   100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 201, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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;  FILE REFERENCE: GNE.1618P2C61
;  CURRENT APPLICATION NUMBER: US/09/906,722A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
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;  PRIOR APPLICATION NUMBER: PCT/US99/20594
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;  PRIOR FILING DATE: 1999-09-13
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;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-722A-201

  Query Match             100.0%;  Score 1657;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60

Qy         61 CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV 120
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Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
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RESULT 15
US-09-949-016-7765
; Sequence 7765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7765
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7765

  Query Match             100.0%;  Score 1657;  DB 2;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-159;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 60
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Db         23 MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA 82

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Db        143 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA 202

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Db        203 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL 262

Qy        241 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT 322

Qy        301 DKNPEESKSPSKTTVRCLEAEV 322
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GenCore version 5.1.7
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OM protein - protein search, using sw model

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	209.5	18.4	363	2	A37009	CD44 homolog membr
3	207	18.2	362	2	A35616	T-cell surface gly
4	203.5	17.9	362	2	A30901	lymphocyte adhesio
5	202	17.8	742	2	A47195	lymphocyte homing
6	199.5	17.6	493	2	S13530	CD44E protein, epi
7	198.5	17.5	365	2	A34424	CD44 membrane glyc
8	198.5	17.5	426	2	JH0518	lymphocyte homing
9	197	17.3	361	2	JH0417	cell adhesion mole
10	196.5	17.3	699	2	I37369	epican - human
11	196	17.3	395	2	I77371	CD44R5 - human
12	194	17.1	351	2	S45305	CD44 antigen precu
13	194	17.1	366	2	A53286	cell-surface glyco
14	183.5	16.2	359	2	S24240	lymphocyte surface
15	145.5	12.8	3562	2	A47171	chondroitin sulfat
16	145	12.8	277	2	A41735	hyaluronate-bindin
17	144	12.7	275	2	JC6506	tumor necrosis fac
18	143	12.6	2109	1	I50421	aggrecan precursor
19	137	12.1	276	2	A47290	TSG-6 homolog PS4
20	131.5	11.6	2124	2	A28452	proteoglycan core
21	131	11.5	2132	1	A55182	aggrecan precursor
22	130.5	11.5	883	2	S57653	brevican precursor
23	130.5	11.5	2415	1	A39086	aggrecan precursor
24	128	11.3	2327	2	T42630	aggrecan - bovine
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28	116	10.2	2397	1	A55535	versican precursor
29	115	10.1	370	2	S29139	aggrecan - pig (fr
30	115	10.1	1643	2	T14274	versican precursor
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32	112.5	9.9	340	2	JC7505	brain link protein
33	111	9.8	2409	1	A60979	versican precursor
34	110.5	9.7	1257	2	S28764	neurocan precursor
35	109	9.6	1069	2	T42681	hypothetical prote
36	108	9.5	354	1	LKHU	proteoglycan link
37	107	9.4	355	1	LKCH	proteoglycan link
38	107	9.4	371	2	A53908	brevican precursor
39	107	9.4	408	1	LKRT2	proteoglycan link
40	107	9.4	1268	2	S52781	neurocan - mouse
41	105.5	9.3	113	2	A55885	chondroitin sulfat
42	104.5	9.2	862	2	S43922	versican - pig-tai
43	104	9.2	354	1	S04243	proteoglycan link
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45	102	9.0	739	2	T21769	hypothetical prote
46	101.5	8.9	380	2	T28081	hypothetical prote
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51	92.5	8.1	851	2	T22696	hypothetical prote
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53	91	8.0	645	2	T29818	hypothetical prote
54	91	8.0	747	2	T34329	hypothetical prote
55	90.5	8.0	402	2	S73773	dihydrolipoamide a
56	90	7.9	388	2	S36500	E2 protein - human
57	89.5	7.9	411	2	A33664	96K lysosomal memb
58	89.5	7.9	518	2	T49778	hypothetical prote
59	89	7.8	307	1	GSFF3	salivary glue prot
60	89	7.8	416	1	A31959	lysosome-associate
61	89	7.8	429	1	JC5861	endo-1,4-beta-xyla
62	89	7.8	517	2	T20658	probable zinc meta
63	88.5	7.8	662	2	A45155	mucin FIM-C.1 - Af
64	88.5	7.8	770	2	T22808	hypothetical prote
65	88.5	7.8	1101	2	S15271	endoglucanase C (E
66	88	7.7	456	2	T31483	hypothetical prote
67	88	7.7	602	2	AD2067	hypothetical prote
68	88	7.7	1229	2	T25697	hypothetical prote
69	87.5	7.7	1085	2	S40476	Ca(2+)-sensing rec
70	87	7.7	235	2	PC2022	mucin like protein
71	87	7.7	721	2	B90487	hypothetical prote
72	87	7.7	1506	2	T30886	integumentary muci
73	86.5	7.6	400	1	A28172	spasmolysin precur
74	86.5	7.6	477	2	S53362	mucin 5AC (clone J
75	86.5	7.6	768	2	T00073	hypothetical prote
76	86.5	7.6	909	1	QRXLL2	LDL receptor 2 pre
77	86.5	7.6	1007	2	T24643	hypothetical prote
78	86.5	7.6	2616	2	A57096	nudel protein prec
79	85.5	7.5	786	2	T16509	hypothetical prote
80	85.5	7.5	895	2	T02597	Mutator-like trans
81	85.5	7.5	1367	1	S48478	glucan 1,4-alpha-g
82	85	7.5	265	2	T33695	hypothetical prote
83	85	7.5	449	2	T33257	hypothetical prote
84	85	7.5	569	2	AI1347	hypothetical prote
85	85	7.5	627	2	G86860	serine/threonine p
86	85	7.5	660	2	JW0067	chitinase (EC 3.2.
87	85	7.5	1016	2	H71460	probable outer mem
88	85	7.5	1162	2	T21557	hypothetical prote
89	84.5	7.4	752	2	E72616	hypothetical prote
90	84.5	7.4	1161	2	S57180	probable membrane
91	84	7.4	262	2	S76772	hypothetical prote
92	84	7.4	335	2	H96667	AP2-containing DNA
93	84	7.4	543	2	S35047	mucin JUL7 - human
94	84	7.4	927	2	T24031	hypothetical prote
95	84	7.4	1331	2	A48954	mannan endo-1,4-be
96	84	7.4	1362	2	A75207	amylopullulanase P
97	84	7.4	1779	2	T31085	xylanase - Caldice
98	84	7.4	1832	2	T31113	mucin-like glycopr
99	84	7.4	3020	2	A43932	mucin 2 precursor,
100	83.5	7.4	216	2	I51920	mucin - rhesus mac
101	83.5	7.4	279	2	S53363	mucin 5AC (clone J
102	83.5	7.4	967	2	S66852	hypothetical prote

103	83.5	7.4	1286	2	A88396	protein M01E10.2 [
104	83	7.3	409	2	S44346	RAD23 protein homo
105	83	7.3	605	2	S48940	hypothetical prote
106	83	7.3	977	2	T16232	hypothetical prote
107	82.5	7.3	383	1	S15624	E2 protein - human
108	82.5	7.3	726	2	S67044	NFI1 protein - yea
109	82.5	7.3	825	2	S62042	probable membrane
110	82.5	7.3	1206	2	S24407	formin isoform IV
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112	82.5	7.3	1420	2	T18385	latrophilin-2 (spl
113	82.5	7.3	1422	2	T18383	latrophilin-2, spl
114	82.5	7.3	1435	2	T18387	latrophilin-2 (spl
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117	82.5	7.3	1465	2	T18384	latrophilin-2 (spl
118	82.5	7.3	1468	2	S11515	formin - mouse
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121	82	7.2	463	2	T38444	hypothetical prote
122	82	7.2	476	2	A46118	myosin-binding pro
123	82	7.2	693	2	T19551	mucin-like protein
124	82	7.2	973	2	A97522	ribonuclease E, RN
125	82	7.2	977	2	AC2741	ribonuclease E [im
126	81.5	7.2	386	2	B97212	protein containing
127	81.5	7.2	584	2	T19061	hypothetical prote
128	81.5	7.2	860	2	AG1612	DNA mismatch repai
129	81.5	7.2	1216	2	F88473	protein F40H6.5 [i
130	81.5	7.2	1513	2	T23681	hypothetical prote
131	81.5	7.2	1777	2	T34369	hypothetical prote
132	81.5	7.2	3175	1	RRWVEV	genome polyprotein
133	81	7.1	221	2	S53649	ribosomal protein
134	81	7.1	1128	2	A49960	bud emergence prot
135	81	7.1	1251	2	T21389	hypothetical prote
136	81	7.1	1537	2	S53465	flocculation prote
137	81	7.1	1609	2	S25345	probable membrane
138	80.5	7.1	148	1	S07723	immediate-early se
139	80.5	7.1	391	1	S15617	E2 protein - human
140	80.5	7.1	441	2	T31482	hypothetical prote
141	80.5	7.1	742	2	T33514	hypothetical prote
142	80.5	7.1	798	2	T34248	hypothetical prote
143	80.5	7.1	896	2	T22061	hypothetical prote
144	80.5	7.1	2225	2	T26063	hypothetical prote
145	80	7.0	725	2	A41258	a-agglutinin core
146	80	7.0	881	2	S56032	probable membrane
147	79.5	7.0	354	2	T46740	microfilarial shea
148	79.5	7.0	860	2	AC1250	DNA mismatch repai
149	79.5	7.0	3570	2	T45025	mucin MUC5B, trach
150	79	7.0	249	2	G84781	hypothetical prote
151	79	7.0	339	2	T25562	hypothetical prote
152	79	7.0	352	2	T51659	myb-related transc
153	79	7.0	359	2	T13478	hypothetical prote
154	79	7.0	410	1	B31959	lysosome-associate
155	79	7.0	410	1	JC4317	lysosome-associate
156	79	7.0	575	2	T21775	hypothetical prote
157	78.5	6.9	164	2	I53641	mucin 5AC - human
158	78.5	6.9	232	2	A60095	larval glue protei
159	78.5	6.9	294	2	A37232	mucin, tracheal (A
160	78.5	6.9	322	2	A53715	apomucin precursor
161	78.5	6.9	562	2	A57088	nucleoporin-like p
162	78.5	6.9	577	2	G89430	protein K02E2.3 [i
163	78.5	6.9	825	2	T29634	hypothetical prote
164	78.5	6.9	1420	2	T17158	CL2AB protein - ra
165	78.5	6.9	1435	2	T46611	CL2BB protein - ra
166	78.5	6.9	1452	2	T17157	CL2AA protein - ra
167	78.5	6.9	1463	2	T17159	CL2AC protein - ra
168	78.5	6.9	1467	2	T17160	CL2BA protein - ra
169	78.5	6.9	1478	2	T17185	CL2BC protein - ra
170	78.5	6.9	1487	2	T14324	alpha-latrotoxin r
171	78	6.9	253	2	S76719	hypothetical prote
172	78	6.9	293	2	G87018	probable membrane
173	78	6.9	434	2	B84684	hypothetical prote
174	78	6.9	530	2	A45690	transactivator EBN
175	78	6.9	1050	2	T31853	hypothetical prote
176	78	6.9	1091	1	IJCHNL	neural cell adhesi
177	78	6.9	1723	2	H86557	polymorphic membra
178	78	6.9	1723	2	E72067	polymorphic membra
179	78	6.9	1732	2	C81601	polymorphic membra
180	78	6.9	1955	1	AGCH	agrin precursor -
181	77.5	6.8	514	2	JQ1317	activin receptor p
182	77.5	6.8	592	2	T34446	hypothetical prote
183	77.5	6.8	623	2	T18892	hypothetical prote
184	77.5	6.8	688	2	T18263	S-layer protein -
185	77.5	6.8	1127	2	E86386	probable mutator-l
186	77.5	6.8	2761	2	T21064	hypothetical prote
187	77	6.8	350	2	E75341	peptidyl-prolyl ci
188	77	6.8	453	2	F75206	maltose-binding pe
189	77	6.8	598	2	T22610	hypothetical prote
190	77	6.8	639	2	T33166	hypothetical prote
191	77	6.8	771	2	JC7388	M83 protein - huma
192	77	6.8	1092	1	JN0635	neural cell adhesi
193	77	6.8	1513	2	A54895	mucin 2, intestina
194	77	6.8	2187	2	T30826	nascent polypeptid
195	76.5	6.7	349	2	T43457	hypothetical prote
196	76.5	6.7	433	2	H84120	methyl-accepting c
197	76.5	6.7	505	2	B46629	mucin 6, gastric (
198	76.5	6.7	542	2	I39540	chitinase (EC 3.2.
199	76.5	6.7	658	2	T39500	serine/threonine-s
200	76.5	6.7	658	2	S60170	protein kinase Pak
201	76.5	6.7	718	2	T29708	hypothetical prote
202	76.5	6.7	750	2	T42614	probable envelope
203	76.5	6.7	1023	2	JC4013	major acidic nucle
204	76.5	6.7	1672	2	C81675	polymorphic membra
205	76	6.7	167	2	A33532	mucin SMUC-40 - hu
206	76	6.7	243	2	B41710	promastigote surfa
207	76	6.7	340	2	AH0940	probable ABC trans
208	76	6.7	368	2	S36564	E2 protein - human
209	76	6.7	382	2	B88561	protein F58A4.7b [
210	76	6.7	389	2	E97305	NADH-dependent but
211	76	6.7	389	2	A47013	butanol dehydrogen
212	76	6.7	532	2	T28784	hypothetical prote
213	76	6.7	549	2	T49298	hypothetical prote
214	76	6.7	569	2	B84470	Mutator-like trans
215	76	6.7	576	2	S59829	hypothetical prote
216	76	6.7	592	2	T16725	hypothetical prote
217	76	6.7	1016	2	T41720	hypothetical prote
218	76	6.7	1360	2	T33922	hypothetical prote
219	76	6.7	1489	2	G71406	probable retroviru
220	76	6.7	5376	2	T42215	zonadhesin - mouse
221	75.5	6.6	194	2	F72525	hypothetical prote
222	75.5	6.6	260	1	G69223	molybdate-binding
223	75.5	6.6	273	2	T44657	protein GP80 [impo
224	75.5	6.6	321	2	T26152	hypothetical prote
225	75.5	6.6	348	1	B46216	transcription fact
226	75.5	6.6	430	1	A46216	transcription fact
227	75.5	6.6	468	2	A55116	vacuolar ATPase (E
228	75.5	6.6	496	2	B41322	N-acetylmuramoyl-L
229	75.5	6.6	511	1	VGBEF4	glycoprotein C - h
230	75.5	6.6	609	2	G87496	peptidase, M23/M37
231	75.5	6.6	665	2	G97213	probable membrane-
232	75.5	6.6	737	1	S64767	probable serine/th
233	75.5	6.6	780	2	A48143	HF-1 regulatory el
234	75.5	6.6	1212	2	T13804	shs protein - frui
235	75	6.6	94	2	S53365	mucin 5AC (clone C
236	75	6.6	310	1	H71054	hypothetical prote
237	75	6.6	475	2	E84745	probable splicing
238	75	6.6	554	2	A56596	chitinase (EC 3.2.
239	75	6.6	604	2	T37994	probable splicing
240	75	6.6	651	2	T16450	hypothetical prote
241	75	6.6	793	2	AH1094	probable peptidogl
242	75	6.6	796	2	E96654	hypothetical prote
243	75	6.6	940	2	D89723	protein F39D8.1b [
244	75	6.6	945	2	T21998	hypothetical prote
245	75	6.6	3375	2	T19821	hypothetical prote
246	74.5	6.6	262	2	T33597	hypothetical prote
247	74.5	6.6	290	2	S66355	lectin-related sto
248	74.5	6.6	382	2	T25280	hypothetical prote

249	74.5	6.6	388	2	T16861	hypothetical prote
250	74.5	6.6	407	2	T26938	hypothetical prote
251	74.5	6.6	482	2	T22754	hypothetical prote
252	74.5	6.6	575	2	S29315	chaperonin 60 - cu
253	74.5	6.6	709	2	T28712	hypothetical prote
254	74.5	6.6	860	2	JC4566	chitinase (EC 3.2.
255	74.5	6.6	909	1	QRXLL1	LDL receptor 1 pre
256	74.5	6.6	998	2	S37627	protein-tyrosine k
257	74.5	6.6	1042	2	T48801	hypothetical prote
258	74.5	6.6	1075	2	S48992	flocculation prote
259	74.5	6.6	1388	2	A53317	collagen alpha 1(X
260	74.5	6.6	1838	1	CGHU1V	collagen alpha 1(V
261	74.5	6.6	2688	2	I49477	alpha-A-crystallin
262	74	6.5	147	2	S09762	hypothetical prote
263	74	6.5	223	2	T21930	hypothetical prote
264	74	6.5	313	2	AH0734	probable bacteriop
265	74	6.5	384	2	T21929	hypothetical prote
266	74	6.5	397	2	E97176	N-terminal domain
267	74	6.5	417	2	T20327	hypothetical prote
268	74	6.5	418	2	T16713	hypothetical prote
269	74	6.5	515	2	AD1162	flagellar motor sw
270	74	6.5	518	2	G88961	protein F59A7.8 [i
271	74	6.5	542	2	S64030	probable membrane
272	74	6.5	586	2	S66697	probable membrane
273	74	6.5	600	2	T06292	hypothetical prote
274	74	6.5	906	2	G90281	conserved hypothet
275	74	6.5	1047	2	A55617	masquerade precurs
276	74	6.5	2414	2	A54277	transcription adap
277	73.5	6.5	263	2	T38003	hypothetical ser-t
278	73.5	6.5	358	2	AD2378	hypothetical prote
279	73.5	6.5	371	2	S20075	promastigote surfa
280	73.5	6.5	435	2	AG1028	prepilin [imported
281	73.5	6.5	447	2	A39321	mucin - rat (fragm
282	73.5	6.5	451	2	S71754	cellular hepatitis
283	73.5	6.5	484	1	A24994	cellulose 1,4-beta
284	73.5	6.5	511	1	VGBE1K	glycoprotein C - h
285	73.5	6.5	542	2	T19952	hypothetical prote
286	73.5	6.5	595	2	A42086	CD30 antigen precu
287	73.5	6.5	601	2	H90270	hypothetical prote
288	73.5	6.5	626	2	AB1328	probable peptidogl
289	73.5	6.5	708	2	F87245	penicillin-bonding
290	73.5	6.5	806	2	E69424	hypothetical prote
291	73.5	6.5	866	2	T45462	membrane glycoprot
292	73.5	6.5	901	2	A44825	phosphoprotein, sy
293	73.5	6.5	905	2	T02205	Lu-ECAM-1 protein
294	73.5	6.5	976	2	A87576	peptidase, M16 fam
295	73.5	6.5	989	2	T47503	hypothetical prote
296	73.5	6.5	998	2	S31735	NAD ADP-ribosyltra
297	73.5	6.5	1004	2	T38074	hypothetical prote
298	73.5	6.5	1016	2	T19006	ankyrin related pr
299	73.5	6.5	2232	2	T34434	hypothetical prote
300	73.5	6.5	3176	2	CGHU3A	collagen alpha 3(V
301	73	6.4	260	2	I50109	gastrulation prote
302	73	6.4	327	2	S20074	promastigote surfa
303	73	6.4	461	2	T51044	related to spore c
304	73	6.4	486	2	S66097	cell-cycle protein
305	73	6.4	492	1	CHBOA3	gamma-aminobutyric
306	73	6.4	528	2	S69589	hypothetical prote
307	73	6.4	550	2	C75557	hypothetical prote
308	73	6.4	600	2	E72027	phosphoenolpyruvat
309	73	6.4	600	2	A86597	phosphoenolpyruvat
310	73	6.4	639	2	T13151	adapter protein CM
311	73	6.4	681	2	S33316	structural protein
312	73	6.4	728	2	T20561	hypothetical prote
313	73	6.4	771	2	T34376	hypothetical prote
314	73	6.4	781	2	T49472	hormone-sensitive
315	73	6.4	814	2	T33140	hypothetical prote
316	73	6.4	825	2	T48431	hypothetical prote
317	73	6.4	884	2	AE3166	ATP-dependent DNA
318	73	6.4	918	2	A36337	membrane glycoprot
319	73	6.4	993	2	F97717	hypothetical prote
320	73	6.4	1235	2	T13710	protein-tyrosine k
321	73	6.4	2179	1	GNNYH4	genome polyprotein
322	73	6.4	2468	2	A83412	hypothetical prote
323	72.5	6.4	263	2	I51225	snail1 protein - z
324	72.5	6.4	321	2	T26153	hypothetical prote
325	72.5	6.4	382	2	T27058	hypothetical prote
326	72.5	6.4	463	1	A36479	milk fat globule m
327	72.5	6.4	498	1	VGXPLM	surface glycoprote
328	72.5	6.4	560	2	T32661	hypothetical prote
329	72.5	6.4	575	2	S39484	DNA-binding protei
330	72.5	6.4	648	2	PC4395	mucin 3 - human (f
331	72.5	6.4	729	2	G96559	hypothetical prote
332	72.5	6.4	765	1	T44946	transducer protein
333	72.5	6.4	797	1	VGBEX1	glycoprotein X pre
334	72.5	6.4	867	2	T45463	membrane glycoprot
335	72.5	6.4	896	2	S36326	clathrin assembly
336	72.5	6.4	907	1	QQBE21	membrane antigen g
337	72.5	6.4	915	2	S36327	clathrin assembly
338	72.5	6.4	930	2	B72537	hypothetical prote
339	72.5	6.4	1021	2	S64506	protein kinase BUB
340	72.5	6.4	1180	2	E86719	hypothetical prote
341	72.5	6.4	1737	2	A59235	unconventional myo
342	72.5	6.4	1965	2	T33216	hypothetical prote
343	72	6.3	159	2	F72758	hypothetical prote
344	72	6.3	182	2	T30078	hypothetical prote
345	72	6.3	199	2	JE0351	OX40 ligand protei
346	72	6.3	236	2	T03041	hypothetical prote
347	72	6.3	246	2	PC4397	mucin 3 T10 - huma
348	72	6.3	324	2	S36646	integrin-associate
349	72	6.3	405	2	A60534	P2B/LAMP-1 precurs
350	72	6.3	448	2	G88639	protein C34H4.2 [i
351	72	6.3	481	2	T38149	pre-mrna splicing
352	72	6.3	482	2	A44997	merozoite surface
353	72	6.3	576	2	T38293	hypothetical serin
354	72	6.3	592	2	D70863	hypothetical prote
355	72	6.3	1176	2	T49482	hypothetical prote
356	72	6.3	1203	2	T17415	mycelial surface a
357	72	6.3	1367	2	S51959	hypothetical prote
358	72	6.3	1419	2	T30531	agglutinin-like ad
359	72	6.3	1489	2	T31108	cyst germination s
360	72	6.3	2526	2	T20531	hypothetical prote
361	72	6.3	2722	2	T20532	hypothetical prote
362	72	6.3	2738	2	E88320	protein F07A11.6 [
363	72	6.3	2971	2	T08026	hypothetical prote
364	71.5	6.3	141	2	A38196	non-structural hyp
365	71.5	6.3	152	2	T15170	hypothetical prote
366	71.5	6.3	152	2	T28759	hypothetical prote
367	71.5	6.3	162	2	C84948	NADH2 dehydrogenas
368	71.5	6.3	281	2	T49537	hypothetical prote
369	71.5	6.3	305	2	AB2149	hypothetical prote
370	71.5	6.3	363	2	T25278	hypothetical prote
371	71.5	6.3	477	2	T32938	hypothetical prote
372	71.5	6.3	496	2	E90181	hypothetical prote
373	71.5	6.3	499	2	AI2449	hypothetical prote
374	71.5	6.3	540	2	H98086	chaperonin GroEL [
375	71.5	6.3	540	2	G95222	chaperonin, 60 kDa
376	71.5	6.3	675	2	T47378	probable transposa
377	71.5	6.3	755	2	T20950	hypothetical prote
378	71.5	6.3	822	2	JC4076	dextranase (EC 3.2
379	71.5	6.3	882	2	T01168	hypothetical prote
380	71.5	6.3	1166	2	S37692	probable tumor sup
381	71.5	6.3	1557	2	D41214	protein-tyrosine-p
382	71.5	6.3	1630	2	C41214	protein-tyrosine-p
383	71	6.2	98	2	S53367	mucin 5AC (clone M
384	71	6.2	240	2	T33698	hypothetical prote
385	71	6.2	292	2	S24169	mucin - rat
386	71	6.2	304	2	T15922	hypothetical prote
387	71	6.2	343	2	S75435	hypothetical prote
388	71	6.2	349	2	T05857	hypothetical prote
389	71	6.2	378	2	S00842	leukosialin precur
390	71	6.2	379	1	S71571	alcohol dehydrogen
391	71	6.2	384	2	A41710	promastigote surfa
392	71	6.2	410	1	S68153	cellulase (EC 3.2.
393	71	6.2	415	2	A35560	lysosomal membrane
394	71	6.2	416	2	T20448	hypothetical prote

395	71	6.2	534	2	G97703	hypothetical prote
396	71	6.2	626	1	NBHUIA	platelet glycoprot
397	71	6.2	727	2	A88131	protein F10G7.9 [i
398	71	6.2	738	2	I40719	isocitrate dehydro
399	71	6.2	739	1	A34873	transcription fact
400	71	6.2	791	2	T39924	hypothetical prote
401	71	6.2	1014	1	A29725	NAD ADP-ribosyltra
402	71	6.2	1156	2	T43326	germline RNA helic
403	71	6.2	1172	2	T32759	hypothetical prote
404	71	6.2	1241	2	S01827	period clock prote
405	71	6.2	1272	2	S26180	neurofascin - chic
406	71	6.2	1367	2	T33819	hypothetical prote
407	71	6.2	1595	2	T31082	endo-1,4-beta-xyla
408	71	6.2	1993	2	AF1450	probable peptidogl
409	70.5	6.2	118	2	S49913	cryptogein - Phyto
410	70.5	6.2	128	2	A35690	mucin 3 (clone SIB
411	70.5	6.2	168	2	A31196	prespore-specific
412	70.5	6.2	172	2	F49247	merozoite surface
413	70.5	6.2	174	2	E49247	merozoite surface
414	70.5	6.2	254	2	D88560	protein F58A4.1 [i
415	70.5	6.2	255	2	I46606	MHC SLA-DQ alpha c
416	70.5	6.2	275	2	T21933	hypothetical prote
417	70.5	6.2	308	2	T29756	hypothetical prote
418	70.5	6.2	321	2	T19259	hypothetical prote
419	70.5	6.2	330	2	S28102	rlx protein - Stap
420	70.5	6.2	350	2	AI0139	UTP-hexose-1-phosp
421	70.5	6.2	385	2	F70591	probable kefB prot
422	70.5	6.2	403	1	S35541	transcription fact
423	70.5	6.2	427	2	C88883	protein JC8.10 [im
424	70.5	6.2	431	1	JC2002	transcription fact
425	70.5	6.2	478	2	A32555	major merozoite su
426	70.5	6.2	496	2	T30976	hypothetical prote
427	70.5	6.2	534	2	T39903	serine-rich protei
428	70.5	6.2	562	2	A85042	hypothetical prote
429	70.5	6.2	610	2	S35049	mucin JER57 - huma
430	70.5	6.2	616	2	T29234	hypothetical prote
431	70.5	6.2	674	2	S74506	ribonuclease E - S
432	70.5	6.2	802	2	T21315	hypothetical prote
433	70.5	6.2	893	2	T18271	hypothetical prote
434	70.5	6.2	910	1	S73361	dnaJ homolog prote
435	70.5	6.2	968	2	T00353	hypothetical prote
436	70.5	6.2	1032	2	G89427	protein T08D2.3 [i
437	70.5	6.2	1032	2	T18293	guanylate kinase-i
438	70.5	6.2	1123	2	T18270	hypothetical prote
439	70.5	6.2	1131	2	T15787	hypothetical prote
440	70.5	6.2	1369	2	S70713	protein-tyrosine k
441	70.5	6.2	1742	2	T17120	cellulase (EC 3.2.
442	70.5	6.2	1904	2	T13256	tail-host specific
443	70.5	6.2	3054	1	GNBVEV	genome polyprotein
444	70.5	6.2	3069	2	H70656	fatty-acid synthas
445	70	6.2	147	2	JC7938	type II antifreeze
446	70	6.2	209	2	AB2218	hypothetical prote
447	70	6.2	311	2	H96002	probable sugar kin
448	70	6.2	329	2	S38082	pathogenesis-relat
449	70	6.2	340	2	C90894	probable LACI-type
450	70	6.2	340	2	F85723	probable LACI-type
451	70	6.2	340	2	G64905	sugar-binding prot
452	70	6.2	357	2	E72245	hydrolase, ama/hip
453	70	6.2	358	2	A88082	protein T05A8.7 [i
454	70	6.2	408	2	A46712	glycoprotein IIa -
455	70	6.2	412	1	AJBORS	argininosuccinate
456	70	6.2	497	2	T51195	hypothetical prote
457	70	6.2	542	2	B47022	chitinase (EC 3.2.
458	70	6.2	589	2	AI0684	hypothetical prote
459	70	6.2	613	2	B90294	hypothetical prote
460	70	6.2	767	1	JU0474	glucan 1,4-alpha-g
461	70	6.2	775	1	WMBE19	ribonucleoside-dip
462	70	6.2	778	1	ALBYG	glucan 1,4-alpha-g
463	70	6.2	835	2	JC6140	cell surface-assoc
464	70	6.2	1048	1	S61388	dotA protein - Leg
465	70	6.2	1213	2	A41724	limb deformity (ld
466	70	6.2	1726	2	A39401	merozoite surface
467	70	6.2	3507	2	T34513	hypothetical prote
468	69.5	6.1	120	1	W4WL42	E4 protein - human
469	69.5	6.1	124	2	E84613	hypothetical prote
470	69.5	6.1	150	2	T48611	agp6 protein - Ara
471	69.5	6.1	172	2	T21753	hypothetical prote
472	69.5	6.1	202	2	AB2378	hypothetical prote
473	69.5	6.1	299	2	G70784	probable mmpS3 pro
474	69.5	6.1	372	2	T48660	heat shock protein
475	69.5	6.1	373	2	F81333	chaperone DnaJ Cj1
476	69.5	6.1	400	2	T32705	hypothetical prote
477	69.5	6.1	425	1	FOMVGC	gag polyprotein -
478	69.5	6.1	432	2	T08771	hypothetical prote
479	69.5	6.1	458	2	F86433	protein T17H7.5 [i
480	69.5	6.1	465	2	S46759	hypothetical prote
481	69.5	6.1	476	2	B44997	merozoite surface
482	69.5	6.1	514	2	A44100	cell adhesion mole
483	69.5	6.1	514	2	A31643	cell adhesion 80K
484	69.5	6.1	519	2	S69989	unspecific monooxy
485	69.5	6.1	540	1	FOMVHL	gag polyprotein -
486	69.5	6.1	558	2	A98199	translocated intim
487	69.5	6.1	558	2	E86045	probable transloca
488	69.5	6.1	621	2	T20307	hypothetical prote
489	69.5	6.1	640	2	T25367	hypothetical prote
490	69.5	6.1	672	2	T20310	hypothetical prote
491	69.5	6.1	736	2	T19366	hypothetical prote
492	69.5	6.1	833	2	AF2089	hypothetical prote
493	69.5	6.1	852	2	T46091	hypothetical prote
494	69.5	6.1	963	2	T40290	hypothetical prote
495	69.5	6.1	993	2	AE1905	outer membrane sec
496	69.5	6.1	1051	2	JC4091	glycoprotein A - P
497	69.5	6.1	1071	2	T22327	hypothetical prote
498	69.5	6.1	1118	2	A48292	mucin, tracheobron
499	69.5	6.1	1785	2	A45546	major merozoite su
500	69.5	6.1	2717	2	A34203	DNA-binding protei
501	69	6.1	171	2	T31478	hypothetical prote
502	69	6.1	217	2	S01358	salivary glue prot
503	69	6.1	255	2	T22429	hypothetical prote
504	69	6.1	258	2	S23106	priA protein - shi
505	69	6.1	266	2	T30919	hypothetical prote
506	69	6.1	284	2	T42367	a-agglutinin core
507	69	6.1	299	2	S44554	citrate transport
508	69	6.1	338	2	F69437	hypothetical prote
509	69	6.1	356	2	S73315	protoporphyrin IX
510	69	6.1	382	2	A28067	lysosomal membrane
511	69	6.1	416	2	T34279	hypothetical prote
512	69	6.1	420	2	AB2426	hypothetical prote
513	69	6.1	483	2	G86902	dextransucrase (EC
514	69	6.1	511	2	I50114	early growth respo
515	69	6.1	530	2	S62439	hypothetical serin
516	69	6.1	608	2	A46312	gag polyprotein -
517	69	6.1	652	2	S50210	surface layer prot
518	69	6.1	658	2	T41309	hypothetical threo
519	69	6.1	670	2	F84540	hypothetical prote
520	69	6.1	790	2	T34293	hypothetical prote
521	69	6.1	814	2	T49207	receptor kinase-li
522	69	6.1	850	1	MMHUE4	erythrocyte membra
523	69	6.1	854	1	QRHYLD	LDL receptor precu
524	69	6.1	1169	2	S38181	flocculation prote
525	69	6.1	1199	2	A40670	nuclear envelope p
526	69	6.1	1630	2	A53577	ascites sialoglyco
527	69	6.1	1868	2	S48938	hypothetical prote
528	69	6.1	2035	2	A40718	host cell factor C
529	69	6.1	2067	2	A42854	probable spindle p
530	69	6.1	2282	2	T42717	DNA-binding protei
531	69	6.1	2481	2	D90011	FmtB protein [impo
532	69	6.1	26926	1	I38344	titin, cardiac mus
533	68.5	6.0	204	2	S51232	gibberellin-respon
534	68.5	6.0	213	2	A86228	hypothetical prote
535	68.5	6.0	218	2	AH1837	hypothetical prote
536	68.5	6.0	246	2	S47805	hypothetical 27.4K
537	68.5	6.0	246	2	D91186	probable outer mem
538	68.5	6.0	246	2	C86033	probable outer mem
539	68.5	6.0	257	2	C84890	hypothetical prote
540	68.5	6.0	261	2	T30170	hypothetical prote

541	68.5	6.0	280	2	AE2031	gamma-tocopherol m
542	68.5	6.0	294	2	AI2016	hypothetical prote
543	68.5	6.0	310	1	YAZQ31	300K antigen Ag231
544	68.5	6.0	318	2	T20063	hypothetical prote
545	68.5	6.0	359	2	G70814	probable far prote
546	68.5	6.0	369	2	T01196	transcription fact
547	68.5	6.0	385	2	H97239	polyferredoxin [im
548	68.5	6.0	420	2	A88962	protein F59A7.1 [i
549	68.5	6.0	426	2	A35641	5-aminoimidazole r
550	68.5	6.0	435	2	C86340	protein F2D10.28 [
551	68.5	6.0	435	2	T25350	hypothetical prote
552	68.5	6.0	498	1	VGXPLA	surface glycoprote
553	68.5	6.0	500	1	S60929	probable aldehyde
554	68.5	6.0	507	2	S05542	hypothetical prote
555	68.5	6.0	509	2	T48459	cytochrome P450-li
556	68.5	6.0	514	1	A47692	fumarate hydratase
557	68.5	6.0	535	2	B84443	hypothetical prote
558	68.5	6.0	553	2	A49364	59 protein, brain
559	68.5	6.0	607	2	S63395	probable membrane
560	68.5	6.0	654	2	T33044	hypothetical prote
561	68.5	6.0	659	2	T40383	hypothetical prote
562	68.5	6.0	699	2	T09483	Cys-rich protein R
563	68.5	6.0	700	2	A54641	interspersed repea
564	68.5	6.0	721	2	E70766	hypothetical prote
565	68.5	6.0	737	2	AG2156	hypothetical prote
566	68.5	6.0	795	2	T20609	hypothetical prote
567	68.5	6.0	865	2	AC1966	hypothetical prote
568	68.5	6.0	942	2	T19553	hypothetical prote
569	68.5	6.0	1200	1	SNPSO	ice nucleation pro
570	68.5	6.0	1379	2	T45119	FIM protein [impor
571	68.5	6.0	1438	2	A48216	neurexin III-alpha
572	68.5	6.0	1471	2	B48218	neurexin III-alpha
573	68.5	6.0	1541	2	S46686	hypothetical prote
574	68.5	6.0	3122	2	T17202	DNA-directed DNA p
575	68	6.0	62	2	S53366	mucin 5AC (clone M
576	68	6.0	211	2	H72608	hypothetical prote
577	68	6.0	248	2	AF1914	carbon dioxide con
578	68	6.0	295	2	S50316	CIN5 protein - yea
579	68	6.0	301	2	H70644	hypothetical prote
580	68	6.0	303	2	S40973	hypothetical prote
581	68	6.0	333	2	T15367	hypothetical prote
582	68	6.0	339	2	AH0050	probable periplasm
583	68	6.0	372	2	T45628	glycerophosphodies
584	68	6.0	378	2	S61992	SLG1 protein - yea
585	68	6.0	380	1	S51826	alcohol dehydrogen
586	68	6.0	387	2	A56275	1,3-propanediol de
587	68	6.0	388	2	T43019	probable DNA-bindi
588	68	6.0	423	2	T14531	S-locus-specific g
589	68	6.0	426	2	I48379	gene hb protein -
590	68	6.0	452	2	T46147	zinc finger protei
591	68	6.0	456	2	T38221	hypothetical serin
592	68	6.0	479	2	A84588	probable tyrosine
593	68	6.0	500	2	AI1913	apolipoprotein N-a
594	68	6.0	502	2	T21935	hypothetical prote
595	68	6.0	515	2	B84406	TRK potassium upta
596	68	6.0	537	1	FOMVM7	gag polyprotein -
597	68	6.0	600	2	S56744	mucin (clone pGM7-
598	68	6.0	655	1	A55726	RNA-binding protei
599	68	6.0	669	2	B70186	translation elonga
600	68	6.0	679	2	S64258	hypothetical prote
601	68	6.0	709	2	S51793	dibasic processing
602	68	6.0	730	2	A75486	hypothetical prote
603	68	6.0	749	2	B86403	probable mutator-l
604	68	6.0	816	2	S64439	hypothetical prote
605	68	6.0	871	2	T43427	pob1 protein - fis
606	68	6.0	916	2	T20909	hypothetical prote
607	68	6.0	1016	1	JS0428	NAD ADP-ribosyltra
608	68	6.0	1098	2	T08599	probable transcrip
609	68	6.0	1131	2	T41144	hypothetical serin
610	68	6.0	1203	2	T51029	related to pathway
611	68	6.0	1204	2	F81158	exodeoxyribonuclea
612	68	6.0	1275	2	T33369	hypothetical prote
613	68	6.0	1390	2	T18883	hypothetical prote
614	68	6.0	1401	2	T30247	Werner syndrome pr
615	68	6.0	1578	2	I48216	neurexin III-alpha
616	68	6.0	1711	2	T31337	1,4-beta-glucanase
617	68	6.0	2440	2	S39162	transcription coac
618	68	6.0	2441	2	S39161	CREB-binding prote
619	68	6.0	3191	2	T22945	hypothetical prote
620	68	6.0	3712	2	S18253	laminin alpha-1 ch
621	67.5	5.9	150	2	T52587	probable arabinoga
622	67.5	5.9	159	2	T31598	hypothetical prote
623	67.5	5.9	191	2	S38117	hypothetical prote
624	67.5	5.9	210	2	B88082	protein T05A8.6 [i
625	67.5	5.9	256	2	H36857	B26R protein - var
626	67.5	5.9	297	2	S55063	conserved hypothet
627	67.5	5.9	338	2	S28004	probable cell surf
628	67.5	5.9	345	2	E88103	protein W10G11.5 [
629	67.5	5.9	346	2	T46916	hypothetical prote
630	67.5	5.9	376	2	S52137	MID2 protein - yea
631	67.5	5.9	387	2	A86302	hypothetical prote
632	67.5	5.9	391	2	A44063	paired box transcr
633	67.5	5.9	399	2	T42242	hypothetical 44.2K
634	67.5	5.9	431	2	G86277	F14L17.11 protein
635	67.5	5.9	433	2	S37790	probable serine/th
636	67.5	5.9	476	2	T32032	hypothetical prote
637	67.5	5.9	476	2	T27051	hypothetical prote
638	67.5	5.9	493	2	A34130	gamma-aminobutyric
639	67.5	5.9	527	2	T28878	hypothetical prote
640	67.5	5.9	530	2	T32812	hypothetical prote
641	67.5	5.9	538	2	S65764	chitinase (EC 3.2.
642	67.5	5.9	601	2	S56144	SH3 domain binding
643	67.5	5.9	642	2	T39607	fork head protein
644	67.5	5.9	644	2	H75141	oligopeptide-bindi
645	67.5	5.9	651	2	T21175	hypothetical prote
646	67.5	5.9	656	1	A49358	RNA-binding protei
647	67.5	5.9	670	2	T49510	fibroin-3 related
648	67.5	5.9	710	2	A99486	ABC transporter, b
649	67.5	5.9	736	2	T41259	hypothetical prote
650	67.5	5.9	749	2	T50397	probable serine/th
651	67.5	5.9	792	2	S70305	hypothetical prote
652	67.5	5.9	815	2	C84287	hypothetical prote
653	67.5	5.9	839	2	T41826	P95 orf83 - Bombyx
654	67.5	5.9	872	2	JH0561	metabotropic gluta
655	67.5	5.9	882	2	T23807	hypothetical prote
656	67.5	5.9	886	2	S29605	glycoprotein 350/2
657	67.5	5.9	971	2	F88448	protein C45G9.10 [
658	67.5	5.9	1051	2	T51904	hypothetical prote
659	67.5	5.9	1203	2	T04294	hypothetical prote
660	67.5	5.9	1348	2	S27812	probable epidermal
661	67.5	5.9	1348	2	A43917	probable epidermal
662	67.5	5.9	1633	2	T01879	hypothetical prote
663	67.5	5.9	1751	2	A45604	major blood-stage
664	67.5	5.9	1784	2	T10532	gag-pol polyprotei
665	67.5	5.9	1896	2	B72175	D15R protein - var
666	67.5	5.9	1897	2	T28621	hypothetical prote
667	67.5	5.9	3345	2	T13423	hypothetical prote
668	67	5.9	148	2	S50653	hypothetical prote
669	67	5.9	149	2	S12913	cystatin - fruit f
670	67	5.9	153	2	S67294	hypothetical prote
671	67	5.9	201	1	WMBEHL	UL4 protein - huma
672	67	5.9	214	2	A46629	mucin 6, gastric (
673	67	5.9	232	1	WMADC2	early E1A 25K prot
674	67	5.9	233	2	T22977	hypothetical prote
675	67	5.9	264	2	A49149	mesoderm developme
676	67	5.9	276	2	T51685	myb-related transc
677	67	5.9	305	2	T24283	hypothetical prote
678	67	5.9	308	1	B48008	electron transfer
679	67	5.9	319	2	T43040	hypothetical prote
680	67	5.9	398	2	AE0975	probable racemase
681	67	5.9	402	2	E86185	hypothetical prote
682	67	5.9	412	2	E88736	protein F33D4.6a [
683	67	5.9	426	2	F75394	hypothetical prote
684	67	5.9	433	2	T14329	dermal glycoprotei
685	67	5.9	438	1	S70602	cellulose 1,4-beta
686	67	5.9	441	2	C75076	heme biosynthesis

687	67	5.9	443	2	T14916	mitosis-specific c
688	67	5.9	466	2	S45419	hypothetical prote
689	67	5.9	476	2	C39481	serum response fac
690	67	5.9	486	2	B39481	serum response fac
691	67	5.9	494	1	A29079	lymphocyte surface
692	67	5.9	514	2	H70699	probable ppp prote
693	67	5.9	536	2	H71563	hypothetical prote
694	67	5.9	549	2	S04845	Ig heavy chain pre
695	67	5.9	558	2	S57953	C4BP protein alpha
696	67	5.9	579	2	D84137	methyl-accepting c
697	67	5.9	581	2	E86408	F3H9.11 protein -
698	67	5.9	588	2	B70618	probable PE protei
699	67	5.9	610	1	I46001	C4b-binding protei
700	67	5.9	617	2	T15408	hypothetical prote
701	67	5.9	620	2	A70525	hypothetical prote
702	67	5.9	634	2	T49415	hypothetical prote
703	67	5.9	636	2	S63131	probable membrane
704	67	5.9	644	2	F81411	probable ribonucle
705	67	5.9	650	2	S22835	alpha-agglutinin -
706	67	5.9	672	2	T32557	hypothetical prote
707	67	5.9	698	1	JX0202	long-chain-fatty-a
708	67	5.9	710	2	T21339	hypothetical prote
709	67	5.9	723	2	H85092	hypothetical prote
710	67	5.9	732	2	T25937	hypothetical prote
711	67	5.9	784	2	S26638	SPR-1 protein - hu
712	67	5.9	824	2	T23923	hypothetical prote
713	67	5.9	826	2	G90283	hypothetical prote
714	67	5.9	850	2	S56015	gastric mucin MUC5
715	67	5.9	855	2	T19405	hypothetical prote
716	67	5.9	910	2	C69456	subtilisin sendai
717	67	5.9	948	2	T11678	hypothetical prote
718	67	5.9	1060	2	T31763	hypothetical prote
719	67	5.9	1140	2	D88690	protein F41H10.3 [
720	67	5.9	1140	2	S73786	hypothetical prote
721	67	5.9	1228	2	C98219	proline dehydrogen
722	67	5.9	1228	2	AG3067	proline dehydrogen
723	67	5.9	1401	2	T17452	Werner syndrome pr
724	67	5.9	1804	2	H96597	hypothetical prote
725	67	5.9	1819	2	T32008	hypothetical prote
726	67	5.9	1900	2	S45530	probable 1-phospha
727	67	5.9	2476	2	T34022	zonadhesin - pig
728	67	5.9	4377	2	A55575	ankyrin 3, long sp
729	66.5	5.9	128	2	T05635	hypothetical prote
730	66.5	5.9	149	2	E71227	hypothetical prote
731	66.5	5.9	175	2	T50094	hypothetical prote
732	66.5	5.9	217	2	S45446	hypothetical prote
733	66.5	5.9	238	2	T07921	probable starch sy
734	66.5	5.9	240	2	S31573	hypothetical prote
735	66.5	5.9	263	2	S01360	salivary glue prot
736	66.5	5.9	319	1	A35163	carbonate dehydrat
737	66.5	5.9	327	2	H82554	conserved hypothet
738	66.5	5.9	345	2	AH0457	UDP-N-acetylmurama
739	66.5	5.9	348	1	B37760	UTP-hexose-1-phosp
740	66.5	5.9	348	2	AE0594	galactose-1-phosph
741	66.5	5.9	359	2	S42787	serine/threonine-r
742	66.5	5.9	369	2	E84291	iron (III) ABC tra
743	66.5	5.9	371	1	AJMSQ3	glutamate-ammonia
744	66.5	5.9	371	1	FOMVCS	gag polyprotein -
745	66.5	5.9	373	1	AJHUQ	glutamate-ammonia
746	66.5	5.9	385	2	T38113	hypothetical serin
747	66.5	5.9	397	2	T22932	hypothetical prote
748	66.5	5.9	413	2	S48756	transcription fact
749	66.5	5.9	452	2	T26827	hypothetical prote
750	66.5	5.9	458	2	T31631	hypothetical prote
751	66.5	5.9	461	2	D72414	anthranilate synth
752	66.5	5.9	506	2	AG1864	hypothetical prote
753	66.5	5.9	507	2	T50398	hypothetical serin
754	66.5	5.9	507	2	T23375	hypothetical prote
755	66.5	5.9	516	2	A31270	radial spoke prote
756	66.5	5.9	521	2	S69559	hypothetical prote
757	66.5	5.9	521	2	C87474	hypothetical prote
758	66.5	5.9	527	2	T16022	hypothetical prote
759	66.5	5.9	542	2	JN0661	heat shock protein
760	66.5	5.9	542	2	S32106	groEL protein - La
761	66.5	5.9	562	2	B41035	chitinase (EC 3.2.
762	66.5	5.9	562	2	S50371	chitinase (EC 3.2.
763	66.5	5.9	571	2	H97070	membrane associate
764	66.5	5.9	575	2	S29316	chaperonin 60 - cu
765	66.5	5.9	615	2	T47395	hypothetical prote
766	66.5	5.9	637	2	T20981	hypothetical prote
767	66.5	5.9	648	2	T43337	polo-like kinase-1
768	66.5	5.9	650	2	I49523	tumor necrosis fac
769	66.5	5.9	681	2	A45705	type I transmembra
770	66.5	5.9	710	2	S67098	probable membrane
771	66.5	5.9	719	2	T33170	hypothetical prote
772	66.5	5.9	739	2	I56187	transcription fact
773	66.5	5.9	811	2	A41054	fasciclin II, tran
774	66.5	5.9	843	2	S44868	kinesin heavy chai
775	66.5	5.9	880	2	S44833	F54H12.5 protein -
776	66.5	5.9	913	2	D82885	multiple banded an
777	66.5	5.9	919	2	T16693	hypothetical prote
778	66.5	5.9	948	2	C75265	hexagonally packed
779	66.5	5.9	996	2	JE0237	apolipoprotein E r
780	66.5	5.9	1059	2	T22545	hypothetical prote
781	66.5	5.9	1219	2	H84464	probable helicase
782	66.5	5.9	1221	2	AI0193	ribonuclease E (EC
783	66.5	5.9	1655	2	T32633	hypothetical prote
784	66	5.8	162	2	T02072	probable glycine c
785	66	5.8	169	2	A49247	merozoite surface
786	66	5.8	193	2	D72643	hypothetical prote
787	66	5.8	253	2	T27279	hypothetical prote
788	66	5.8	255	2	B75309	hypothetical prote
789	66	5.8	256	2	JC2398	PMS3 homolog misma
790	66	5.8	259	2	E82029	methionyl aminopep
791	66	5.8	282	2	B90313	conserved hypothet
792	66	5.8	315	2	S74357	hypothetical prote
793	66	5.8	329	2	T43012	conserved hypothet
794	66	5.8	360	2	T33835	hypothetical prote
795	66	5.8	367	1	W2WL11	E2 protein - human
796	66	5.8	369	2	AI1079	conserved hypothet
797	66	5.8	375	2	S36547	E2 protein - human
798	66	5.8	380	1	S00912	alcohol dehydrogen
799	66	5.8	383	2	E96972	riboflavin biosynt
800	66	5.8	393	1	HVRKC1	Ig mu chain C regi
801	66	5.8	407	2	A30200	120K lysosomal mem
802	66	5.8	426	2	B53580	neurexin III beta
803	66	5.8	459	2	T17364	NADH2 dehydrogenas
804	66	5.8	463	1	P2WL13	L2 protein - human
805	66	5.8	471	1	A38979	cellulose 1,4-beta
806	66	5.8	471	1	A26160	cellulose 1,4-beta
807	66	5.8	482	2	S76376	hypothetical prote
808	66	5.8	584	2	JC7809	sulfakinin recepto
809	66	5.8	599	2	G71481	probable phosphoen
810	66	5.8	611	2	T04510	hypothetical prote
811	66	5.8	614	2	A43390	gamma-aminobutyric
812	66	5.8	619	2	T15969	hypothetical prote
813	66	5.8	627	2	T27123	hypothetical prote
814	66	5.8	643	2	H84305	Htr8 transducer [i
815	66	5.8	645	2	T16078	hypothetical prote
816	66	5.8	655	2	AD2422	DNA polymerase III
817	66	5.8	657	2	E96812	protein F3F9.10 [i
818	66	5.8	657	2	H71422	hypothetical prote
819	66	5.8	674	2	G70875	probable oxidoredu
820	66	5.8	687	2	A49636	soluble vascular e
821	66	5.8	730	2	A53064	folded gastrulatio
822	66	5.8	733	2	T01875	probable long-chai
823	66	5.8	786	1	A47547	serine proteinease
824	66	5.8	816	2	A49151	fibroblast growth
825	66	5.8	897	2	S50550	SIN1-associated pr
826	66	5.8	978	1	RGBYI3	regulatory protein
827	66	5.8	994	1	MNWVM	nonstructural prot
828	66	5.8	1039	2	T09883	hypothetical prote
829	66	5.8	1041	2	S55862	probable membrane
830	66	5.8	1273	2	S58782	SEC31 protein - ye
831	66	5.8	1338	2	S09982	protein-tyrosine k
832	66	5.8	1422	2	T42636	protein-tyrosine-p

833	66	5.8	1711	2	AB1283	peptidoglycan link
834	66	5.8	1829	2	T24583	hypothetical prote
835	66	5.8	2271	2	F90073	hypothetical prote
836	66	5.8	2405	2	T08164	dynein alpha heavy
837	65.5	5.8	157	2	JP0075	lectin CEL-IV, C-t
838	65.5	5.8	198	2	A40709	ecdysone receptor
839	65.5	5.8	211	1	MUKAD	lysozyme (EC 3.2.1
840	65.5	5.8	248	2	T40149	hypothetical prote
841	65.5	5.8	282	2	T21222	hypothetical prote
842	65.5	5.8	287	2	S65765	chitinase (EC 3.2.
843	65.5	5.8	290	2	A43897	spicule matrix pro
844	65.5	5.8	314	2	D96703	hypothetical prote
845	65.5	5.8	316	2	G86333	hypothetical prote
846	65.5	5.8	328	2	S69715	hypothetical prote
847	65.5	5.8	356	2	D86382	hypothetical prote
848	65.5	5.8	365	2	T26564	hypothetical prote
849	65.5	5.8	377	2	A48018	mucin 7 precursor,
850	65.5	5.8	443	2	C88427	protein R07E5.6 [i
851	65.5	5.8	459	2	G84752	En/Spm-like transp
852	65.5	5.8	460	2	T23955	hypothetical prote
853	65.5	5.8	461	2	T39862	hypothetical prote
854	65.5	5.8	463	2	T15416	hypothetical prote
855	65.5	5.8	493	2	JC5486	membrane glycoprot
856	65.5	5.8	497	2	D81723	conserved hypothet
857	65.5	5.8	516	2	T24644	hypothetical prote
858	65.5	5.8	526	2	C84552	hypothetical prote
859	65.5	5.8	540	2	T19956	hypothetical prote
860	65.5	5.8	541	2	T44725	chaperonin 60K [im
861	65.5	5.8	575	2	T34280	hypothetical prote
862	65.5	5.8	588	2	A25902	65K antigen - Myco
863	65.5	5.8	592	2	S43597	coiled-coil protei
864	65.5	5.8	594	2	S62529	hypothetical prote
865	65.5	5.8	604	1	JP0001	glucan 1,4-alpha-g
866	65.5	5.8	628	2	F84219	Htr16 transducer [
867	65.5	5.8	631	2	T32761	hypothetical prote
868	65.5	5.8	642	1	T44253	transducer protein
869	65.5	5.8	649	2	JQ0103	hypothetical 70K p
870	65.5	5.8	667	2	T15710	hypothetical prote
871	65.5	5.8	679	2	T19703	hypothetical prote
872	65.5	5.8	713	2	T44447	neuregulin-3 [impo
873	65.5	5.8	746	2	G02838	enhancer-of-zeste
874	65.5	5.8	759	2	T44142	DR1 protein [impor
875	65.5	5.8	784	2	AH2560	hypothetical prote
876	65.5	5.8	790	1	FOMVHZ	gag-kit polyprotei
877	65.5	5.8	815	2	H84199	dihydropteroate sy
878	65.5	5.8	821	2	S39983	eps8 protein - mou
879	65.5	5.8	826	2	T46060	hypothetical prote
880	65.5	5.8	841	2	B71212	hypothetical prote
881	65.5	5.8	877	2	F90070	Clumping factor B
882	65.5	5.8	894	2	T13029	beta-adaptin homol
883	65.5	5.8	975	2	T29908	hypothetical prote
884	65.5	5.8	1011	1	JH0581	NAD ADP-ribosyltra
885	65.5	5.8	1043	2	F97302	hypothetical prote
886	65.5	5.8	1161	2	A27069	lethal (2) giant l
887	65.5	5.8	1306	2	S25370	MSB2 protein - yea
888	65.5	5.8	1442	1	B48148	protein-tyrosine-p
889	65.5	5.8	1524	2	S68553	surface layer prot
890	65.5	5.8	1650	2	S28721	hypothetical prote
891	65.5	5.8	3124	2	A40020	collagen alpha 1(X
892	65.5	5.8	7576	2	T17428	FK506 polyketide s
893	65	5.7	179	2	T26929	hypothetical prote
894	65	5.7	194	2	B72642	hypothetical prote
895	65	5.7	244	2	D90783	probable outer mem
896	65	5.7	244	2	F85643	outer membrane pre
897	65	5.7	271	2	B96773	hypothetical prote
898	65	5.7	275	2	T48436	hypothetical prote
899	65	5.7	282	2	T26397	hypothetical prote
900	65	5.7	284	2	A97203	2-oxoacid ferredox
901	65	5.7	332	2	T31928	hypothetical prote
902	65	5.7	348	2	AD3264	electron transfer
903	65	5.7	373	2	AG3191	amide hydrolase [i
904	65	5.7	380	1	S53307	alcohol dehydrogen
905	65	5.7	392	2	T49471	mucin (muc3) relat
906	65	5.7	393	2	A49008	paired box transcr
907	65	5.7	402	2	T20595	hypothetical prote
908	65	5.7	427	2	E83711	hypothetical prote
909	65	5.7	434	2	S62168	hypothetical prote
910	65	5.7	459	2	T17358	NADH2 dehydrogenas
911	65	5.7	465	2	T34984	probable integral
912	65	5.7	473	2	G90401	flagella-related p
913	65	5.7	503	2	S63257	probable membrane
914	65	5.7	506	2	A86169	hypothetical prote
915	65	5.7	516	2	JE0134	mannan endo-1,4-be
916	65	5.7	585	2	JC5013	2,4-chlorocatechol
917	65	5.7	593	2	S49525	glycoprotein G - s
918	65	5.7	608	2	S05341	probable reverse t
919	65	5.7	609	2	S36569	E1 protein - human
920	65	5.7	611	2	E86388	probable chaperoni
921	65	5.7	618	2	AI0171	probable exported
922	65	5.7	619	2	A43361	Ets-related transc
923	65	5.7	627	2	S37954	RNA polymerase I t
924	65	5.7	633	2	T04835	probable serine/th
925	65	5.7	648	2	T04837	probable serine/th
926	65	5.7	674	2	T15524	hypothetical prote
927	65	5.7	706	2	S33761	transferrin precur
928	65	5.7	708	2	T29669	hypothetical prote
929	65	5.7	742	2	AH2166	hypothetical prote
930	65	5.7	770	2	G88445	protein C26E6.2 [i
931	65	5.7	786	2	A55501	cyclin F - human
932	65	5.7	792	2	F90566	conserved hypothet
933	65	5.7	817	2	F86742	ribonuclease [impo
934	65	5.7	859	2	T29630	hypothetical prote
935	65	5.7	874	2	AI0281	probable insectici
936	65	5.7	876	2	T05943	probable lipoxygen
937	65	5.7	921	2	A45183	TBP-associated fac
938	65	5.7	921	2	A48184	transcription init
939	65	5.7	955	2	F84914	hypothetical prote
940	65	5.7	973	2	B86547	polymorphic outer
941	65	5.7	973	2	F72076	polymorphic outer
942	65	5.7	995	2	C81593	polymorphic membra
943	65	5.7	1088	1	IJXLNL	neural cell adhesi
944	65	5.7	1095	2	PC1114	SKCDC25 protein -
945	65	5.7	1096	2	H86237	protein F14N23.29
946	65	5.7	1097	2	T49187	hypothetical prote
947	65	5.7	1124	2	F71719	hypothetical prote
948	65	5.7	1139	1	E64234	cytadherence-acces
949	65	5.7	1146	2	S46837	hypothetical prote
950	65	5.7	1216	2	B90580	hypothetical prote
951	65	5.7	1314	2	H86327	protein F18O14.25
952	65	5.7	1459	2	T32271	hypothetical prote
953	65	5.7	1566	2	T20058	hypothetical prote
954	65	5.7	1605	2	T31435	DNA-directed RNA p
955	65	5.7	1634	2	T26517	hypothetical prote
956	65	5.7	1642	2	T19130	hypothetical prote
957	65	5.7	1895	2	T15881	hypothetical prote
958	65	5.7	1970	2	T03284	myoblast city prot
959	65	5.7	2311	1	TVCHSR	kinase-related pro
960	64.5	5.7	69	2	D72852	actin rearrangemen
961	64.5	5.7	117	2	AB0028	50S ribosomal prot
962	64.5	5.7	134	2	T24968	hypothetical prote
963	64.5	5.7	204	2	S67295	probable membrane
964	64.5	5.7	220	2	I50588	fibroblast growth
965	64.5	5.7	224	2	G83392	hypothetical prote
966	64.5	5.7	226	2	T28268	hypothetical prote
967	64.5	5.7	227	2	T50033	capsular polysacch
968	64.5	5.7	231	2	F84311	hypothetical prote
969	64.5	5.7	292	2	JC4741	mosquitocidal toxi
970	64.5	5.7	313	2	A34677	secretory pathway
971	64.5	5.7	319	2	S12104	lipase 1 - Moraxel
972	64.5	5.7	322	2	AH2192	hypothetical prote
973	64.5	5.7	328	2	S67570	hypothetical prote
974	64.5	5.7	336	2	T15837	hypothetical prote
975	64.5	5.7	341	2	C83578	hypothetical prote
976	64.5	5.7	345	2	T12344	NADH2 dehydrogenas
977	64.5	5.7	349	2	T42965	glycoprotein - ate
978	64.5	5.7	354	2	S59521	mucin 5ac - mouse

979	64.5	5.7	378	2	A33271	manganese peroxida
980	64.5	5.7	385	2	AC2857	conserved hypothet
981	64.5	5.7	385	2	A97634	hypothetical prote
982	64.5	5.7	397	2	B69378	probable acyl-CoA
983	64.5	5.7	402	2	D69530	probable acyl-CoA
984	64.5	5.7	412	1	AJMSRS	argininosuccinate
985	64.5	5.7	412	1	AJRTRS	argininosuccinate
986	64.5	5.7	416	2	S65110	chitinase (EC 3.2.
987	64.5	5.7	420	1	AJBYRS	argininosuccinate
988	64.5	5.7	424	1	VGBEE9	glycoprotein gp63
989	64.5	5.7	425	1	A26431	nerve growth facto
990	64.5	5.7	446	2	T07907	hydroxyproline-ric
991	64.5	5.7	471	2	T15155	hypothetical prote
992	64.5	5.7	485	2	T37550	hypothetical coile
993	64.5	5.7	491	2	G86297	F3O9.8 protein - A
994	64.5	5.7	512	2	E59437	F02569_2 protein [
995	64.5	5.7	519	1	S69988	unspecific monooxy
996	64.5	5.7	532	2	B35621	spore germination
997	64.5	5.7	549	2	F71219	probable thermophi
998	64.5	5.7	568	2	A34891	Ig heavy chain pre
999	64.5	5.7	568	2	I58106	gene DMR-N9 protei
1000	64.5	5.7	570	2	H97244	membrane associate
1001	64.5	5.7	574	2	E82282	probable chitinase
1002	64.5	5.7	577	2	A60501	thrombomodulin pre
1003	64.5	5.7	587	2	S21139	amine oxidase (cop
1004	64.5	5.7	590	2	S66956	hypothetical prote
1005	64.5	5.7	623	2	A48123	cell cycle regulat
1006	64.5	5.7	631	2	H70754	probable abc trans
1007	64.5	5.7	648	2	A32576	beta-glucuronidase
1008	64.5	5.7	680	2	S26764	major coat protein
1009	64.5	5.7	680	2	T19939	hypothetical prote
1010	64.5	5.7	690	2	H86464	hypothetical prote
1011	64.5	5.7	757	2	F96518	protein T2B6.10 [i
1012	64.5	5.7	760	1	S07896	transcription fact
1013	64.5	5.7	770	1	S30293	transcription fact
1014	64.5	5.7	802	2	T32448	hypothetical prote
1015	64.5	5.7	833	2	G75621	arylesterase/monox
1016	64.5	5.7	854	1	WMBP12	gene 12 protein -
1017	64.5	5.7	920	1	PXKZP	H+-exporting ATPas
1018	64.5	5.7	1032	2	S65341	probable membrane
1019	64.5	5.7	1033	2	T37715	actin-interacting
1020	64.5	5.7	1079	2	A86220	protein F22O13.29
1021	64.5	5.7	1117	2	S63399	probable membrane
1022	64.5	5.7	1125	2	B41206	microtubule-associ
1023	64.5	5.7	1133	2	T30302	P-type ATPase - Te
1024	64.5	5.7	1152	2	AC1347	probable peptidogl
1025	64.5	5.7	1160	2	A27868	lethal (2) giant l
1026	64.5	5.7	1191	2	T13850	gene u-shaped prot
1027	64.5	5.7	1200	2	T17404	hyalin - sea urchi
1028	64.5	5.7	1205	2	S64819	probable membrane
1029	64.5	5.7	1249	2	A56511	myosin I myoA - Em
1030	64.5	5.7	1277	2	S70306	hypothetical prote
1031	64.5	5.7	1477	2	AG3009	polyketide synthet
1032	64.5	5.7	1489	2	G98274	hypothetical prote
1033	64.5	5.7	1501	2	C84512	probable retroelem
1034	64.5	5.7	1505	2	S26765	genome polyprotein
1035	64.5	5.7	1842	2	T43409	probable fatty-aci
1036	64.5	5.7	1842	2	T38781	fatty acid synthas
1037	64.5	5.7	2570	2	T17451	fimbriae-associate
1038	64	5.6	131	2	T25705	hypothetical prote
1039	64	5.6	171	2	H86413	hypothetical prote
1040	64	5.6	230	2	T33364	hypothetical prote
1041	64	5.6	234	2	E72456	hypothetical prote
1042	64	5.6	259	2	C81008	methionine aminope
1043	64	5.6	268	2	S63630	acid proteinase (E
1044	64	5.6	279	2	E82689	conserved hypothet
1045	64	5.6	298	2	D95354	probable epimerase
1046	64	5.6	309	2	AD0144	hypothetical prote
1047	64	5.6	309	2	S40749	hypothetical prote
1048	64	5.6	314	1	HNVZVW	hemagglutinin prec
1049	64	5.6	314	1	JQ1793	hemagglutinin prec
1050	64	5.6	354	2	F65092	hypothetical prote
1051	64	5.6	360	2	S12850	protein TPX - Ther
1052	64	5.6	364	1	EDBESP	immediate-early pr
1053	64	5.6	376	2	AG0455	thiamin biosynthes
1054	64	5.6	384	2	S36529	E2 protein - human
1055	64	5.6	393	2	S62335	I71-7 protein - fr
1056	64	5.6	394	2	T20778	hypothetical prote
1057	64	5.6	395	2	H75457	hypothetical prote
1058	64	5.6	413	2	AG0632	glucose-1-phosphat
1059	64	5.6	416	2	S68822	neurotensin recept
1060	64	5.6	417	2	S76588	hypothetical prote
1061	64	5.6	417	2	T24618	hypothetical prote
1062	64	5.6	428	2	D86003	hypothetical prote
1063	64	5.6	428	2	F91157	probable membrane
1064	64	5.6	438	1	HVRKCS	Ig mu chain C regi
1065	64	5.6	461	1	HVRKC0	Ig mu chain C regi
1066	64	5.6	461	2	D96647	hypothetical prote
1067	64	5.6	471	2	S46739	hypothetical prote
1068	64	5.6	473	2	T45954	hypothetical prote
1069	64	5.6	519	2	T45764	hypothetical prote
1070	64	5.6	543	1	QFMSL	neurofilament trip
1071	64	5.6	554	2	T45840	GTPase activating-
1072	64	5.6	560	2	S50392	hypothetical prote
1073	64	5.6	561	2	T41097	RNA binding protei
1074	64	5.6	562	2	S69055	TTAGGG repeat-bind
1075	64	5.6	562	2	T49386	hypothetical prote
1076	64	5.6	580	2	T20716	hypothetical prote
1077	64	5.6	583	2	S67571	hypothetical prote
1078	64	5.6	586	2	S44850	K12H4.1 protein -
1079	64	5.6	646	2	JC5583	85K SH3 domain-con
1080	64	5.6	664	2	T48258	kinesin-like prote
1081	64	5.6	716	2	G01627	androgen receptor
1082	64	5.6	745	2	T03119	hypothetical prote
1083	64	5.6	750	2	T10864	transcription acti
1084	64	5.6	756	2	T27642	hypothetical prote
1085	64	5.6	768	2	A29066	DNA ligase (ATP) (
1086	64	5.6	801	2	A37353	membrane protein 4
1087	64	5.6	825	1	GLHQ	beta-glucosidase (
1088	64	5.6	894	2	B96557	probable receptor
1089	64	5.6	982	2	T43676	hunchback-related
1090	64	5.6	1104	2	S59310	probable membrane
1091	64	5.6	1115	2	S64101	PAN2 protein - yea
1092	64	5.6	1132	2	B82538	ribonuclease E XF2
1093	64	5.6	1217	2	T25894	hypothetical prote
1094	64	5.6	1280	2	E95031	alkaline amylopull
1095	64	5.6	1282	2	JE0120	glycoprotein A - m
1096	64	5.6	1328	2	T43060	agrin - electric r
1097	64	5.6	1445	1	A48148	protein-tyrosine-p
1098	64	5.6	1469	2	T19168	hypothetical prote
1099	64	5.6	1547	2	T28657	blackjack protein,
1100	64	5.6	1607	2	T02837	long chain fatty a
1101	64	5.6	1671	2	S71628	sensory transducti
1102	64	5.6	1859	1	A34092	DNA-directed RNA p
1103	64	5.6	1862	2	T29959	DNA-directed RNA p
1104	64	5.6	1870	2	D88486	protein F20H11.2 [
1105	64	5.6	1975	2	B81192	hemagglutinin/hemo
1106	64	5.6	1995	2	G81044	hemagglutinin/hemo
1107	64	5.6	2055	2	T30259	multiple PDZ domai
1108	64	5.6	2274	2	T30258	adenomatous polypo
1109	64	5.6	2292	1	GNNYEB	genome polyprotein
1110	64	5.6	2292	1	GNNYED	genome polyprotein
1111	64	5.6	2292	2	S55401	capsid polyprotein
1112	64	5.6	6805	2	S20901	titin - rabbit (fr
1113	63.5	5.6	101	2	E72458	hypothetical prote
1114	63.5	5.6	149	2	A71074	probable methylmal
1115	63.5	5.6	166	1	C65000	NADH2 dehydrogenas
1116	63.5	5.6	166	2	B85869	NADH dehydrogenase
1117	63.5	5.6	166	2	A91025	NADH dehydrogenase
1118	63.5	5.6	185	2	S20593	alcohol dehydrogen
1119	63.5	5.6	197	2	T19892	hypothetical prote
1120	63.5	5.6	197	2	C49247	merozoite surface
1121	63.5	5.6	205	2	S55670	hypothetical prote
1122	63.5	5.6	255	2	I47093	MHC OVAR-DQ-ALPHA-
1123	63.5	5.6	275	2	S09774	hypothetical prote
1124	63.5	5.6	284	2	T28018	hypothetical prote

1125	63.5	5.6	289	2	T41305	hypothetical prote
1126	63.5	5.6	296	2	I40258	outer surface prot
1127	63.5	5.6	296	2	I40267	outer surface prot
1128	63.5	5.6	296	2	I40256	outer surface prot
1129	63.5	5.6	296	2	I40250	outer surface prot
1130	63.5	5.6	296	2	I40260	outer surface prot
1131	63.5	5.6	313	2	D71363	hypothetical prote
1132	63.5	5.6	322	2	E82505	conserved hypothet
1133	63.5	5.6	327	2	I55459	Fra-2 - rat
1134	63.5	5.6	341	2	F71042	hypothetical prote
1135	63.5	5.6	357	2	A37440	red-sensitive visu
1136	63.5	5.6	366	2	T27912	hypothetical prote
1137	63.5	5.6	373	1	AJMSQ	glutamate-ammonia
1138	63.5	5.6	378	2	AI2180	hypothetical prote
1139	63.5	5.6	423	2	T01559	hypothetical prote
1140	63.5	5.6	427	2	T00465	probable WRKY-type
1141	63.5	5.6	432	2	T25471	hypothetical prote
1142	63.5	5.6	445	2	I38521	inwardly rectifyin
1143	63.5	5.6	445	2	S45713	potassium channel
1144	63.5	5.6	446	2	S66268	inward rectifier p
1145	63.5	5.6	451	2	F97230	probable maltodext
1146	63.5	5.6	462	2	S05050	retinoic acid nucl
1147	63.5	5.6	484	2	T20451	hypothetical prote
1148	63.5	5.6	498	2	H85040	hypothetical prote
1149	63.5	5.6	509	2	A35016	cystathionine gamm
1150	63.5	5.6	512	2	S21171	activin receptor S
1151	63.5	5.6	532	2	G70986	probable coA ligas
1152	63.5	5.6	541	2	S40245	heat shock protein
1153	63.5	5.6	542	2	B86674	60 KD chaperonin [
1154	63.5	5.6	546	2	H89780	hypothetical prote
1155	63.5	5.6	560	2	D83759	methyl-accepting c
1156	63.5	5.6	630	2	A39344	tumor-associated m
1157	63.5	5.6	631	2	I52257	episialin - mouse
1158	63.5	5.6	649	2	T04606	protein kinase hom
1159	63.5	5.6	651	2	C56653	membrane glycoprot
1160	63.5	5.6	653	2	AI3404	transposase BMEI12
1161	63.5	5.6	675	2	D85065	receptor protein k
1162	63.5	5.6	688	2	T23108	hypothetical prote
1163	63.5	5.6	694	2	S68442	Grb2-associated bi
1164	63.5	5.6	699	2	C43674	US4 protein - huma
1165	63.5	5.6	702	2	E69498	hypothetical prote
1166	63.5	5.6	708	2	H64631	outer membrane pro
1167	63.5	5.6	713	2	B86315	F2H15.20 protein -
1168	63.5	5.6	733	1	S33643	transforming prote
1169	63.5	5.6	756	2	JC5886	signaling mediator
1170	63.5	5.6	761	2	T00940	hypothetical prote
1171	63.5	5.6	761	2	T03719	probable thyroid r
1172	63.5	5.6	764	2	A84328	Htr2 transducer [i
1173	63.5	5.6	767	1	WMBEP6	ribonucleoside-dip
1174	63.5	5.6	774	2	T22309	hypothetical prote
1175	63.5	5.6	777	2	C86454	hypothetical prote
1176	63.5	5.6	782	2	S04047	finger protein zfy
1177	63.5	5.6	799	2	H71255	probable cell divi
1178	63.5	5.6	808	2	T23129	hypothetical prote
1179	63.5	5.6	826	2	T46061	hypothetical prote
1180	63.5	5.6	854	1	WMBP22	gene 12 protein -
1181	63.5	5.6	861	2	S77409	hypothetical prote
1182	63.5	5.6	865	2	A47282	calcium-binding pr
1183	63.5	5.6	880	2	D89756	protein T23E7.2b [
1184	63.5	5.6	890	2	T21000	hypothetical prote
1185	63.5	5.6	926	2	T38198	COPII coated vesic
1186	63.5	5.6	937	2	A56517	nucleoporin Nup98
1187	63.5	5.6	977	2	S49004	tyrosine kinase Mp
1188	63.5	5.6	988	2	I50611	protein-tyrosine k
1189	63.5	5.6	1009	2	S60248	protein-tyrosine k
1190	63.5	5.6	1013	1	S04200	NAD ADP-ribosyltra
1191	63.5	5.6	1043	2	T13172	gag-like protein p
1192	63.5	5.6	1067	2	T30061	hypothetical prote
1193	63.5	5.6	1138	2	S64484	phosphatidylserine
1194	63.5	5.6	1199	2	T15826	hypothetical prote
1195	63.5	5.6	1208	2	T27822	hypothetical prote
1196	63.5	5.6	1218	2	AC3580	1-pyrroline-5-carb
1197	63.5	5.6	1262	2	T25168	hypothetical prote
1198	63.5	5.6	1324	2	S06187	RNA2 polyprotein -
1199	63.5	5.6	1326	2	B56395	secretory phosphol
1200	63.5	5.6	1332	2	T23024	hypothetical prote
1201	63.5	5.6	1382	2	S70310	hypothetical prote
1202	63.5	5.6	1460	2	T00095	hypothetical prote
1203	63.5	5.6	1465	2	A56395	secretory phosphol
1204	63.5	5.6	1466	2	T17138	CL1AA protein - ra
1205	63.5	5.6	1467	2	T18411	latrophilin-1, bra
1206	63.5	5.6	1471	2	T17149	CL1BA protein - ra
1207	63.5	5.6	1472	2	T18413	latrophilin-1, bra
1208	63.5	5.6	1475	2	S42718	nuclear pore compl
1209	63.5	5.6	1510	2	T17145	CL1AB protein - ra
1210	63.5	5.6	1515	2	T17156	CL1BB protein - ra
1211	63.5	5.6	1544	2	T29482	hypothetical prote
1212	63.5	5.6	1624	2	T25592	hypothetical prote
1213	63.5	5.6	1729	2	T18396	erythrocyte membra
1214	63.5	5.6	1796	2	S65004	probable membrane
1215	63.5	5.6	1854	2	S36859	cipA protein - Clo
1216	63.5	5.6	2145	2	JC4747	adenylate cyclase
1217	63.5	5.6	2211	1	KFBO5	coagulation factor
1218	63.5	5.6	2512	1	XYCHFA	enoyl-[acyl-carrie
1219	63.5	5.6	2700	2	D88450	protein F21H11.2 [
1220	63.5	5.6	3027	2	JQ1917	polyprotein - pars
1221	63	5.5	125	2	S24703	Ig heavy chain V6
1222	63	5.5	126	2	S14131	hypothetical prote
1223	63	5.5	135	2	T49996	AtAGP4 - Arabidops
1224	63	5.5	139	2	T05847	hypothetical prote
1225	63	5.5	154	2	C71162	hypothetical prote
1226	63	5.5	190	2	T26357	hypothetical prote
1227	63	5.5	204	2	AG2437	hypothetical prote
1228	63	5.5	204	2	S49031	cadmium-induced pr
1229	63	5.5	259	2	T09317	glycoprotein - hum
1230	63	5.5	291	2	G81407	hypothetical prote
1231	63	5.5	292	2	B89807	exotoxin 9 [import
1232	63	5.5	309	2	E70319	phosphoribosylanth
1233	63	5.5	309	2	T17557	procyclin homolog
1234	63	5.5	321	2	T50966	hypothetical prote
1235	63	5.5	326	2	S15749	transforming prote
1236	63	5.5	326	2	I48351	fos-related antige
1237	63	5.5	326	2	G69366	homoserine dehydro
1238	63	5.5	346	2	H84512	hypothetical prote
1239	63	5.5	348	2	D87097	conserved hypothet
1240	63	5.5	348	2	JQ0431	hypothetical 35.5K
1241	63	5.5	361	2	T19395	hypothetical prote
1242	63	5.5	371	1	TVXLT1	transforming prote
1243	63	5.5	375	2	T33797	hypothetical prote
1244	63	5.5	376	2	S71558	probable cell wall
1245	63	5.5	380	2	T32944	hypothetical prote
1246	63	5.5	382	1	WZVZI6	I6 43.5K protein -
1247	63	5.5	396	1	C64907	chloramphenicol re
1248	63	5.5	396	2	H85721	probable resistanc
1249	63	5.5	396	2	G90895	hypothetical prote
1250	63	5.5	402	2	S42367	lag-2 protein - Ca
1251	63	5.5	412	1	AJHURS	argininosuccinate
1252	63	5.5	426	2	T04985	probable transamin
1253	63	5.5	443	2	E82046	proteinase HslVU,
1254	63	5.5	451	2	T15718	hypothetical prote
1255	63	5.5	453	2	S59436	hypothetical prote
1256	63	5.5	482	2	AI2094	hypothetical prote
1257	63	5.5	486	2	AF1575	acetaldehyde dehyd
1258	63	5.5	486	2	AC1222	acetaldehyde dehyd
1259	63	5.5	487	2	S40820	probable permease
1260	63	5.5	519	2	A49367	transducin homolog
1261	63	5.5	535	2	S18606	phosphoenolpyruvat
1262	63	5.5	535	2	T38244	hypothetical prote
1263	63	5.5	537	2	B97013	and cellulose-bind
1264	63	5.5	539	2	I46470	estrogen dependent
1265	63	5.5	544	1	S41389	penton protein (II
1266	63	5.5	547	2	S44841	K06H7.1 protein -
1267	63	5.5	559	1	WMBES1	71K upper matrix p
1268	63	5.5	564	2	T12550	hypothetical prote
1269	63	5.5	595	2	B82203	methyl-accepting c
1270	63	5.5	609	2	S36481	E1 protein - human

1271	63	5.5	609	2	T34371	hypothetical prote
1272	63	5.5	610	1	A49082	calcium-dependent
1273	63	5.5	611	2	S76211	hypothetical prote
1274	63	5.5	623	2	H69435	indolepyruvate fer
1275	63	5.5	630	2	A34041	dnaK-type molecula
1276	63	5.5	632	2	C98264	5'-nucleotidase pr
1277	63	5.5	635	2	T37239	serotonin receptor
1278	63	5.5	636	2	AF3020	5'-nucleotidase [i
1279	63	5.5	638	2	S36723	FUN36 protein - ye
1280	63	5.5	640	2	F75114	hypothetical prote
1281	63	5.5	672	2	T43716	dnaK-type molecula
1282	63	5.5	672	2	T43723	dnaK-type molecula
1283	63	5.5	677	2	T39590	hypothetical prote
1284	63	5.5	683	2	T37240	serotonin receptor
1285	63	5.5	714	2	AF2479	ABC transporter AT
1286	63	5.5	719	2	T47727	hypothetical prote
1287	63	5.5	722	2	E71403	hypothetical prote
1288	63	5.5	729	2	T15076	hypothetical prote
1289	63	5.5	763	2	T22843	hypothetical prote
1290	63	5.5	776	2	A55448	Ah receptor nuclea
1291	63	5.5	779	2	A57177	NIMA-like protein
1292	63	5.5	813	2	A72203	cellobiose-phospho
1293	63	5.5	838	2	G81444	molybdopterin-cont
1294	63	5.5	843	2	T01438	hypothetical prote
1295	63	5.5	862	2	S51493	major nitrogen reg
1296	63	5.5	865	2	B96558	probable protein k
1297	63	5.5	918	1	PXBY1P	H+-exporting ATPas
1298	63	5.5	986	2	T33135	hypothetical prote
1299	63	5.5	1002	2	T19226	hypothetical prote
1300	63	5.5	1028	2	E85089	probable transposo
1301	63	5.5	1028	2	C88364	protein C13B4.1 [i
1302	63	5.5	1036	2	B69368	hypothetical prote
1303	63	5.5	1065	2	S19482	hypothetical prote
1304	63	5.5	1106	2	T18739	hypothetical prote
1305	63	5.5	1215	2	T43916	chitinase A [impor
1306	63	5.5	1279	2	T13613	hypothetical prote
1307	63	5.5	1320	1	S66279	proline dehydrogen
1308	63	5.5	1320	2	AE0633	proline dehydrogen
1309	63	5.5	1636	2	S60403	probable membrane
1310	63	5.5	1817	2	T34249	hypothetical prote
1311	63	5.5	1820	2	S71853	genome polyprotein
1312	63	5.5	1902	2	C97702	cell surface antig
1313	63	5.5	1972	2	S68176	TOG protein - huma
1314	63	5.5	2628	2	T28651	hemagglutinin A -
1315	63	5.5	2697	2	T25444	hypothetical prote
1316	63	5.5	3066	1	JQ1662	genome polyprotein
1317	63	5.5	3163	1	JQ1895	genome polyprotein
1318	63	5.5	6420	2	T30283	polyketide synthas
1319	62.5	5.5	123	2	B75546	hypothetical prote
1320	62.5	5.5	130	2	T12478	hypothetical prote
1321	62.5	5.5	139	2	G98226	hypothetical prote
1322	62.5	5.5	139	2	AI3059	hypothetical prote
1323	62.5	5.5	142	2	G84194	hypothetical prote
1324	62.5	5.5	147	2	T34803	hypothetical prote
1325	62.5	5.5	157	2	S36784	mucin - rat (fragm
1326	62.5	5.5	177	2	G75285	hypothetical prote
1327	62.5	5.5	198	2	S48994	hypothetical prote
1328	62.5	5.5	210	2	S53300	self-incompatibili
1329	62.5	5.5	219	2	F65018	hypothetical prote
1330	62.5	5.5	220	2	AC2961	thiamin-phosphate
1331	62.5	5.5	234	2	T35448	hypothetical prote
1332	62.5	5.5	238	2	C98322	probable thiamin b
1333	62.5	5.5	245	2	S43565	R01H10.4 protein (
1334	62.5	5.5	252	2	T04739	hypothetical prote
1335	62.5	5.5	277	2	H97266	minD family ATPase
1336	62.5	5.5	287	2	S45662	histone H1 - tomat
1337	62.5	5.5	289	2	T52354	hypothetical prote
1338	62.5	5.5	290	2	T44550	hypothetical prote
1339	62.5	5.5	290	2	D70974	probable dehydroge
1340	62.5	5.5	299	2	F84810	hypothetical prote
1341	62.5	5.5	304	2	H86332	T20H2.26 protein -
1342	62.5	5.5	306	2	T48715	hypothetical prote
1343	62.5	5.5	314	2	B75588	FraH-related prote
1344	62.5	5.5	343	2	F95915	probable sugar ABC
1345	62.5	5.5	348	2	B90727	galactose-1-phosph
1346	62.5	5.5	348	2	C85578	galactose-1-phosph
1347	62.5	5.5	356	2	A32945	GTP-binding protei
1348	62.5	5.5	359	2	T31821	hypothetical prote
1349	62.5	5.5	364	2	T16837	hypothetical prote
1350	62.5	5.5	372	2	T23680	hypothetical prote
1351	62.5	5.5	385	2	JC7783	RAD 23B protein -
1352	62.5	5.5	389	2	A38302	pepsin (EC 3.4.23.
1353	62.5	5.5	391	2	JC6193	tumor suppressor p
1354	62.5	5.5	393	2	T33103	lin-1 protein - Ca
1355	62.5	5.5	396	2	S54999	ubiquinol-cytochro
1356	62.5	5.5	396	2	PC4236	trans-cinnamate 4-
1357	62.5	5.5	398	1	W2WL42	E2 protein - human
1358	62.5	5.5	412	2	A57468	P-selectin glycopr
1359	62.5	5.5	426	2	T50944	hypothetical prote
1360	62.5	5.5	428	1	Q4ECAD	damX protein (aroB
1361	62.5	5.5	433	2	T49675	origin recognition
1362	62.5	5.5	458	1	MHRB	Ig mu chain C regi
1363	62.5	5.5	462	1	A29491	retinoic acid rece
1364	62.5	5.5	479	1	MHRBM	Ig mu chain C regi
1365	62.5	5.5	493	2	S73752	hypothetical prote
1366	62.5	5.5	503	2	T37119	probable membrane-
1367	62.5	5.5	513	2	S11439	cellulose 1,4-beta
1368	62.5	5.5	513	2	S50915	SIN3 protein-bindi
1369	62.5	5.5	518	2	T33196	hypothetical prote
1370	62.5	5.5	521	2	C82922	methionyl-tRNA syn
1371	62.5	5.5	538	2	AG2902	conserved hypothet
1372	62.5	5.5	545	2	T10662	aromatic amino-aci
1373	62.5	5.5	550	2	H97677	hypothetical prote
1374	62.5	5.5	557	2	JC5487	cellulase (EC 3.2.
1375	62.5	5.5	585	1	B70747	probable serine/th
1376	62.5	5.5	586	2	D84710	hypothetical prote
1377	62.5	5.5	596	2	S61146	probable membrane
1378	62.5	5.5	601	2	T34396	hypothetical prote
1379	62.5	5.5	609	2	F87237	phosphoenolpyruvat
1380	62.5	5.5	617	2	A90644	probable membrane
1381	62.5	5.5	617	2	A85495	probable membrane
1382	62.5	5.5	621	1	YRNC	monophenol monooxy
1383	62.5	5.5	626	2	S53871	Pmel 17 protein -
1384	62.5	5.5	647	2	S26386	transcription fact
1385	62.5	5.5	653	2	E86787	hypothetical prote
1386	62.5	5.5	671	1	VCMVCE	env polyprotein -
1387	62.5	5.5	697	2	E96752	hypothetical prote
1388	62.5	5.5	706	2	T49700	related to AP-1-li
1389	62.5	5.5	722	2	T37970	probable G2-specif
1390	62.5	5.5	725	2	JC1300	endo-beta-1,4-gluc
1391	62.5	5.5	728	2	F72693	probable phosphoes
1392	62.5	5.5	761	2	A96810	probable Mutator-l
1393	62.5	5.5	761	2	A81985	pilus secretin NMA
1394	62.5	5.5	823	2	G90848	probable exonuclea
1395	62.5	5.5	823	2	F90914	hypothetical prote
1396	62.5	5.5	823	2	E85706	probable exonuclea
1397	62.5	5.5	853	2	H70939	probable nirB prot
1398	62.5	5.5	873	2	B41054	fasciclin II PI-li
1399	62.5	5.5	874	2	AC2287	hypothetical prote
1400	62.5	5.5	887	2	G88484	protein F23F12.8 [
1401	62.5	5.5	893	2	A47550	bride of sevenless
1402	62.5	5.5	899	2	C84765	hypothetical prote
1403	62.5	5.5	903	2	T00074	hypothetical prote
1404	62.5	5.5	907	2	T04820	aconitate hydratas
1405	62.5	5.5	929	2	JC6124	diacylglycerol kin
1406	62.5	5.5	955	4	C40045	probable transcrip
1407	62.5	5.5	968	2	S46992	protein p130 - rat
1408	62.5	5.5	988	1	S35362	protein kinase C (
1409	62.5	5.5	1018	2	T40253	hypothetical prote
1410	62.5	5.5	1033	2	I48775	Smcx protein (esca
1411	62.5	5.5	1117	2	T19727	hypothetical prote
1412	62.5	5.5	1197	2	D86317	protein F15H18.21
1413	62.5	5.5	1203	2	H87687	helicase, UvrD/Rep
1414	62.5	5.5	1302	2	T23236	hypothetical prote
1415	62.5	5.5	1309	1	BVBYD9	RAD9 protein - yea
1416	62.5	5.5	1337	2	T30291	dextranase - Strep

1417	62.5	5.5	1387	2	JC5502	G-protein signalin
1418	62.5	5.5	1560	2	I54361	SMCX protein - hum
1419	62.5	5.5	1577	2	T30858	glucosyltransferas
1420	62.5	5.5	1784	2	A49420	tuberous sclerosis
1421	62.5	5.5	1802	2	S69703	HKR1 protein precu
1422	62.5	5.5	1872	2	T00339	hypothetical prote
1423	62.5	5.5	2054	2	T46612	multi PDZ domain p
1424	62.5	5.5	2090	2	S26058	probable transform
1425	62.5	5.5	2114	2	E96505	hypothetical prote
1426	62.5	5.5	2366	2	S10317	toxin B - Clostrid
1427	62.5	5.5	2367	2	S70172	toxin B - Clostrid
1428	62.5	5.5	3002	2	A47221	fibrillin 1 precur
1429	62.5	5.5	3011	1	GNWVC3	genome polyprotein
1430	62.5	5.5	3011	1	S40770	genome polyprotein
1431	62.5	5.5	3033	1	JQ1303	genome polyprotein
1432	62.5	5.5	3343	2	S44887	ZK112.7 protein -
1433	62.5	5.5	5107	2	T29144	partial CDS - Caen
1434	62	5.5	125	2	E90350	hypothetical prote
1435	62	5.5	165	1	KTHUB	choriogonadotropin
1436	62	5.5	170	2	E84257	flagellin A2 precu
1437	62	5.5	174	2	AH1979	hypothetical prote
1438	62	5.5	181	2	T31481	hypothetical prote
1439	62	5.5	189	2	G70512	probable lppK prot
1440	62	5.5	192	2	T51463	hypothetical prote
1441	62	5.5	194	1	B28944	flagellin A2 precu
1442	62	5.5	196	2	F72356	hypothetical prote
1443	62	5.5	197	2	B49247	merozoite surface
1444	62	5.5	222	2	T16381	hypothetical prote
1445	62	5.5	250	2	D71710	hypothetical prote
1446	62	5.5	269	2	T30468	hypothetical prote
1447	62	5.5	277	2	C97335	methyl-accepting c
1448	62	5.5	292	1	MGNZ60	major surface glyc
1449	62	5.5	315	2	T42682	hypothetical prote
1450	62	5.5	317	2	T27485	hypothetical prote
1451	62	5.5	320	2	JC1311	cell protein precu
1452	62	5.5	324	2	T49143	hypothetical prote
1453	62	5.5	337	2	AF0086	periplasmic bindin
1454	62	5.5	341	2	A75313	DNA-directed RNA p
1455	62	5.5	341	2	S33650	heat shock protein
1456	62	5.5	370	2	S49008	fork head protein
1457	62	5.5	372	1	QQBE88	glycoprotein I pre
1458	62	5.5	382	2	S33075	I6L protein - vari
1459	62	5.5	382	2	T28498	hypothetical prote
1460	62	5.5	385	2	G87006	probable transmemb
1461	62	5.5	392	2	A53580	neurexin III beta
1462	62	5.5	395	2	A54949	syndecan precursor
1463	62	5.5	396	2	T50229	probable transmemb
1464	62	5.5	405	2	G86848	conserved hypothet
1465	62	5.5	409	2	A84602	hypothetical prote
1466	62	5.5	416	2	T44423	dihydrolipoamide S
1467	62	5.5	431	2	T29850	hypothetical prote
1468	62	5.5	434	2	T44911	hypothetical prote
1469	62	5.5	439	2	I60916	HNF-3/forkhead hom
1470	62	5.5	450	2	C75316	conserved hypothet
1471	62	5.5	453	2	C40511	hypothetical prote
1472	62	5.5	459	2	T17141	NADH2 dehydrogenas
1473	62	5.5	470	2	S28303	hypothetical prote
1474	62	5.5	474	2	S15921	protein TPX-VT3 -
1475	62	5.5	477	2	T46666	N-ethylammeline ch
1476	62	5.5	485	2	T28076	hypothetical prote
1477	62	5.5	493	2	G70589	probable malate de
1478	62	5.5	511	2	S10527	endoglucanase B pr
1479	62	5.5	517	2	T19962	hypothetical prote
1480	62	5.5	528	2	I47141	gastric mucin (clo
1481	62	5.5	528	2	D70968	hypothetical prote
1482	62	5.5	532	2	T49467	related to COP1-in
1483	62	5.5	535	2	S65762	chitinase (EC 3.2.
1484	62	5.5	539	2	F72288	methyl-accepting c
1485	62	5.5	555	1	RGASWA	regulatory protein
1486	62	5.5	556	2	S51892	probable membrane
1487	62	5.5	573	2	I40496	methylation enzyme
1488	62	5.5	582	2	T07952	lectin-like protei
1489	62	5.5	587	2	A34084	extracellular prot
1490	62	5.5	589	1	NDECAS	type I site-specif
1491	62	5.5	592	2	T47821	methylenetetrahydr
1492	62	5.5	595	2	F85438	nucleoporin-like p
1493	62	5.5	606	2	T01221	malate dehydrogena
1494	62	5.5	606	2	T37217	probable ATP/GTP b
1495	62	5.5	606	2	A75554	ABC transporter, A
1496	62	5.5	617	2	T15104	hypothetical prote
1497	62	5.5	624	2	S49000	hypothetical prote
1498	62	5.5	632	2	T48616	hypothetical prote
1499	62	5.5	638	2	B34285	NADH2 dehydrogenas
1500	62	5.5	654	2	S70905	transferrin-bindin

ALIGNMENTS

RESULT 1
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.; Matzku, S
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcino
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: UNIPROT:P26051; UNIPARC:UPI000012736D; GB:M61874; NID:g576534; PIDN
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: UNIPARC:UPI0000179A9B; GB:M61875
C;Keywords: cell adhesion

Query Match 18.8%; Score 213.5; DB 2; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.6e-11;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

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Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              |:| ||  ::: : ::||  |:  | |     :: ||| : |    :|    |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  |  || |    :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST 162
                  |:   : |:     |   :  | | ||    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 167
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RESULT 2
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CA
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <ZHO>
A;Cross-references: UNIPROT:P15379; UNIPARC:UPI000002A5F4; GB:M30655; NID:g200332; PIDN
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

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  Query Match           18.4%;  Score 209.5;  DB 2;  Length 363;
  Best Local Similarity  32.7%;  Pred. No. 8.4e-11;
  Matches   52;  Conservative   25;  Mismatches   75;  Indels    7;  Gaps    3;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              |:| ||  ::: : |:||  |:  | |     :: ||| : |:    :|   ||:: ||
Db         14 LLQLSLAHQQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMKLALS 73

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
Db         74 KGFETCRYGFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCFNASAPPEEDC 132

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST 162
                    |:   : |:     |   :  | | ||    | |
Db        133 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 166


RESULT 3
A35616
T-cell surface glycoprotein CD44 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A35616
R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A;Title: CD44 is the principal cell surface receptor for hyaluronate.
A;Reference number: A35616; MUID:90304889; PMID:1694723
A;Accession: A35616
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-362 <ARU>
A;Cross-references: UNIPROT:P20944; UNIPARC:UPI0000179518
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein

  Query Match           18.2%;  Score 207;  DB 2;  Length 362;
  Best Local Similarity  32.8%;  Pred. No. 1.4e-10;
  Matches   57;  Conservative   23;  Mismatches   82;  Indels   12;  Gaps    5;

Qy          9 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFE 68
              ||  |:: : ::||  |:  | |     :: ||| : |:    :|   ||:  ||   ||
Db         18 SLAHEQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVMALSKGFE 77

Qy         69 TCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI 128
              || ||:: :| ||| || ||  |  |  || |     |  :  ||:|:|      |
Db         78 TCRYGFI-EGHVVIPRIQPNAICAANHTGVYILTSNTS-HYDTYCFNASAPLEEDC---- 131

Qy        129 ITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPTTTPPAPASTS 177
               |:   : |:     |   :  | | ||    | |    | |  ||    :| |
Db        132 -TSVTDLPNSFEGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNTTDDDVSSGS 184


RESULT 4
A30901
lymphocyte adhesion receptor precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 21-Jul-2000
C;Accession: A33935; A30901
R;Idzerda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John, T
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recep
A;Reference number: A33935; MUID:89282830; PMID:2471974
A;Accession: A33935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <IDZ>
A;Cross-references: UNIPARC:UPI000012736C; GB:M22452; NID:g176576; PID:g176577
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD44; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antig
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>
F;21-270/Domain: extracellular #status predicted <EXT>
F;271-290/Domain: transmembrane #status predicted <TMM>
F;291-362/Domain: intracellular #status predicted <CYT>
F;25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match           17.9%;  Score 203.5;  DB 2;  Length 362;
  Best Local Similarity  27.3%;  Pred. No. 2.8e-10;
  Matches   70;  Conservative   27;  Mismatches   92;  Indels   67;  Gaps    9;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              ||| ||   :: : ::||  ||  | |     :: ||| : |:    :|    |:| ||
Db         14 LVQLSL--AQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS 71

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPGEDC 129

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP------APT---------- 167
                    |:   : |      |   :  | | |     | | |      :||
Db        130 -----TSVTDLPNAFDGPITITIVNRDGTRYVKKGEYRTNPEDINPSSPTDDDVSSGSSS 184

Qy        168 ----------------TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAF 211
                             |:|| |                         | ||:  |   :: ||
Db        185 ERSSTLGGYIFYNHFSTSPPIPDEDG--------------PWITDSTDRTPATRDQGAF 229

Qy        212 K----------NEAAG 217
                       :|:||
Db        230 DPSGGSHTTHGSESAG 245


RESULT 5
A47195
lymphocyte homing receptor isoform CD44 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47195
R;Screaton, G.R.; Bell, M.V.; Jackson, D.G.; Cornelis, F.B.; Gerth, U.; Bell, J.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 12160-12164, 1992
A;Title: Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals at
A;Reference number: A47195; MUID:93101687; PMID:1465456
A;Accession: A47195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-742 <SCR>
A;Cross-references: UNIPROT:Q9UJ36; UNIPARC:UPI000017C297
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120739,
, NCBIN:120764, NCBIN:120766, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:120776, NCB

  Query Match           17.8%;  Score 202;  DB 2;  Length 742;
  Best Local Similarity  26.0%;  Pred. No. 9.4e-10;
  Matches   61;  Conservative   30;  Mismatches   84;  Indels   60;  Gaps    7;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 125
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        126 ----------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 155
                                         || |   :|  : :: ::|   :   |
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        156 VASPYSTI-PAPTTTPP--------APASTSIPRRKKLICVTEVFMETSTMSTET 201
              :   :||: | |    |         ||:|              | ||  :|||
Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATT-------------LMSTSATATET 234


RESULT 6
```

```
S13530
CD44E protein, epithelial - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S13530
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with d
A;Reference number: S13530; MUID:91122041; PMID:1991450
A;Accession: S13530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-493 <STA>
A;Cross-references: UNIPARC:UPI0000159271; EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID
C;Keywords: transmembrane protein

  Query Match             17.6%;  Score 199.5;  DB 2;  Length 493;
  Best Local Similarity   23.6%;  Pred. No. 9.4e-10;
  Matches   66;  Conservative   39;  Mismatches  100;  Indels   75;  Gaps    8;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |    :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 125
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        126 ------------------------------PEIITTKDPIFNTQTATQTTE-------FI 148
                                           || |   :|  :  ::  ::|       :|
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        149 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 186
                              ::|||      :: | :||   ||  |       : |   |
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        187 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAG 217
               |:    : : ||  |   |:|         :: :|:  |
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTG 293


RESULT 7
A34424
CD44 membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
A;Reference number: A34424; MUID:90046829; PMID:2682651
A;Accession: A34424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <NOT>
A;Cross-references: UNIPARC:UPI00000E88CD; GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:
R;Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antige
A;Reference number: A34907; MUID:90094420; PMID:2403559
A;Accession: A34907
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 8-195,'G',197-365 <WOL>
A;Cross-references: UNIPARC:UPI000016CFB0; GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

  Query Match             17.5%;  Score 198.5;  DB 2;  Length 365;
  Best Local Similarity   31.8%;  Pred. No. 7.9e-10;
  Matches   48;  Conservative   24;  Mismatches   72;  Indels    7;  Gaps    3;

Qy         13 EELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSY 72
              :::: : |:||  |:  | |     :: ||| : |:    :|   ||:: ||   |||| |
Db         24 QQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMKLALSKGFETCRY 83

Qy         73 GWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEIITTK 132
              |:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |     |:
Db         84 GFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCFNASAPPEEDC-----TSV 137

Qy        133 DPIFNTQTATQTTEFIVSDST-YSVASPYST 162
                : |:      |   :  | | ||    | |
Db        138 TDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 168


RESULT 8
JH0518
lymphocyte homing receptor CD44, splice form CD44R1 - human
N;Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surfac
N;Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing rece
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R;Dougherty, G.J.; Lansdorp, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A;Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 l
A;Reference number: JH0518; MUID:91277598; PMID:2056274
A;Accession: JH0518
A;Molecule type: mRNA
A;Residues: 1-426 <DOU>
A;Cross-references: UNIPROT:Q9UCB0; UNIPARC:UPI0000179519
A;Experimental source: lymphocytes, cell line KG1a
A;Accession: JH0519
A;Molecule type: mRNA
A;Residues: 1-223,288-426 <DO2>
A;Cross-references: UNIPARC:UPI000017951A
A;Experimental source: lymphocyte, cell line KG1a
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta
Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal
A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
A;Molecule type: DNA
A;Residues: 223-357 <COO>
A;Cross-references: UNIPARC:UPI000017951B
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfa
A;Reference number: A39209; MUID:91177958; PMID:2007624
A;Accession: A39209
A;Molecule type: mRNA
A;Residues: 184-376 <BRO>
A;Cross-references: UNIPARC:UPI000016A690; GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:
R;Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by in
A;Reference number: A42402; MUID:92165834; PMID:1537855
A;Accession: A42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-223,288-359 <JAC>
A;Cross-references: UNIPARC:UPI000017951C
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
A;Note: variant B
A;Accession: C42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-320 <JA2>
A;Cross-references: UNIPARC:UPI000017951D
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
A;Note: variant D
R;Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy
A;Reference number: A53029; MUID:94149816; PMID:7508992
A;Accession: A53029
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76,'X',78-89 <SHE>
A;Cross-references: UNIPARC:UPI000006D03F
C;Genetics:
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 35/1; 65/1; 133/1
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycc
F;1-426/Product: lymphocyte homing receptor CD44, splice form CD44R1 #status predicted <
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

  Query Match             17.5%;  Score 198.5;  DB 2;  Length 426;
  Best Local Similarity   23.6%;  Pred. No. 9.6e-10;
  Matches   66;  Conservative   39;  Mismatches  100;  Indels   75;  Gaps    8;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 125
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|     |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        126 ------------------------------PEIITTKDPIFNTQTATQTTE-------FI 148
                                           || |   :|  :  ::  ::|        :|
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        149 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 186
                              ::|||      :: | :||   ||  |       : |   |
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        187 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAG 217
              |:    : : ||  |   |:|          :: :|:  |
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTG 293


RESULT 9
JH0417
cell adhesion molecule CD44 - human
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 31-Dec-2004
C;Accession: JH0417; A32376; G02251; A32377
R;Harn, H.J.; Isola, N.; Cooper, D.L.
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991
A;Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte cD
A;Reference number: JH0417; MUID:91337049; PMID:1840487
A;Accession: JH0417
A;Molecule type: mRNA
A;Residues: 1-361 <HAR>
A;Cross-references: UNIPROT:Q92493; UNIPARC:UPI000016A68F; GB:M59040; NID:g180129; PIDN:
A;Experimental source: reticulocyte
A;Note: the authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA
R;Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.
Cell 56, 1057-1062, 1989
A;Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil
A;Reference number: A32376; MUID:89168434; PMID:2466575
A;Accession: A32376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238,'E',240-361 <STA>
A;Cross-references: UNIPARC:UPI0000143A5B; GB:M24915; NID:g180196; PIDN:AAA35674.1; PID:
R;Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.
submitted to the EMBL Data Library, November 1995
A;Reference number: H00921
A;Accession: G02251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-25,'M',27-108,'S',110-361 <BOS>
A;Cross-references: UNIPARC:UPI000016A285; EMBL:U40373; NID:g1101785; PID:g1101786
R;Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.; I
Cell 56, 1063-1072, 1989
A;Title: A human lymphocyte homing receptor, the hermes antigen, is related to cartilage
A;Reference number: A32377; MUID:89168435; PMID:2466576
A;Accession: A32377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108,'S',110-293,'S' <GOL>
A;Cross-references: UNIPARC:UPI0000070BED; GB:M25078; NID:g186660; PIDN:AAA36138.1; PID:g
C;Keywords: alternative splicing; cell adhesion; surface antigen; transmembrane protein
F;269-285/Domain: transmembrane #status predicted <TMM>

  Query Match             17.3%;  Score 197;  DB 2;  Length 361;
  Best Local Similarity   30.9%;  Pred. No. 1.1e-09;
  Matches   54;  Conservative   23;  Mismatches   84;  Indels   14;  Gaps    5;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 129
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|     |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDC----- 129

Qy        130 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA------PTTTPPAPASTS 177
              |:   : |      |   :  | | |     | | |       ||    :  |:|
Db        130 TSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSS 184


RESULT 10
I37369
epican - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: I37369; S24631
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.
J. Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is
A;Reference number: I37369; PMID:1281868
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Accession: I37369
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-699 <RES>
A;Cross-references: UNIPARC:UPI000016A89D; EMBL:X66733; NID:g31190; PID:g31191

  Query Match             17.3%;  Score 196.5;  DB 2;  Length 699;
  Best Local Similarity   25.4%;  Pred. No. 2.7e-09;
  Matches   60;  Conservative   34;  Mismatches   93;  Indels   49;  Gaps    7;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 125
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|     |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        126 ------------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 155
                                           || |   :|  :  ::  ::|   :   |
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        156 VASPYSTI-PAPTTTPP--APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENK 208
              :   :||: | |     |    ::  ||               ::|:|   ||  ||:
Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATS---------TSSNTISAGWEPNEENE 240


RESULT 11
I77371
CD44R5 - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I77371
```

```
R;Tanabe, K.K.; Nishi, T.; Saya, H.
Mol. Carcinog. 7, 212-220, 1993
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 a
A;Reference number: I57483; MUID:93356912; PMID:8352881
A;Accession: I77371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-395 <RES>
A;Cross-references: UNIPARC:UPI000016B3F6; GB:S66400; NID:g435697; PIDN:AAB27919.1; PID:
C;Genetics:
A;Gene: GDB:CD44
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 257/1
C;Superfamily: human cell adhesion protein CD44

  Query Match             17.3%;  Score 196;  DB 2;  Length 395;
  Best Local Similarity   30.9%;  Pred. No. 1.4e-09;
  Matches   54;  Conservative   23;  Mismatches   84;  Indels   14;  Gaps    5;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 129
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDC----- 129

Qy        130 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA------PTTTPPAPASTS 177
              |:   : |       |   :  | | |     | | |       ||    :  |:|
Db        130 TSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSS 184


RESULT 12
S45305
CD44 antigen precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S45305
R;Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.
Biochim. Biophys. Acta 1218, 112-114, 1994
A;Title: Molecular cloning of the canine CD44 antigen cDNA.
A;Reference number: S45305; MUID:94250687; PMID:7514890
A;Accession: S45305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <MIL>
A;Cross-references: UNIPROT:Q28284; UNIPARC:UPI0000127367; EMBL:Z27115; NID:g473226; PID
C;Superfamily: human cell adhesion protein CD44

  Query Match             17.1%;  Score 194;  DB 2;  Length 351;
  Best Local Similarity   30.3%;  Pred. No. 1.9e-09;
  Matches   53;  Conservative   25;  Mismatches   83;  Indels   14;  Gaps    5;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: | | : |:    :|    |:| ||   |||
Db         10 LSLAQIDLNITCRYAGVFHVEKNGRYSISRTAAADLCKAFNSTLPTMAQMERALSVGFET 69

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 129
              | ||:: :| ||| || ||  |  |  || |  :  : |:  ||:|:|      |
Db         70 CRYGFI-EGHVVIPRIQPNAICAANHTGVYI-LISNTSQYDTYCFNASAPPEEDC----- 122

Qy        130 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA------PTTTPPAPASTS 177
              |:   : |       |   :  | | ||    | | |       ||    :  |:|
Db        123 TSVTHLPNAFDGPITITIVNRDGTRYSQKGEYRTNPEDINPSNPTDDDVSSGSSS 177


RESULT 13
A53286
cell-surface glycoprotein CD44 precursor - bovine
N;Alternate names: CD44 protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53286; S22123
R;Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A;Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A;Reference number: A53286; MUID:92017904; PMID:1922105
A;Accession: A53286
A;Molecule type: mRNA
A;Residues: 1-366 <BOS>
A;Cross-references: UNIPROT:Q29423; UNIPARC:UPI0000127366; EMBL:X62881; NID:g186; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F;274-294/Domain: transmembrane #status predicted <TMM>
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match             17.1%;  Score 194;  DB 2;  Length 366;
  Best Local Similarity   29.9%;  Pred. No. 2e-09;
  Matches   56;  Conservative   27;  Mismatches   86;  Indels   18;  Gaps    6;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              ||| ||   :: : ::||  |:  | |     :: ||| : |:    :|    |:| |
Db         14 LVQLSL--AQIDLNITCRYAGVFHVEKNGRYSISKTEAADLCKAFNSTLPTMAQMEAARN 71

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  | || |     | |:   |:|:|      |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTICFNASAPPGEDC 129

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP--------APTTTPPAPAS 175
                  |:   : |       |   :  | | |:    | | |         :|:: |    |
Db        130 -----TSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSVVSPSSPPDDEMS 184

Qy        176 TSIPRRK 182
              :  |  :
Db        185 SGSPSER 191


RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; But
Immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <TA2>
A;Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NID:g1059; PIDN
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

  Query Match             16.2%;  Score 183.5;  DB 2;  Length 359;
  Best Local Similarity   29.4%;  Pred. No. 1.6e-08;
  Matches   50;  Conservative   24;  Mismatches   87;  Indels    9;  Gaps    5;

Qy         10 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 69
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:: ||   |||
Db         17 LSLAQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMQKALNIGFET 76

Qy         70 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 129
              | |:: :| |||  | ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRIGFI-EGHVVIPPIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDC----- 129

Qy        130 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPAPTTTPPAPASTSI 178
              |:   : |       |   :  | | |:    | | |       |  ||   :
Db        130 TSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNP-EDINPSTPADDDV 178
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```
RESULT 15
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during

A;Reference number: A47171; MUID:93300846; PMID:8314802
A;Accession: A47171
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3562 <SHI>
A;Cross-references: UNIPROT:Q90953; UNIPARC:UPI000013178A; GB:D13542; NID:g391643; PIDN:
A;Experimental source: stage 22-23 developing limb buds
A;Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-345/Domain: link protein repeat homology <LNK2>
F;3258-3289/Domain: EGF homology <EGF1>
F;3296-3327/Domain: EGF homology <EGF>
F;3334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>

  Query Match             12.8%;  Score 145.5;  DB 2;  Length 3562;
  Best Local Similarity   26.1%;  Pred. No. 0.00062;
  Matches   47;  Conservative   25;  Mismatches   89;  Indels   19;  Gaps    5;

Qy         35 QQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKN 94
              ::| | |||| ||     ||    :  | :  |: | |||: || |          |:||
Db        258 EKLTFEEAKELCRKRDGVLASVGNMYVAWRNGFDQCDYGWLADGSVRYPASVARPQCGGG 317

Qy         95 GVGVLI---------WKVPVSRQFAAYCYNSSDTWTNSCIPEIITT--KDPIFNTQTATQ 143
               :||           :  | |: | ||||      :     :::||   | :  :
Db        318 LLGVRTLYRYENQTGFPYPDSK-FDAYCYERKKIVSEPTTVKLVTTLKTDSVELSSAKVT 376

Qy        144 TTEFIVSDSTYSVASPYSTIP----APTTTPPAPASTSIPRRKKLICVTEVFMETSTMST 199
                 :   |   ||   : :|    |   |     :| :   |: :   || ||   ::|
Db        377 LKPSVFESSVTEVAVTKTKVPAWEEATLETEDTKMTTEVAEEKREM---EVLMENIKLTT 433


Search completed: March 20, 2006, 14:09:51
Job time : 21.8585 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:48 ; Search time 47.4764 Seconds
(without alignments)
3269.333 Million cell updates/sec

Title: US-10-063-510-6_COPY_16_235
Perfect score: 1136
Sequence: 1 TTRLLVQGSLRAEELSIQVS.....TEPFVENKAAFKNEAAGFGG 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1136	100.0	322	2	Q9UNF4_HUMAN	Q9unf4 homo sapien
2	1122	98.8	322	2	Q8TC18_HUMAN	Q8tc18 homo sapien
3	1117	98.3	322	2	Q9Y5Y7_HUMAN	Q9y5y7 homo sapien
4	730	64.3	322	2	Q6UC88_BOVIN	Q6uc88 bos taurus
5	680	59.9	318	2	Q8BHC0_MOUSE	Q8bhc0 mus musculu
6	680	59.9	318	2	Q99NE4_MOUSE	Q99ne4 mus musculu
7	526.5	46.3	201	2	Q7YS22_PIG	Q7ys22 sus scrofa
8	245	21.6	392	2	Q58E15_XENLA	Q58e15 xenopus lae
9	241	21.2	441	2	Q6GM56_XENLA	Q6gm56 xenopus lae
10	226	19.9	437	2	Q6P8A2_XENTR	Q6p8a2 xenopus tro
11	213.5	18.8	503	1	CD44_RAT	P26051 rattus norv
12	213.5	18.8	780	2	O08779_RAT	O08779 rattus norv
13	211.5	18.6	364	2	O70509_RAT	O70509 rattus norv
14	211	18.6	265	2	Q98SR5_ANAPL	Q98sr5 anas platyr
15	209.5	18.4	398	2	Q90ZL8_ANAPL	Q90zl8 anas platyr
16	209.5	18.4	778	1	CD44_MOUSE	P15379 mus musculu
17	207	18.2	362	1	CD44_CRIGR	P20944 cricetulus
18	205	18.0	431	1	CD44_MESAU	Q60522 m cd44 anti
19	203.5	17.9	362	1	CD44_PAPHA	P14745 papio hamad
20	203	17.9	742	2	Q9UJ36_HUMAN	Q9uj36 homo sapien
21	202	17.8	742	1	CD44_HUMAN	P16070 h cd44 anti
22	200.5	17.6	580	2	Q80X37_MOUSE	Q80x37 mus musculu
23	198.5	17.5	168	2	Q90ZL6_ANAPL	Q90zl6 anas platyr
24	198.5	17.5	493	2	Q86Z27_HUMAN	Q86z27 homo sapien
25	198.5	17.5	493	2	Q5R9V4_PONPY	Q5r9v4 pongo pygma
26	197	17.3	396	2	Q9W6S4_CHICK	Q9w6s4 gallus gall
27	197	17.3	719	2	Q9H5A5_HUMAN	Q9h5a5 homo sapien
28	196	17.3	294	2	Q92493_HUMAN	Q92493 homo sapien
29	196	17.3	361	2	Q86T72_HUMAN	Q86t72 homo sapien
30	196	17.3	361	2	Q8N694_HUMAN	Q8n694 homo sapien
31	195	17.2	364	2	O97569_CERSI	O97569 ceratotheri
32	194	17.1	351	1	CD44_CANFA	Q28284 canis famil
33	194	17.1	366	1	CD44_BOVIN	Q29423 bos taurus
34	191.5	16.9	676	2	Q9H5A7_HUMAN	Q9h5a7 homo sapien
35	191	16.8	271	2	Q9H5A3_HUMAN	Q9h5a3 homo sapien
36	191	16.8	338	2	Q9H5A4_HUMAN	Q9h5a4 homo sapien
37	191	16.8	470	2	Q9H5A6_HUMAN	Q9h5a6 homo sapien
38	183.5	16.2	359	1	CD44_HORSE	Q05078 equus cabal
39	173.5	15.3	153	2	Q4SI95_TETNG	Q4si95 tetraodon n
40	150	13.2	537	1	PGCA_PIG	Q29011 sus scrofa
41	145.5	12.8	494	2	Q9BGH3_PIG	Q9bgh3 sus scrofa
42	145.5	12.8	3562	1	CSPG2_CHICK	Q90953 gallus gall
43	145	12.8	277	1	TSG6_HUMAN	P98066 homo sapien
44	145	12.8	277	2	Q53TI7_HUMAN	Q53ti7 homo sapien
45	144	12.7	275	1	TSG6_MOUSE	O08859 mus musculu
46	144	12.7	280	2	Q5W1C4_BOVIN	Q5w1c4 bos taurus
47	143	12.6	2109	1	PGCA_CHICK	P07898 gallus gall
48	141.5	12.5	243	2	Q4S9S8_TETNG	Q4s9s8 tetraodon n
49	140	12.3	2571	1	STAB1_MOUSE	Q8r4y4 mus musculu
50	139.5	12.3	2333	1	PGCA_CANFA	Q28343 canis famil
51	139	12.2	2109	2	P79787_CHICK	P79787 gallus gall
52	137	12.1	276	1	TSG6_RABIT	P98065 oryctolagus
53	133	11.7	514	2	Q62913_RAT	Q62913 rattus norv
54	132.5	11.7	721	2	Q6PID9_HUMAN	Q6pid9 homo sapien
55	132	11.6	1046	2	Q4S1V9_TETNG	Q4s1v9 tetraodon n
56	131.5	11.6	2124	1	PGCA_RAT	P07897 rattus norv
57	131	11.5	314	2	Q4SE78_TETNG	Q4se78 tetraodon n
58	131	11.5	2132	1	PGCA_MOUSE	Q61282 mus musculu
59	130.5	11.5	883	1	PGCB_MOUSE	Q61361 mus musculu
60	130.5	11.5	883	2	Q80WT7_MOUSE	Q80wt7 mus musculu
61	130.5	11.5	2415	1	PGCA_HUMAN	P16112 homo sapien
62	129	11.4	1431	1	STAB2_RAT	Q8cfm6 rattus norv
63	128	11.3	2149	2	Q6XL68_BOVIN	Q6xl68 bos taurus
64	128	11.3	2327	2	Q6XL66_BOVIN	Q6xl66 bos taurus
65	128	11.3	2364	1	PGCA_BOVIN	P13608 bos taurus
66	128	11.3	2365	2	Q6XL67_BOVIN	Q6xl67 bos taurus
67	127.5	11.2	671	2	Q5T3I5_HUMAN	Q5t3i5 homo sapien
68	127.5	11.2	850	2	Q59F90_HUMAN	Q59f90 homo sapien
69	127.5	11.2	883	1	PGCB_RAT	P55068 rattus norv
70	127.5	11.2	911	1	PGCB_HUMAN	Q96gw7 homo sapien
71	127.5	11.2	911	2	Q5SZ10_HUMAN	Q5sz10 homo sapien
72	127	11.2	266	2	Q5I051_XENLA	Q5i051 xenopus lae
73	125.5	11.0	536	2	Q5RG03_BRARE	Q5rg03 brachydanio
74	125.5	11.0	845	2	Q4RV64_TETNG	Q4rv64 tetraodon n
75	124.5	11.0	1515	2	Q4T6A4_TETNG	Q4t6a4 tetraodon n
76	124	10.9	2586	2	Q4RUP1_TETNG	Q4rup1 tetraodon n
77	123.5	10.9	386	2	Q4S472_TETNG	Q4s472 tetraodon n
78	123.5	10.9	2760	2	Q4T8G9_TETNG	Q4t8g9 tetraodon n
79	123	10.8	2570	1	STAB1_HUMAN	Q9ny15 homo sapien
80	122	10.7	383	2	Q5BJ60_XENTR	Q5bj60 xenopus tro
81	122	10.7	394	1	PGCA_RABIT	Q28670 oryctolagus
82	121.5	10.7	360	1	HPLN3_HUMAN	Q96s86 homo sapien
83	121	10.7	516	2	Q8IWX2_HUMAN	Q8iwx2 homo sapien
84	121	10.7	1091	2	Q4SE77_TETNG	Q4se77 tetraodon n
85	121	10.7	1152	2	Q90WM2_XENLA	Q90wm2 xenopus lae
86	120.5	10.6	912	1	PGCB_BOVIN	Q28062 bos taurus
87	120.5	10.6	1570	2	Q75ZI3_BRARE	Q75zi3 brachydanio
88	120.5	10.6	2559	1	STAB2_MOUSE	Q8r4u0 mus musculu
89	120	10.6	313	2	Q4SHL9_TETNG	Q4shl9 tetraodon n
90	119	10.5	359	2	Q7ZX17_XENLA	Q7zx17 xenopus lae
91	118.5	10.4	3396	1	CSPG2_HUMAN	P13611 homo sapien
92	118.5	10.4	3410	2	Q59FG9_HUMAN	Q59fg9 homo sapien
93	116	10.2	368	2	Q8BS97_MOUSE	Q8bs97 mus musculu
94	116	10.2	368	2	Q4VA91_MOUSE	Q4va91 mus musculu
95	116	10.2	2738	1	CSPG2_RAT	Q9erb4 rattus norv
96	116	10.2	3358	1	CSPG2_MOUSE	Q62059 mus musculu
97	115.5	10.2	744	2	Q4RLD6_TETNG	Q4rld6 tetraodon n
98	115	10.1	370	2	Q7M2W7_PIG	Q7m2w7 sus scrofa
99	115	10.1	394	2	Q6DCI6_XENLA	Q6dci6 xenopus lae
100	115	10.1	3381	1	CSPG2_BOVIN	P81282 bos taurus
101	114.5	10.1	1039	2	Q4S473_TETNG	Q4s473 tetraodon n
102	113.5	10.0	341	1	HPLN2_MOUSE	Q9esm3 mus musculu
103	112.5	9.9	340	1	HPLN2_HUMAN	Q9gzv7 homo sapien
104	112.5	9.9	340	2	Q5T3J0_HUMAN	Q5t3j0 homo sapien

105	112.5	9.9	417	1	PGCB_FELCA	P41725	felis silve	178	93	8.2	1155	2	Q4JA20_SULAC	Q4ja20	sulfolobus
106	112	9.9	210	2	Q8C9U7_MOUSE	Q8c9u7	mus musculu	179	92.5	8.1	215	2	Q614I3_CAEBR	Q614i3	caenorhabdi
107	112	9.9	2551	1	STAB2_HUMAN	Q8wwq8	h stabilin-	180	92.5	8.1	232	2	Q4V3Z2_DROME	Q4v3z2	drosophila
108	111	9.8	354	2	Q86W61_HUMAN	Q86w61	homo sapien	181	92.5	8.1	236	2	Q4V400_DROME	Q4v400	drosophila
109	111	9.8	359	2	Q5R1X6_RAT	Q5r1x6	rattus norv	182	92.5	8.1	247	2	Q8MKY7_DROME	Q8mky7	drosophila
110	111	9.8	537	2	Q4IQU7_GIBZE	Q4iqu7	gibberella	183	92.5	8.1	276	2	Q54NG3_DICDI	Q54ng3	dictyosteli
111	110.5	9.7	1257	1	CSPG3_RAT	P55067	rattus norv	184	92.5	8.1	289	2	Q60TZ2_CAEBR	Q60tz2	caenorhabdi
112	110	9.7	363	2	Q6NV41_BRARE	Q6nv41	brachydanio	185	92.5	8.1	400	1	HPLN4_MOUSE	Q80wm4	mus musculu
113	110	9.7	1290	2	Q9W6E1_CHICK	Q9w6e1	gallus gall	186	92.5	8.1	448	2	Q61C0I_CAEBR	Q61c01	caenorhabdi
114	109	9.6	1321	1	CSPG3_HUMAN	O14594	homo sapien	187	92.5	8.1	1034	2	Q613E9_CAEBR	Q613e9	caenorhabdi
115	109	9.6	1335	2	Q4LE67_HUMAN	Q4le67	homo sapien	188	92.5	8.1	1491	2	Q4QDK4_LEIMA	Q4qdk4	leishmania
116	108.5	9.6	341	1	HPLN2_RAT	Q9esm2	rattus norv	189	92	8.1	347	2	Q8SYW5_DROME	Q8syw5	drosophila
117	108.5	9.6	1441	2	Q4S3C4_TETNG	Q4s3c4	tetraodon n	190	92	8.1	500	2	Q864U4_BOVIN	Q864u4	bos taurus
118	108	9.5	354	1	HPLN1_HUMAN	P10915	homo sapien	191	92	8.1	504	2	Q54FD8_DICDI	Q54fd8	dictyosteli
119	108	9.5	359	1	HPLN3_MOUSE	Q80wm5	mus musculu	192	92	8.1	738	2	Q5WN81_CAEBR	Q5wn81	caenorhabdi
120	107	9.4	354	1	HPLN1_RAT	P03994	rattus norv	193	92	8.1	846	2	O01699_CAEEL	O01699	caenorhabdi
121	107	9.4	355	1	HPLN1_CHICK	P07354	gallus gall	194	92	8.1	989	2	Q83U76_CHLTR	Q83u76	chlamydia t
122	107	9.4	356	1	HPLN1_MOUSE	Q9qup5	mus musculu	195	92	8.1	989	2	Q84FU9_CHLTR	Q84fu9	chlamydia t
123	107	9.4	862	2	Q9UF98_HUMAN	Q9uf98	homo sapien	196	92	8.1	1121	2	Q59YM6_CANAL	Q59ym6	candida alb
124	107	9.4	1268	1	CSPG3_MOUSE	P55066	mus musculu	197	92	8.1	1121	2	Q7Z884_CANAL	Q7z884	candida alb
125	107	9.4	1321	1	CSPG3_PANTR	Q5is41	pan troglod	198	92	8.1	1879	2	Q4VZL0_CUCSA	Q4vzl0	cucumis sat
126	106.5	9.4	816	2	O70474_RAT	O70474	rattus norv	199	91.5	8.1	288	2	Q6QPC9_9ADEN	Q6qpc9	simian aden
127	106	9.3	1059	2	Q5ISN4_MACFA	Q5isn4	macaca fasc	200	91.5	8.1	651	2	Q61YZ5_CAEBR	Q61yz5	caenorhabdi
128	105	9.2	354	1	HPLN1_BOVIN	P55252	bos taurus	201	91.5	8.1	860	2	Q7RZN3_NEUCR	Q7rzn3	neurospora
129	104.5	9.2	862	1	CSPG2_MACNE	Q28858	macaca neme	202	91.5	8.1	1126	2	Q9VGK5_DROME	Q9vgk5	drosophila
130	104	9.2	139	2	O95370_HUMAN	O95370	homo sapien	203	91	8.0	174	2	Q7YTP1_CAEEL	Q7ytp1	caenorhabdi
131	104	9.2	354	1	HPLN1_HORSE	Q28381	equus cabal	204	91	8.0	213	2	Q5T3I7_HUMAN	Q5t3i7	homo sapien
132	104	9.2	354	1	HPLN1_PIG	P10859	sus scrofa	205	91	8.0	488	2	Q09586_CAEEL	Q09586	caenorhabdi
133	103.5	9.1	1197	2	Q5IS86_9PRIM	Q5is86	saimiri bol	206	91	8.0	576	2	Q61MD1_CAEBR	Q61md1	caenorhabdi
134	103	9.1	80	2	Q86UZ1_HUMAN	Q86uz1	homo sapien	207	91	8.0	624	2	Q19780_CAEEL	Q19780	caenorhabdi
135	103	9.1	231	2	Q5T3I6_HUMAN	Q5t3i6	homo sapien	208	91	8.0	644	2	Q54D31_DICDI	Q54d31	dictyosteli
136	102	9.0	739	2	O02360_CAEEL	O02360	caenorhabdi	209	91	8.0	698	2	Q61SH2_CAEBR	Q61sh2	caenorhabdi
137	101.5	8.9	380	2	O02343_CAEEL	O02343	caenorhabdi	210	91	8.0	876	2	Q619L5_CAEBR	Q619l5	caenorhabdi
138	101.5	8.9	411	2	Q702X4_HHV1	Q702x4	human herpe	211	90.5	8.0	278	2	Q4WIP3_ASPFU	Q4wip3	aspergillus
139	101.5	8.9	1853	2	Q7KT96_DROME	Q7kt96	drosophila	212	90.5	8.0	402	1	ODP2_MYCPN	P75392	mycoplasma
140	101.5	8.9	1893	2	Q9NKC9_DROME	Q9nkc9	drosophila	213	90.5	8.0	411	2	Q6P6W1_RAT	Q6p6w1	rattus norv
141	101	8.9	708	2	Q18175_CAEEL	Q18175	caenorhabdi	214	90.5	8.0	497	2	Q8QVC4_9REOV	Q8qvc4	eyach virus
142	101	8.9	2535	2	Q755B8_ASHGO	Q755b8	ashbya goss	215	90.5	8.0	699	2	Q8QVE9_9REOV	Q8qve9	eyach virus
143	100.5	8.8	402	1	HPLN4_HUMAN	Q86uw8	homo sapien	216	90.5	8.0	952	2	Q86AH0_DICDI	Q86ah0	dictyosteli
144	100	8.8	319	2	Q4S1V7_TETNG	Q4s1v7	tetraodon n	217	90.5	8.0	972	2	Q60Q42_CAEBR	Q60q42	caenorhabdi
145	99.5	8.8	335	2	Q60H44_BRARE	Q60h44	brachydanio	218	90.5	8.0	1165	2	Q60NC3_CAEBR	Q60nc3	caenorhabdi
146	99.5	8.8	397	2	Q702X3_HHV1	Q702x3	human herpe	219	90.5	8.0	1175	2	Q9VRL7_DROME	Q9vrl7	drosophila
147	99.5	8.8	577	2	Q52GY0_CAEEL	Q52gy0	caenorhabdi	220	90.5	8.0	1976	2	Q9V9I8_DROME	Q9v9i8	drosophila
148	99	8.7	388	2	Q4H2F0_HPV27	Q4h2f0	human papil	221	90	7.9	388	1	VE2_HPV27	P36789	human papil
149	98.5	8.7	441	2	Q5BA48_EMENI	Q5ba48	aspergillus	222	90	7.9	812	2	Q61KE5_CAEBR	Q61ke5	caenorhabdi
150	98.5	8.7	573	2	Q8CJD9_RAT	Q8cjd9	rattus norv	223	90	7.9	948	2	Q86AV9_DICDI	Q86av9	d phosphati
151	98.5	8.7	4370	2	Q4Q1Q2_LEIMA	Q4q1q2	leishmania	224	90	7.9	1167	2	Q7RWQ7_NEUCR	Q7rwq7	neurospora
152	98	8.6	527	2	Q54VQ0_DICDI	Q54vq0	dictyosteli	225	89.5	7.9	411	1	LAMP2_RAT	P17046	rattus norv
153	98	8.6	2112	2	Q9VEL9_DROME	Q9vel9	drosophila	226	89.5	7.9	440	2	Q9P566_NEUCR	Q9p566	neurospora
154	97.5	8.6	297	2	Q7PR65_ANOGA	Q7pr65	anopheles g	227	89.5	7.9	471	2	Q9VMG7_DROME	Q9vmg7	drosophila
155	97	8.5	390	1	VGLI_HHV11	P06487	human herpe	228	89.5	7.9	558	2	Q4JK70_DERPT	Q4jk70	dermatophag
156	97	8.5	390	2	Q702X7_HHV1	Q702x7	human herpe	229	89.5	7.9	560	2	Q54LP6_DICDI	Q54lp6	dictyosteli
157	97	8.5	889	2	Q4RUP0_TETNG	Q4rup0	tetraodon n	230	89.5	7.9	917	2	Q7QJI6_ANOGA	Q7qji6	anopheles g
158	97	8.5	1604	2	Q4SNA3_TETNG	Q4sna3	tetraodon n	231	89.5	7.9	1349	2	Q8WWQ4_HUMAN	Q8wwq4	homo sapien
159	96	8.5	173	2	Q4KTX2_CEREL	Q4ktx2	cervus elap	232	89	7.8	232	2	Q5BDD1_EMENI	Q5bdd1	aspergillus
160	96	8.5	3178	1	YS89_CAEEL	Q09624	caenorhabdi	233	89	7.8	307	1	SGS3_DROME	P02840	drosophila
161	95.5	8.4	481	2	Q9XUF4_CAEEL	Q9xuf4	caenorhabdi	234	89	7.8	316	2	Q9U9J0_TOXCA	Q9u9j0	toxocara ca
162	95.5	8.4	732	2	Q54FU3_DICDI	Q54fu3	dictyosteli	235	89	7.8	359	2	Q5KCB0_CRYNE	Q5kcb0	cryptococcu
163	95	8.4	294	2	Q54FY4_DICDI	Q54fy4	dictyosteli	236	89	7.8	392	2	Q59FZ0_HUMAN	Q59fz0	homo sapien
164	95	8.4	424	2	Q9FGW0_ARATH	Q9fgw0	arabidopsis	237	89	7.8	416	1	LAMP1_HUMAN	P11279	homo sapien
165	94.5	8.3	182	2	Q8I0D8_DROME	Q8i0d8	drosophila	238	89	7.8	417	2	Q8WU33_HUMAN	Q8wu33	homo sapien
166	94.5	8.3	183	2	Q9VT37_DROME	Q9vt37	drosophila	239	89	7.8	429	2	P79046_9ASCO	P79046	humicola gr
167	94.5	8.3	281	2	Q4KSI9_9ADEN	Q4ksi9	human adeno	240	89	7.8	482	2	Q6BSZ9_DEBHA	Q6bsz9	debaryomyce
168	94.5	8.3	407	2	Q564S9_CAEEL	Q564s9	caenorhabdi	241	89	7.8	503	1	NAS14_CAEEL	Q19269	caenorhabdi
169	94.5	8.3	519	2	Q7YTR7_CAEEL	Q7ytr7	caenorhabdi	242	89	7.8	603	2	Q6CE49_YARLI	Q6ce49	yarrowia li
170	94.5	8.3	1079	2	Q9N4S7_CAEEL	Q9n4s7	caenorhabdi	243	89	7.8	648	2	Q4QGJ2_LEIMA	Q4qgj2	leishmania
171	94.5	8.3	1748	2	Q54FL9_DICDI	Q54fl9	dictyosteli	244	89	7.8	860	2	Q5WNQ1_CAEBR	Q5wnq1	caenorhabdi
172	94.5	8.3	1795	2	O76894_DROME	O76894	drosophila	245	89	7.8	1521	2	Q7Q1W8_ANOGA	Q7q1w8	anopheles g
173	94	8.3	1117	2	Q54SZ6_DICDI	Q54sz6	dictyosteli	246	89	7.8	1569	2	Q54DM4_DICDI	Q54dm4	dictyosteli
174	93.5	8.2	397	2	Q702X6_HHV1	Q702x6	human herpe	247	89	7.8	1708	2	Q7XWZ9_ORYSA	Q7xwz9	oryza sativ
175	93	8.2	405	2	Q66HZ2_BRARE	Q66hz2	brachydanio	248	88.5	7.8	389	2	Q611Z9_CAEBR	Q611z9	caenorhabdi
176	93	8.2	478	2	Q7YX15_CAEEL	Q7yx15	caenorhabdi	249	88.5	7.8	582	2	Q8IR74_DROME	Q8ir74	drosophila
177	93	8.2	916	2	Q7YZI0_MONBE	Q7yzi0	monosiga br	250	88.5	7.8	662	1	MUC1_XENLA	Q05049	xenopus lae

251	88.5	7.8	764	2	Q4WYI0_ASPFU	Q4wyi0	aspergillus
252	88.5	7.8	901	2	Q9H195_HUMAN	Q9h195	homo sapien
253	88.5	7.8	956	2	Q60MG7_CAEBR	Q60mg7	caenorhabdi
254	88.5	7.8	1038	2	Q4T3K8_TETNG	Q4t3k8	tetraodon n
255	88.5	7.8	1101	1	GUNC_CELFI	P14090	cellulomona
256	88.5	7.8	1148	2	Q6CBJ2_YARLI	Q6cbj2	yarrowia li
257	88.5	7.8	2273	2	Q63HU2_BURPS	Q63hu2	burkholderi
258	88	7.7	103	2	Q9TTB3_PIG	Q9ttb3	sus scrofa
259	88	7.7	239	2	Q55C69_DICDI	Q55c69	dictyosteli
260	88	7.7	302	2	Q55XK5_CRYNE	Q55xk5	cryptococcu
261	88	7.7	302	2	Q5KMC9_CRYNE	Q5kmc9	cryptococcu
262	88	7.7	359	2	Q55JE9_CRYNE	Q55je9	cryptococcu
263	88	7.7	382	2	Q6C971_YARLI	Q6c971	yarrowia li
264	88	7.7	456	2	Q9U2W2_CAEEL	Q9u2w2	caenorhabdi
265	88	7.7	487	2	Q4U479_ANOGA	Q4u479	anopheles g
266	88	7.7	602	2	Q8YV91_ANASP	Q8yv91	anabaena sp
267	88	7.7	616	2	Q8R0X0_MOUSE	Q8r0x0	mus musculu
268	88	7.7	656	2	Q8BUE7_MOUSE	Q8bue7	mus musculu
269	88	7.7	716	2	Q9NYE4_HUMAN	Q9nye4	homo sapien
270	88	7.7	730	2	Q86AZ8_DICDI	Q86az8	dictyosteli
271	88	7.7	931	2	Q51LJ1_MAGGR	Q51lj1	magnaporthe
272	88	7.7	1007	2	Q5P0E5_AZOSE	Q5p0e5	azoarcus sp
273	88	7.7	1051	2	Q6C1J9_YARLI	Q6c1j9	yarrowia li
274	88	7.7	1254	2	Q94185_CAEEL	Q94185	caenorhabdi
275	87.5	7.7	299	2	Q5H2T1_XANOR	Q5h2t1	xanthomonas
276	87.5	7.7	555	2	Q9U6R7_DERFA	Q9u6r7	dermatophag
277	87.5	7.7	653	2	Q59YC5_CANAL	Q59yc5	candida alb
278	87.5	7.7	653	2	Q8NK55_CANAL	Q8nk55	candida alb
279	87.5	7.7	752	2	Q52CR1_MAGGR	Q52cr1	magnaporthe
280	87.5	7.7	997	1	VGNM_APMV	P38485	andean pota
281	87.5	7.7	1085	1	CASR_BOVIN	P35384	bos taurus
282	87	7.7	235	2	Q63349_RAT	Q63349	rattus norv
283	87	7.7	264	2	Q80XS5_MOUSE	Q80xs5	mus musculu
284	87	7.7	391	2	Q753G3_ASHGO	Q753g3	ashbya goss
285	87	7.7	463	2	Q5A3K1_CANAL	Q5a3k1	candida alb
286	87	7.7	532	2	Q4JK69_DERPT	Q4jk69	dermatophag
287	87	7.7	567	2	Q60X66_CAEBR	Q60x66	caenorhabdi
288	87	7.7	612	2	Q7QJB6_ANOGA	Q7qjb6	anopheles g
289	87	7.7	661	2	O13444_CLAFU	O13444	cladosporiu
290	87	7.7	701	2	Q8ZWG4_PYRAE	Q8zwg4	pyrobaculum
291	87	7.7	721	2	Q97UG7_SULSO	Q97ug7	sulfolobus
292	87	7.7	722	2	O59644_SULSO	O59644	sulfolobus
293	87	7.7	802	2	Q60LR3_CAEBR	Q60lr3	caenorhabdi
294	87	7.7	881	2	Q8IMS9_DROME	Q8ims9	drosophila
295	87	7.7	1055	2	Q55G65_DICDI	Q55g65	dictyosteli
296	87	7.7	1506	2	P79927_XENLA	P79927	xenopus lae
297	86.5	7.6	400	1	MUA1_XENLA	P10667	xenopus lae
298	86.5	7.6	483	2	Q5AT96_EMENI	Q5at96	aspergillus
299	86.5	7.6	585	2	Q5SE79_9MONO	Q5se79	avian pneum
300	86.5	7.6	629	2	Q4QGJ0_LEIMA	Q4qgj0	leishmania
301	86.5	7.6	768	2	O60279_HUMAN	O60279	homo sapien
302	86.5	7.6	838	2	Q7UNP4_RHOBA	Q7unp4	rhodopirell
303	86.5	7.6	928	2	Q4SL40_TETNG	Q4sl40	tetraodon n
304	86.5	7.6	941	2	Q9LTH0_ARATH	Q9lth0	arabidopsis
305	86.5	7.6	965	2	Q22286_CAEEL	Q22286	caenorhabdi
306	86.5	7.6	980	2	Q84FU6_CHLTR	Q84fu6	chlamydia t
307	86.5	7.6	980	2	Q84FU8_CHLTR	Q84fu8	chlamydia t
308	86.5	7.6	981	2	Q84FU7_CHLTR	Q84fu7	chlamydia t
309	86.5	7.6	4509	2	Q54T85_DICDI	Q54t85	dictyosteli
310	86	7.6	390	2	Q70LM3_PHLRA	Q70lm3	phlebia rad
311	86	7.6	390	2	Q96TS5_PHLRA	Q96ts5	phlebia rad
312	86	7.6	431	2	Q51WX9_MAGGR	Q51wx9	magnaporthe
313	86	7.6	477	2	Q86YC5_HUMAN	Q86yc5	homo sapien
314	86	7.6	591	2	Q4WHJ8_ASPFU	Q4whj8	aspergillus
315	86	7.6	678	2	Q54U48_DICDI	Q54u48	dictyosteli
316	86	7.6	709	2	Q4P7Y7_USTMA	Q4p7y7	ustilago ma
317	86	7.6	1266	2	Q626F7_CAEBR	Q626f7	caenorhabdi
318	86	7.6	2044	2	Q4HZP9_GIBZE	Q4hzp9	gibberella
319	85.5	7.5	178	2	Q8FQU3_COREF	Q8fqu3	corynebacte
320	85.5	7.5	346	2	Q5R230_9ZYGO	Q5r230	phycomyces
321	85.5	7.5	363	2	Q91YK8_MOUSE	Q91yk8	mus musculu
322	85.5	7.5	510	2	Q6SCJ8_ASPFU	Q6scj8	aspergillus
323	85.5	7.5	734	2	Q7S939_NEUCR	Q7s939	neurospora
324	85.5	7.5	786	2	Q21027_CAEEL	Q21027	caenorhabdi
325	85.5	7.5	841	2	Q6R8J4_BRARE	Q6r8j4	brachydanio
326	85.5	7.5	866	2	Q4PDE9_USTMA	Q4pde9	ustilago ma
327	85.5	7.5	895	2	O80973_ARATH	O80973	arabidopsis
328	85.5	7.5	908	2	Q59PF9_CANAL	Q59pf9	candida alb
329	85.5	7.5	935	2	Q6R8J3_BRARE	Q6r8j3	brachydanio
330	85.5	7.5	951	2	Q9FVX8_ORYSA	Q9fvx8	oryza sativ
331	85.5	7.5	977	2	Q6R8J2_BRARE	Q6r8j2	brachydanio
332	85.5	7.5	1209	2	Q4SFS8_TETNG	Q4sfs8	tetraodon n
333	85.5	7.5	1367	1	MUC1_YEAST	P08640	saccharomyc
334	85.5	7.5	1367	2	Q6LCS8_SACDI	Q6lcs8	saccharomyc
335	85.5	7.5	2448	2	Q8WWQ5_HUMAN	Q8wwq5	homo sapien
336	85.5	7.5	4862	2	Q5RI27_BRARE	Q5ri27	brachydanio
337	85.5	7.5	6995	2	Q96RK2_HUMAN	Q96rk2	homo sapien
338	85	7.5	172	2	Q8VC95_MOUSE	Q8vc95	mus musculu
339	85	7.5	265	2	Q9GZE5_CAEEL	Q9gze5	caenorhabdi
340	85	7.5	345	2	Q691Y8_ANOSA	Q691y8	anolis sagr
341	85	7.5	429	2	O76430_CAEEL	O76430	caenorhabdi
342	85	7.5	449	2	Q71UN8_CAEEL	Q71un8	caenorhabdi
343	85	7.5	569	2	Q9KGV9_LISMO	Q9kgv9	listeria mo
344	85	7.5	612	2	Q622S9_CAEBR	Q622s9	caenorhabdi
345	85	7.5	626	2	Q9NDD1_LEITR	Q9ndd1	leishmania
346	85	7.5	627	1	PKNB_LACLA	Q9cef5	lactococcus
347	85	7.5	852	2	Q6CIA5_YARLI	Q6cia5	yarrowia li
348	85	7.5	879	2	Q4IC17_GIBZE	Q4ic17	gibberella
349	85	7.5	961	2	Q5ATY9_EMENI	Q5aty9	aspergillus
350	85	7.5	961	2	Q92223_EMENI	Q92223	emericella
351	85	7.5	991	2	Q83UW2_CHLTR	Q83uw2	chlamydia t
352	85	7.5	991	2	Q84FV0_CHLTR	Q84fv0	chlamydia t
353	85	7.5	991	2	Q84FV1_CHLTR	Q84fv1	chlamydia t
354	85	7.5	1016	1	PMPH_CHLTR	O84880	chlamydia t
355	85	7.5	1025	2	Q626Q9_CAEBR	Q626q9	caenorhabdi
356	85	7.5	1049	2	Q960E6_DROME	Q960e6	drosophila
357	85	7.5	1049	2	Q9V6L1_DROME	Q9v6l1	drosophila
358	85	7.5	1153	2	Q4IAN9_GIBZE	Q4ian9	gibberella
359	85	7.5	1170	2	Q95011_CAEEL	Q95011	caenorhabdi
360	85	7.5	1286	2	Q9VR49_DROME	Q9vr49	drosophila
361	84.5	7.4	220	2	Q9EQG0_MOUSE	Q9eqg0	mus musculu
362	84.5	7.4	245	2	Q564Z3_CAEEL	Q564z3	caenorhabdi
363	84.5	7.4	250	2	Q5AP52_CANAL	Q5ap52	candida alb
364	84.5	7.4	274	2	Q54WW2_DICDI	Q54ww2	dictyosteli
365	84.5	7.4	320	2	Q4SCG1_TETNG	Q4scg1	tetraodon n
366	84.5	7.4	333	2	Q60JT6_CAEBR	Q60jt6	caenorhabdi
367	84.5	7.4	346	2	Q7S973_NEUCR	Q7s973	neurospora
368	84.5	7.4	752	2	Q9YC61_AERPE	Q9yc61	aeropyrum p
369	84.5	7.4	814	2	Q6C247_YARLI	Q6c247	yarrowia li
370	84.5	7.4	834	2	Q877B7_ASPOR	Q877b7	aspergillus
371	84.5	7.4	1161	1	DAN4_YEAST	P47179	saccharomyc
372	84.5	7.4	1186	2	Q54I94_DICDI	Q54i94	dictyosteli
373	84.5	7.4	1218	2	Q54YZ6_DICDI	Q54yz6	dictyosteli
374	84.5	7.4	2163	2	Q61TS1_CAEBR	Q61ts1	caenorhabdi
375	84.5	7.4	22152	2	Q8WXI7_HUMAN	Q8wxi7	homo sapien
376	84	7.4	259	2	Q9N3B9_CAEEL	Q9n3b9	caenorhabdi
377	84	7.4	262	2	P74577_SYNY3	P74577	synechocyst
378	84	7.4	273	2	Q61002_MOUSE	Q61002	mus musculu
379	84	7.4	335	2	Q9C7W2_ARATH	Q9c7w2	arabidopsis
380	84	7.4	421	2	Q6KCA6_CANDU	Q6kca6	candida dub
381	84	7.4	475	2	Q8FQJ1_COREF	Q8fqj1	corynebacte
382	84	7.4	543	2	Q14879_HUMAN	Q14879	homo sapien
383	84	7.4	641	2	Q6AJU8_DESPS	Q6aju8	desulfotale
384	84	7.4	648	2	Q95QX0_CAEEL	Q95qx0	caenorhabdi
385	84	7.4	668	2	Q4QGK4_LEIMA	Q4qgk4	leishmania
386	84	7.4	713	2	Q55RT5_CRYNE	Q55rt5	cryptococcu
387	84	7.4	927	2	Q21811_CAEEL	Q21811	caenorhabdi
388	84	7.4	1331	1	MANB_CALSA	P22533	caldocellum
389	84	7.4	1362	2	Q9V294_PYRAB	Q9v294	pyrococcus
390	84	7.4	1370	2	Q6C3B8_YARLI	Q6c3b8	yarrowia li
391	84	7.4	1413	2	Q54FI2_DICDI	Q54fi2	dictyosteli
392	84	7.4	1779	2	O52374_9FIRM	O52374	caldicellul
393	84	7.4	1832	2	O96503_CRYPV	O96503	cryptospori
394	83.5	7.4	216	2	Q28501_MACMU	Q28501	macaca mula
395	83.5	7.4	279	2	Q14888_HUMAN	Q14888	homo sapien
396	83.5	7.4	571	2	Q4YHW1_PLABE	Q4yhw1	plasmodium

397	83.5	7.4	615	2	Q9M6E8_PHAVU	Q9m6e8	phaseolus v
398	83.5	7.4	788	2	O18510_TRINI	O18510	trichoplusi
399	83.5	7.4	800	2	Q8TFG4_SCHPO	Q8tfg4	schizosacch
400	83.5	7.4	807	2	O18511_TRINI	O18511	trichoplusi
401	83.5	7.4	892	1	LDLR2_XENLA	Q99088	xenopus lae
402	83.5	7.4	967	2	Q08294_YEAST	Q08294	saccharomyc
403	83.5	7.4	1001	2	Q05164_YEAST	Q05164	saccharomyc
404	83.5	7.4	1214	2	Q54LU4_DICDI	Q54lu4	dictyosteli
405	83.5	7.4	1286	2	Q9TXR6_CAEEL	Q9txr6	caenorhabdi
406	83.5	7.4	1713	2	Q8TGE1_YEAST	Q8tge1	saccharomyc
407	83.5	7.4	2048	2	Q55GC1_DICDI	Q55gc1	dictyosteli
408	83.5	7.4	5179	1	MUC2_HUMAN	Q02817	homo sapien
409	83	7.3	198	2	Q7QB72_ANOGA	Q7qb72	anopheles g
410	83	7.3	244	2	Q54RQ4_DICDI	Q54rq4	dictyosteli
411	83	7.3	262	2	Q7PRG9_ANOGA	Q7prg9	anopheles g
412	83	7.3	269	2	Q9U9J2_TOXCA	Q9u9j2	toxocara ca
413	83	7.3	309	2	Q63549_RAT	Q63549	rattus norv
414	83	7.3	316	2	Q8TD14_HUMAN	Q8td14	homo sapien
415	83	7.3	337	2	Q7Z5K8_HUMAN	Q7z5k8	homo sapien
416	83	7.3	378	2	Q8SXS5_DROME	Q8sxs5	drosophila
417	83	7.3	404	2	Q702X0_HHV1	Q702x0	human herpe
418	83	7.3	404	2	Q702Y3_HHV1	Q702y3	human herpe
419	83	7.3	409	1	RD23B_HUMAN	P54727	homo sapien
420	83	7.3	409	2	Q53F10_HUMAN	Q53f10	homo sapien
421	83	7.3	419	2	Q8TD11_HUMAN	Q8td11	homo sapien
422	83	7.3	422	2	Q8TD13_HUMAN	Q8td13	homo sapien
423	83	7.3	477	2	Q14887_HUMAN	Q14887	homo sapien
424	83	7.3	485	2	Q9V8B0_DROME	Q9v8b0	drosophila
425	83	7.3	487	2	Q4UHA9_THEAN	Q4uha9	theileria a
426	83	7.3	492	2	Q6CGC6_YARLI	Q6cgc6	yarrowia li
427	83	7.3	552	2	Q4N6B9_THEPA	Q4n6b9	theileria p
428	83	7.3	559	2	Q9VN36_DROME	Q9vn36	drosophila
429	83	7.3	605	1	WSC4_YEAST	P38739	saccharomyc
430	83	7.3	630	2	Q5ELS1_DROME	Q5els1	drosophila
431	83	7.3	665	2	Q4IIW3_GIBZE	Q4iiw3	gibberella
432	83	7.3	769	2	Q17921_CAEEL	Q17921	caenorhabdi
433	83	7.3	794	2	Q55CQ4_DICDI	Q55cq4	dictyosteli
434	83	7.3	985	2	Q5KL22_CRYNE	Q5kl22	cryptococcu
435	83	7.3	985	2	Q55V60_CRYNE	Q55v60	cryptococcu
436	83	7.3	993	2	Q83TJ6_CHLTR	Q83tj6	chlamydia t
437	83	7.3	1002	2	Q6CBD5_YARLI	Q6cbd5	yarrowia li
438	83	7.3	1030	2	Q7QV30_GIALA	Q7qv30	giardia lam
439	83	7.3	1066	2	Q76NW3_DICDI	Q76nw3	dictyosteli
440	83	7.3	1086	2	Q54X99_DICDI	Q54x99	dictyosteli
441	83	7.3	1118	2	Q550H5_DICDI	Q550h5	dictyosteli
442	83	7.3	1458	2	Q54PJ4_DICDI	Q54pj4	dictyosteli
443	83	7.3	1646	2	Q5CFZ6_CRYHO	Q5cfz6	cryptospori
444	83	7.3	1777	2	Q54FB8_DICDI	Q54fb8	dictyosteli
445	82.5	7.3	184	2	Q7PRM2_ANOGA	Q7prm2	anopheles g
446	82.5	7.3	197	2	Q26878_TRYCR	Q26878	trypanosoma
447	82.5	7.3	252	2	Q6GZ06_9MONO	Q6gz06	avian pneum
448	82.5	7.3	268	2	Q5ATR9_EMENI	Q5atr9	aspergillus
449	82.5	7.3	346	2	Q52J88_9SAUR	Q52j88	heteronotia
450	82.5	7.3	346	2	Q52J76_9SAUR	Q52j76	heteronotia
451	82.5	7.3	383	1	VE2_HPV57	P22155	human papil
452	82.5	7.3	389	2	Q64BB8_9ARCH	Q64bb8	uncultured
453	82.5	7.3	389	2	Q6GXX0_9VIRU	Q6gxx0	swine hepat
454	82.5	7.3	389	2	Q6GXX2_9VIRU	Q6gxx2	swine hepat
455	82.5	7.3	389	2	Q6GXX3_9VIRU	Q6gxx3	swine hepat
456	82.5	7.3	391	2	Q54XF0_DICDI	Q54xf0	dictyosteli
457	82.5	7.3	459	2	Q55SZ8_CRYNE	Q55sz8	cryptococcu
458	82.5	7.3	540	1	CH60_STRAP	Q8kj20	streptococc
459	82.5	7.3	599	2	Q6C2K2_YARLI	Q6c2k2	yarrowia li
460	82.5	7.3	625	2	Q5ELP7_DROSI	Q5elp7	drosophila
461	82.5	7.3	627	2	Q7RWT2_NEUCR	Q7rwt2	neurospora
462	82.5	7.3	635	2	O66065_FIBSU	O66065	fibrobacter
463	82.5	7.3	641	2	Q5KHD0_CRYNE	Q5khd0	cryptococcu
464	82.5	7.3	726	1	NFI1_YEAST	Q12216	saccharomyc
465	82.5	7.3	825	2	Q03088_YEAST	Q03088	saccharomyc
466	82.5	7.3	833	2	Q602T7_METCA	Q602t7	methylococc
467	82.5	7.3	843	2	Q9VYH8_DROME	Q9vyh8	drosophila
468	82.5	7.3	876	2	Q6XLI5_BRARE	Q6xli5	brachydanio
469	82.5	7.3	1206	1	FMN1B_MOUSE	Q05859	mus musculu
470	82.5	7.3	1261	2	Q7R2F4_GIALA	Q7r2f4	giardia lam
471	82.5	7.3	1371	2	Q9VU22_DROME	Q9vu22	drosophila
472	82.5	7.3	1468	1	FMN1A_MOUSE	Q05860	mus musculu
473	82.5	7.3	1472	2	Q6V9R4_STRPU	Q6v9r4	strongyloce
474	82.5	7.3	1478	1	LPHN2_BOVIN	O97817	bos taurus
475	82.5	7.3	1711	1	NU214_DROME	Q9w1x4	drosophila
476	82.5	7.3	1809	2	Q4Q8Z9_LEIMA	Q4q8z9	leishmania
477	82.5	7.3	1851	2	Q9ESP3_RAT	Q9esp3	rattus norv
478	82.5	7.3	2482	2	Q61GF0_CAEBR	Q61gf0	caenorhabdi
479	82.5	7.3	4483	2	Q51QB7_MAGGR	Q51qb7	magnaporthe
480	82	7.2	166	2	Q5IE00_PINTA	Q5ie00	pinus taeda
481	82	7.2	166	2	Q5IE20_PINTA	Q5ie20	pinus taeda
482	82	7.2	166	2	Q56VT9_9STRA	Q56vt9	pythium aph
483	82	7.2	236	2	Q9LM00_PINTA	Q9lm00	pinus taeda
484	82	7.2	306	2	Q54UW3_DICDI	Q54uw3	dictyosteli
485	82	7.2	311	2	Q55LZ4_CRYNE	Q55lz4	cryptococcu
486	82	7.2	311	2	Q5K8S4_CRYNE	Q5k8s4	cryptococcu
487	82	7.2	318	2	Q86HN3_DICDI	Q86hn3	dictyosteli
488	82	7.2	339	2	Q9VUX8_DROME	Q9vux8	drosophila
489	82	7.2	345	2	Q690W2_ANOSA	Q690w2	anolis sagr
490	82	7.2	374	2	Q9Z209_CRIGR	Q9z209	cricetulus
491	82	7.2	388	2	Q60KQ3_CAEBR	Q60kq3	caenorhabdi
492	82	7.2	389	2	O76573_CAEEL	O76573	caenorhabdi
493	82	7.2	410	2	Q4R5B5_MACFA	Q4r5b5	macaca fasc
494	82	7.2	463	2	O42665_SCHPO	O42665	schizosacch
495	82	7.2	477	1	MYBPH_HUMAN	Q13203	homo sapien
496	82	7.2	479	2	Q61AU9_CAEBR	Q61au9	caenorhabdi
497	82	7.2	483	2	Q9W4M2_DROME	Q9w4m2	drosophila
498	82	7.2	495	2	Q4RZZ8_TETNG	Q4rzz8	tetraodon n
499	82	7.2	505	2	Q4FYQ6_LEIMA	Q4fyq6	leishmania
500	82	7.2	538	2	Q76H84_STRMU	Q76h84	streptococc
501	82	7.2	562	2	Q51ND8_MAGGR	Q51nd8	magnaporthe
502	82	7.2	616	2	Q4WC60_ASPFU	Q4wc60	aspergillus
503	82	7.2	623	2	O57602_ICTPU	O57602	ictalurus p
504	82	7.2	630	2	Q96YH6_SULTO	Q96yh6	sulfolobus
505	82	7.2	644	2	Q6CF33_YARLI	Q6cf33	yarrowia li
506	82	7.2	693	2	Q27394_CAEEL	Q27394	caenorhabdi
507	82	7.2	713	2	Q5KG88_CRYNE	Q5kg88	cryptococcu
508	82	7.2	780	2	Q5CHI0_CRYHO	Q5chi0	cryptospori
509	82	7.2	919	2	Q51BH5_ENTHI	Q51bh5	entamoeba h
510	82	7.2	952	2	Q9U3P1_CAEEL	Q9u3p1	caenorhabdi
511	82	7.2	973	2	Q7CZH1_AGRT5	Q7czh1	agrobacteri
512	82	7.2	977	2	Q8UFQ8_AGRT5	Q8ufq8	agrobacteri
513	82	7.2	1099	2	Q7TUJ6_PROMM	Q7tuj6	prochloroco
514	82	7.2	1113	2	Q7PMD5_ANOGA	Q7pmd5	anopheles g
515	82	7.2	1266	2	Q6CAR3_YARLI	Q6car3	yarrowia li
516	82	7.2	1599	2	Q4QDX1_LEIMA	Q4qdx1	leishmania
517	82	7.2	1689	2	Q5EEN9_9VIRU	Q5een9	crimean-con
518	82	7.2	2523	2	Q4IEB9_GIBZE	Q4ieb9	gibberella
519	81.5	7.2	146	2	Q5W0S5_HUMAN	Q5w0s5	homo sapien
520	81.5	7.2	147	2	O61043_TRYCR	O61043	trypanosoma
521	81.5	7.2	171	1	NUOE_BUCBP	Q89au3	buchnera ap
522	81.5	7.2	224	2	Q8KKT9_RHIET	Q8kkt9	rhizobium e
523	81.5	7.2	342	2	Q54LV1_DICDI	Q54lv1	dictyosteli
524	81.5	7.2	381	2	Q5B2S4_EMENI	Q5b2s4	aspergillus
525	81.5	7.2	386	2	Q97G38_CLOAB	Q97g38	clostridium
526	81.5	7.2	390	2	Q6PND6_EMENI	Q6pnd6	emericella
527	81.5	7.2	411	2	Q702X9_HHV1	Q702x9	human herpe
528	81.5	7.2	460	2	O18984_CERAE	O18984	cercopithec
529	81.5	7.2	579	2	Q4RLQ7_TETNG	Q4rlq7	tetraodon n
530	81.5	7.2	584	1	CEJ1_CAEEL	Q17802	caenorhabdi
531	81.5	7.2	612	2	Q6CD44_YARLI	Q6cd44	yarrowia li
532	81.5	7.2	640	2	Q55CW3_DICDI	Q55cw3	dictyosteli
533	81.5	7.2	682	2	Q60PP2_CAEBR	Q60pp2	caenorhabdi
534	81.5	7.2	741	2	Q6CH88_YARLI	Q6ch88	yarrowia li
535	81.5	7.2	808	2	Q8I123_CAEEL	Q8i123	caenorhabdi
536	81.5	7.2	846	2	Q6ZKY0_ORYSA	Q6zky0	oryza sativ
537	81.5	7.2	860	1	MUTS_LISIN	Q92bv3	listeria in
538	81.5	7.2	860	1	VG12_BPB03	Q37893	bacteriopha
539	81.5	7.2	913	2	Q7NP28_GLOVI	Q7np28	gloeobacter
540	81.5	7.2	957	2	Q9UKN0_HUMAN	Q9ukn0	homo sapien
541	81.5	7.2	980	2	Q54TI9_DICDI	Q54ti9	dictyosteli
542	81.5	7.2	1116	2	Q5AJH8_CANAL	Q5ajh8	candida alb

543	81.5	7.2	1216	1	YPX5_CAEEL	Q09277	caenorhabdi
544	81.5	7.2	1267	2	Q54VU8_DICDI	Q54vu8	dictyosteli
545	81.5	7.2	1320	2	Q96KF5_HUMAN	Q96kf5	homo sapien
546	81.5	7.2	1354	2	Q9VKA7_DROME	Q9vka7	drosophila
547	81.5	7.2	1500	2	Q6AUV2_ORYSA	Q6auv2	oryza sativ
548	81.5	7.2	1570	2	Q61L27_CAEBR	Q61l27	caenorhabdi
549	81.5	7.2	1598	2	Q60RK8_CAEBR	Q60rk8	caenorhabdi
550	81.5	7.2	1844	2	Q22579_CAEEL	Q22579	caenorhabdi
551	81.5	7.2	2338	2	Q629N6_BURMA	Q629n6	burkholderi
552	81.5	7.2	3175	1	RPOA_EAVBU	P19811	e replicase
553	81	7.1	153	2	Q4VT19_PINEC	Q4vt19	pinus echin
554	81	7.1	161	2	Q6CPZ3_KLULA	Q6cpz3	kluyveromyc
555	81	7.1	166	2	Q5IDX6_PINTA	Q5idx6	pinus taeda
556	81	7.1	166	2	Q5IE14_PINTA	Q5ie14	pinus taeda
557	81	7.1	166	2	Q5IE16_PINTA	Q5ie16	pinus taeda
558	81	7.1	282	2	Q52BD2_MAGGR	Q52bd2	magnaporthe
559	81	7.1	301	2	Q628G4_CAEBR	Q628g4	caenorhabdi
560	81	7.1	301	2	Q924G0_CRACA	Q924g0	cratogeomys
561	81	7.1	303	2	Q4QGL0_LEIMA	Q4qgl0	leishmania
562	81	7.1	315	2	Q9VXI1_DROME	Q9vxi1	drosophila
563	81	7.1	345	2	Q691X0_ANOSA	Q691x0	anolis sagr
564	81	7.1	355	2	Q9NP13_HUMAN	Q9np13	homo sapien
565	81	7.1	403	2	Q702W8_HHV1	Q702w8	human herpe
566	81	7.1	404	2	Q702W6_HHV1	Q702w6	human herpe
567	81	7.1	404	2	Q702Y0_HHV1	Q702y0	human herpe
568	81	7.1	404	2	Q702Y6_HHV1	Q702y6	human herpe
569	81	7.1	446	2	Q4QDE7_LEIMA	Q4qde7	leishmania
570	81	7.1	453	2	Q9U301_CAEEL	Q9u301	caenorhabdi
571	81	7.1	455	2	Q4INK6_GIBZE	Q4ink6	gibberella
572	81	7.1	585	2	Q58SH2_DROSI	Q58sh2	drosophila
573	81	7.1	587	2	Q4QGJ9_LEIMA	Q4qgj9	leishmania
574	81	7.1	606	2	Q5ZEJ5_ORYSA	Q5zej5	oryza sativ
575	81	7.1	625	2	Q58SG0_DROSI	Q58sg0	drosophila
576	81	7.1	629	2	Q5ELS5_DROME	Q5els5	drosophila
577	81	7.1	665	2	Q4WIN7_ASPFU	Q4win7	aspergillus
578	81	7.1	668	2	Q6FWR2_CANGA	Q6fwr2	candida gla
579	81	7.1	746	2	Q82GM0_STRAW	Q82gm0	streptomyce
580	81	7.1	782	2	Q6CNV3_KLULA	Q6cnv3	kluyveromyc
581	81	7.1	812	2	Q55D98_DICDI	Q55d98	dictyosteli
582	81	7.1	841	2	Q4Q5Z4_LEIMA	Q4q5z4	leishmania
583	81	7.1	927	2	Q5BE09_EMENI	Q5be09	aspergillus
584	81	7.1	977	2	Q620Q9_CAEBR	Q620q9	caenorhabdi
585	81	7.1	1031	2	Q925N8_MOUSE	Q925n8	mus musculu
586	81	7.1	1031	2	Q9D071_MOUSE	Q9d071	m mus muscu
587	81	7.1	1128	1	BEM3_YEAST	P32873	saccharomyc
588	81	7.1	1139	2	Q54Z39_DICDI	Q54z39	dictyosteli
589	81	7.1	1163	2	Q86AR1_DICDI	Q86ar1	dictyosteli
590	81	7.1	1312	2	Q55RV4_CRYNE	Q55rv4	cryptococcu
591	81	7.1	1317	1	YQU3_CAEEL	Q09550	caenorhabdi
592	81	7.1	1537	1	FLO1_YEAST	P32768	saccharomyc
593	81	7.1	1537	2	Q58HH7_YEAST	Q58hh7	saccharomyc
594	81	7.1	1569	2	Q6W4X9_HUMAN	Q6w4x9	homo sapien
595	81	7.1	1609	1	FIG2_YEAST	P25653	saccharomyc
596	81	7.1	2282	1	ZAN_RABIT	P57999	oryctolagus
597	81	7.1	2977	2	Q9VAP9_DROME	Q9vap9	drosophila
598	80.5	7.1	148	1	CCL2_RAT	P14844	rattus norv
599	80.5	7.1	148	2	Q549R5_RAT	Q549r5	rattus norv
600	80.5	7.1	165	2	Q26877_TRYCR	Q26877	trypanosoma
601	80.5	7.1	242	2	Q86RS8_CAEEL	Q86rs8	caenorhabdi
602	80.5	7.1	294	2	Q5AVM6_EMENI	Q5avm6	aspergillus
603	80.5	7.1	334	2	Q6VAV6_ANOGA	Q6vav6	anopheles g
604	80.5	7.1	391	1	VE2_HPV2A	P25482	human papil
605	80.5	7.1	410	1	LAMP2_CRIGR	P49130	cricetulus
606	80.5	7.1	441	2	Q9U2W3_CAEEL	Q9u2w3	caenorhabdi
607	80.5	7.1	462	2	Q4MZT8_THEPA	Q4mzt8	theileria p
608	80.5	7.1	540	1	CH60_STRA3	Q8cx22	streptococc
609	80.5	7.1	540	1	CH60_STRA5	Q8cx00	streptococc
610	80.5	7.1	624	2	Q58SG1_DROSI	Q58sg1	drosophila
611	80.5	7.1	636	2	Q60LP1_CAEBR	Q60lp1	caenorhabdi
612	80.5	7.1	657	2	Q86ID0_DICDI	Q86id0	dictyosteli
613	80.5	7.1	659	2	Q556Y6_DICDI	Q556y6	dictyosteli
614	80.5	7.1	659	2	Q86AI8_DICDI	Q86ai8	dictyosteli
615	80.5	7.1	747	2	Q7S8F0_NEUCR	Q7s8f0	neurospora
616	80.5	7.1	758	2	Q9TZI4_CAEEL	Q9tzi4	caenorhabdi
617	80.5	7.1	765	2	Q75I27_ORYSA	Q75i27	oryza sativ
618	80.5	7.1	860	1	MUTS_LISMF	Q71zr7	listeria mo
619	80.5	7.1	877	2	Q55CK2_DICDI	Q55ck2	dictyosteli
620	80.5	7.1	896	2	Q20253_CAEEL	Q20253	caenorhabdi
621	80.5	7.1	971	2	Q6W3C4_CAEEL	Q6w3c4	caenorhabdi
622	80.5	7.1	989	2	Q19930_CAEEL	Q19930	caenorhabdi
623	80.5	7.1	1007	2	Q55CR8_DICDI	Q55cr8	dictyosteli
624	80.5	7.1	1111	2	Q611Y9_CAEBR	Q611y9	caenorhabdi
625	80.5	7.1	1184	2	Q6F3A8_ORYSA	Q6f3a8	oryza sativ
626	80.5	7.1	1300	2	Q6BZP6_YARLI	Q6bzp6	yarrowia li
627	80.5	7.1	1372	2	Q8SX99_DROME	Q8sx99	drosophila
628	80.5	7.1	1372	2	Q9VN46_DROME	Q9vn46	drosophila
629	80.5	7.1	1378	2	Q4WLF4_ASPFU	Q4wlf4	aspergillus
630	80.5	7.1	1773	2	Q4N437_THEPA	Q4n437	theileria p
631	80.5	7.1	1816	2	Q4N6E9_THEPA	Q4n6e9	theileria p
632	80.5	7.1	1912	2	Q5CWD9_CRYPV	Q5cwd9	cryptospori
633	80.5	7.1	2225	2	O45881_CAEEL	O45881	caenorhabdi
634	80	7.0	103	2	O46380_RABIT	O46380	oryctolagus
635	80	7.0	153	2	Q4VT16_PINCO	Q4vt16	pinus conto
636	80	7.0	153	2	Q4VT18_PINPO	Q4vt18	pinus ponde
637	80	7.0	166	2	Q5IDZ6_PINTA	Q5idz6	pinus taeda
638	80	7.0	272	2	Q6ZSN5_HUMAN	Q6zsn5	homo sapien
639	80	7.0	272	2	Q5SZI1_HUMAN	Q5szi1	homo sapien
640	80	7.0	291	2	Q6QPG5_9ADEN	Q6qpg5	simian aden
641	80	7.0	334	2	Q6VAW0_ANOGA	Q6vaw0	anopheles g
642	80	7.0	349	2	Q7XEC9_ORYSA	Q7xec9	oryza sativ
643	80	7.0	375	2	Q55F61_DICDI	Q55f61	dictyosteli
644	80	7.0	410	2	Q9UD93_HUMAN	Q9ud93	homo sapien
645	80	7.0	410	2	Q5FVZ7_XENTR	Q5fvz7	xenopus tro
646	80	7.0	449	2	Q9VKS4_DROME	Q9vks4	drosophila
647	80	7.0	480	2	Q5CGY9_CRYHO	Q5cgy9	cryptospori
648	80	7.0	511	2	Q5A7R7_CANAL	Q5a7r7	candida alb
649	80	7.0	521	2	Q4J9N9_SULAC	Q4j9n9	sulfolobus
650	80	7.0	569	2	Q71XI0_LISMF	Q71xi0	listeria mo
651	80	7.0	625	2	Q58SF8_DROSI	Q58sf8	drosophila
652	80	7.0	653	2	Q5WRN8_CAEEL	Q5wrn8	caenorhabdi
653	80	7.0	657	2	Q6AM00_DESPS	Q6am00	desulfotale
654	80	7.0	704	2	Q4QGK1_LEIMA	Q4qgk1	leishmania
655	80	7.0	716	2	Q54BA1_DICDI	Q54ba1	dictyosteli
656	80	7.0	725	1	AGA1_YEAST	P32323	saccharomyc
657	80	7.0	729	2	Q80WY2_MOUSE	Q80wy2	mus musculu
658	80	7.0	732	2	Q80WY1_MOUSE	Q80wy1	mus musculu
659	80	7.0	747	2	Q8CCZ1_MOUSE	Q8ccz1	mus musculu
660	80	7.0	881	1	PRY3_YEAST	P47033	saccharomyc
661	80	7.0	924	2	Q4I966_GIBZE	Q4i966	gibberella
662	80	7.0	1016	2	Q54TA5_DICDI	Q54ta5	dictyosteli
663	80	7.0	1048	2	Q9LAU3_LEGPN	Q9lau3	legionella
664	80	7.0	1082	1	YK02_SCHPO	Q9hdy9	schizosacch
665	80	7.0	1168	2	Q9VZE8_DROME	Q9vze8	drosophila
666	80	7.0	1256	2	Q54RH9_DICDI	Q54rh9	dictyosteli
667	80	7.0	1273	2	Q4S9G2_TETNG	Q4s9g2	tetraodon n
668	80	7.0	1324	2	Q8MMQ2_DICDI	Q8mmq2	dictyosteli
669	80	7.0	1325	2	Q9BKV7_LEIMA	Q9bkv7	leishmania
670	80	7.0	1377	2	Q54ND2_DICDI	Q54nd2	dictyosteli
671	80	7.0	1435	2	Q4FX64_LEIMA	Q4fx64	leishmania
672	80	7.0	1469	2	Q7S353_NEUCR	Q7s353	neurospora
673	80	7.0	1473	2	Q54TV0_DICDI	Q54tv0	dictyosteli
674	80	7.0	1764	2	Q4WB96_ASPFU	Q4wb96	aspergillus
675	80	7.0	4262	2	Q685J2_HUMAN	Q685j2	homo sapien
676	80	7.0	4493	2	Q685J3_HUMAN	Q685j3	homo sapien
677	79.5	7.0	113	2	Q5AF39_CANAL	Q5af39	candida alb
678	79.5	7.0	129	2	Q6UNH4_ICTPU	Q6unh4	ictalurus p
679	79.5	7.0	154	2	Q4VT10_PINMO	Q4vt10	pinus monti
680	79.5	7.0	161	2	Q6IGP4_DROME	Q6igp4	drosophila
681	79.5	7.0	178	2	Q60F71_CAEEL	Q60f71	caenorhabdi
682	79.5	7.0	199	2	Q6C3G4_YARLI	Q6c3g4	yarrowia li
683	79.5	7.0	245	2	Q61MB0_CAEBR	Q61mb0	caenorhabdi
684	79.5	7.0	272	2	Q8A3G1_BACTN	Q8a3g1	bacteroides
685	79.5	7.0	273	2	Q6JK85_9NUCL	Q6jk85	neodiprion
686	79.5	7.0	289	2	Q5AR17_EMENI	Q5ar17	aspergillus
687	79.5	7.0	333	2	Q6VAV7_ANOGA	Q6vav7	anopheles g
688	79.5	7.0	354	2	Q25402_LITSI	Q25402	litomosoide

689	79.5	7.0	373	2	O76810_ANOGA	O76810 anopheles g	762	79	7.0	278	2	Q4WLZ8_ASPFU	Q4wlz8 aspergillus		
690	79.5	7.0	403	2	Q8MVA9_IXOSC	Q8mva9 ixodes scap	763	79	7.0	294	2	Q4V3X0_DROME	Q4v3x0 drosophila		
691	79.5	7.0	413	2	Q5B569_EMENI	Q5b569 aspergillus	764	79	7.0	308	2	Q74KF4_LACJO	Q74kf4 lactobacill		
692	79.5	7.0	418	2	Q5AU55_EMENI	Q5au55 aspergillus	765	79	7.0	321	2	Q4ID50_GIBZE	Q4id50 gibberella		
693	79.5	7.0	433	2	Q88VC0_LACPL	Q88vc0 lactobacill	766	79	7.0	333	2	Q6VAV8_ANOGA	Q6vav8 anopheles g		
694	79.5	7.0	438	2	Q4X548_PLACH	Q4x548 plasmodium	767	79	7.0	345	2	Q691T8_ANOSA	Q691t8 anolis sagr		
695	79.5	7.0	461	2	Q6C2X8_YARLI	Q6c2x8 yarrowia li	768	79	7.0	352	2	O49782_ARATH	O49782 arabidopsis		
696	79.5	7.0	462	2	Q8TUE0_METAC	Q8tue0 methanosarc	769	79	7.0	353	2	Q8VPM3_9MICC	Q8vpm3 micrococcus		
697	79.5	7.0	463	2	Q7RNE3_PLAYO	Q7rne3 plasmodium	770	79	7.0	359	2	Q9XZT0_DROME	Q9xzt0 drosophila		
698	79.5	7.0	495	2	Q9CV82_MOUSE	Q9cv82 mus musculu	771	79	7.0	390	2	Q702W4_HHV1	Q702w4 human herpe		
699	79.5	7.0	497	2	Q8QVC5_9REOV	Q8qvc5 eyach virus	772	79	7.0	390	2	Q702W9_HHV1	Q702w9 human herpe		
700	79.5	7.0	511	2	Q8UYA8_HHV1	Q8uya8 human herpe	773	79	7.0	410	1	LAMP2_HUMAN	P13473 homo sapien		
701	79.5	7.0	511	2	Q8UZ60_HHV1	Q8uz60 human herpe	774	79	7.0	411	2	Q6Q3G8_HUMAN	Q6q3g8 homo sapien		
702	79.5	7.0	511	2	Q8UZ61_HHV1	Q8uz61 human herpe	775	79	7.0	444	2	Q4QBU8_LEIMA	Q4qbu8 leishmania		
703	79.5	7.0	511	2	Q8UZ64_HHV1	Q8uz64 human herpe	776	79	7.0	447	2	Q8BIY6_MOUSE	Q8biy6 mus musculu		
704	79.5	7.0	511	2	Q8UZ66_HHV1	Q8uz66 human herpe	777	79	7.0	462	2	Q5YX93_NOCFA	Q5yx93 nocardia fa		
705	79.5	7.0	511	2	Q8UZ67_HHV1	Q8uz67 human herpe	778	79	7.0	462	2	Q5SRX3_MOUSE	Q5srx3 mus musculu		
706	79.5	7.0	543	2	Q4YVC9_PLABE	Q4yvc9 plasmodium	779	79	7.0	476	2	Q5G2D4_9PEZI	Q5g2d4 chaetomium		
707	79.5	7.0	595	2	Q5ANA0_CANAL	Q5ana0 candida alb	780	79	7.0	486	2	Q8FRY2_COREF	Q8fry2 corynebacte		
708	79.5	7.0	602	2	Q5Z1H2_NOCFA	Q5z1h2 nocardia fa	781	79	7.0	488	2	Q4V3Z8_DROME	Q4v3z8 drosophila		
709	79.5	7.0	624	2	Q5ELP3_DROSI	Q5elp3 drosophila	782	79	7.0	489	2	Q95Q80_CAEEL	Q95q80 caenorhabdi		
710	79.5	7.0	658	2	Q8MQZ8_DROME	Q8mqz8 drosophila	783	79	7.0	503	2	Q95Q82_CAEEL	Q95q82 caenorhabdi		
711	79.5	7.0	706	2	Q9VNZ5_DROME	Q9vnz5 drosophila	784	79	7.0	503	2	Q8VCF0_MOUSE	Q8vcf0 mus musculu		
712	79.5	7.0	779	2	Q5TRJ3_ANOGA	Q5trj3 anopheles g	785	79	7.0	534	2	Q86AL2_DICDI	Q86al2 dictyosteli		
713	79.5	7.0	796	2	Q8MRG9_DROME	Q8mrg9 drosophila	786	79	7.0	555	2	Q9VH46_DROME	Q9vh46 drosophila		
714	79.5	7.0	796	2	Q9VTR4_DROME	Q9vtr4 drosophila	787	79	7.0	561	2	Q556P6_DICDI	Q556p6 dictyosteli		
715	79.5	7.0	805	2	Q61PW9_CAEBR	Q61pw9 caenorhabdi	788	79	7.0	572	2	Q58SM0_DROME	Q58sm0 drosophila		
716	79.5	7.0	812	2	Q5TT09_ANOGA	Q5tt09 anopheles g	789	79	7.0	572	2	Q58SM1_DROME	Q58sm1 drosophila		
717	79.5	7.0	828	2	Q5B8I9_EMENI	Q5b8i9 aspergillus	790	79	7.0	572	2	Q58SM4_DROME	Q58sm4 drosophila		
718	79.5	7.0	860	1	MUTS_LISMO	Q8y789 listeria mo	791	79	7.0	572	2	Q58SM6_DROME	Q58sm6 drosophila		
719	79.5	7.0	873	2	Q9Y076_LEIMA	Q9y076 leishmania	792	79	7.0	572	2	Q58SM7_DROME	Q58sm7 drosophila		
720	79.5	7.0	873	2	Q9W468_DROME	Q9w468 drosophila	793	79	7.0	575	2	O62223_CAEEL	O62223 caenorhabdi		
721	79.5	7.0	878	2	Q55GH4_DICDI	Q55gh4 dictyosteli	794	79	7.0	585	2	Q58SG3_DROSI	Q58sg3 drosophila		
722	79.5	7.0	887	2	Q6XD56_CHICK	Q6xd56 gallus gall	795	79	7.0	585	2	Q58SG5_DROSI	Q58sg5 drosophila		
723	79.5	7.0	939	2	Q592W9_BRARE	Q592w9 brachydanio	796	79	7.0	594	2	Q6PAN1_MOUSE	Q6pan1 mus musculu		
724	79.5	7.0	958	2	Q4WTT4_ASPFU	Q4wtt4 aspergillus	797	79	7.0	601	2	Q6V6S1_DROME	Q6v6s1 drosophila		
725	79.5	7.0	985	2	Q67643_9ALPH	Q67643 gallid herp	798	79	7.0	601	2	Q6V6S2_DROME	Q6v6s2 drosophila		
726	79.5	7.0	1061	2	Q555D2_DICDI	Q555d2 dictyosteli	799	79	7.0	625	2	Q58SH7_DROSI	Q58sh7 drosophila		
727	79.5	7.0	1114	2	Q5AJV5_CANAL	Q5ajv5 candida alb	800	79	7.0	625	2	Q5ELP1_DROSI	Q5elp1 drosophila		
728	79.5	7.0	1123	2	Q5VX82_HUMAN	Q5vx82 homo sapien	801	79	7.0	626	2	Q8KUU5_SYNP7	Q8kuu5 synechococc		
729	79.5	7.0	1170	2	Q54PK2_DICDI	Q54pk2 dictyosteli	802	79	7.0	629	2	Q24017_DROME	Q24017 drosophila		
730	79.5	7.0	1177	2	Q5VX83_HUMAN	Q5vx83 homo sapien	803	79	7.0	629	2	Q5ELR5_DROME	Q5elr5 drosophila		
731	79.5	7.0	1203	2	Q6ZQ56_MOUSE	Q6zq56 mus musculu	804	79	7.0	629	2	Q5ELR7_DROME	Q5elr7 drosophila		
732	79.5	7.0	1212	2	O42347_CHICK	O42347 gallus gall	805	79	7.0	629	2	Q5ELR9_DROME	Q5elr9 drosophila		
733	79.5	7.0	1237	2	Q7WYN2_9CLOT	Q7wyn2 acetivibrio	806	79	7.0	629	2	Q5ELS8_DROME	Q5els8 drosophila		
734	79.5	7.0	1241	2	Q75JC0_DICDI	Q75jc0 dictyosteli	807	79	7.0	629	2	Q5ELT0_DROME	Q5elt0 drosophila		
735	79.5	7.0	1350	2	Q5T9D2_HUMAN	Q5t9d2 homo sapien	808	79	7.0	629	2	Q5ELT4_DROME	Q5elt4 drosophila		
736	79.5	7.0	1403	2	Q5VX81_HUMAN	Q5vx81 homo sapien	809	79	7.0	629	2	Q5ELU4_DROME	Q5elu4 drosophila		
737	79.5	7.0	1416	2	Q5VX78_HUMAN	Q5vx78 homo sapien	810	79	7.0	629	2	Q5ELV0_DROME	Q5elv0 drosophila		
738	79.5	7.0	1431	2	Q5VX75_HUMAN	Q5vx75 homo sapien	811	79	7.0	629	2	Q9V3H7_DROME	Q9v3h7 drosophila		
739	79.5	7.0	1441	2	Q8GU94_ORYSA	Q8gu94 oryza sativ	812	79	7.0	669	2	Q7EZY9_ORYSA	Q7ezy9 oryza sativ		
740	79.5	7.0	1441	2	Q8S628_ORYSA	Q8s628 oryza sativ	813	79	7.0	729	2	Q8BW38_MOUSE	Q8bw38 mus musculu		
741	79.5	7.0	1459	1	LPHN2_HUMAN	O95490 homo sapien	814	79	7.0	732	2	Q5CEB1_CRYHO	Q5ceb1 cryptospori		
742	79.5	7.0	1461	2	Q5VX77_HUMAN	Q5vx77 homo sapien	815	79	7.0	785	2	Q7QQI5_GIALA	Q7qqi5 giardia lam		
743	79.5	7.0	1474	2	Q5VX80_HUMAN	Q5vx80 homo sapien	816	79	7.0	849	2	Q5R7V6_PONPY	Q5r7v6 pongo pygma		
744	79.5	7.0	1486	2	Q967Y2_DROME	Q967y2 drosophila	817	79	7.0	893	2	Q9LHT1_ARATH	Q9lht1 arabidopsis		
745	79.5	7.0	1486	2	Q95RE5_DROME	Q95re5 drosophila	818	79	7.0	919	2	Q76EQ4_STRRT	Q76eq4 streptococc		
746	79.5	7.0	1486	2	Q7KRP7_DROME	Q7krp7 drosophila	819	79	7.0	927	2	Q5DLW0_9VIRU	Q5dlw0 sea perch i		
747	79.5	7.0	1582	2	Q7KRP6_DROME	Q7krp6 drosophila	820	79	7.0	980	2	Q9MA13_ARATH	Q9ma13 arabidopsis		
748	79.5	7.0	1684	2	Q5EEP1_9VIRU	Q5eep1 crimean-con	821	79	7.0	1011	2	Q54B35_DICDI	Q54b35 dictyosteli		
749	79.5	7.0	1707	2	Q6PMR4_9VIRU	Q6pmr4 swine hepat	822	79	7.0	1015	2	Q55MZ8_CRYNE	Q55mz8 cryptococcu		
750	79.5	7.0	1806	2	Q869R4_DICDI	Q869r4 dictyosteli	823	79	7.0	1036	2	Q4PED6_USTMA	Q4ped6 ustilago ma		
751	79.5	7.0	2053	2	Q51SB6_MAGGR	Q51sb6 magnaporthe	824	79	7.0	1142	2	Q6CCL7_YARLI	Q6ccl7 yarrowia li		
752	79.5	7.0	2082	2	Q7PQ78_ANOGA	Q7pq78 anopheles g	825	79	7.0	1157	2	Q5HZI5_MOUSE	Q5hzi5 mus musculu		
753	79.5	7.0	2314	2	Q55F23_DICDI	Q55f23 dictyosteli	826	79	7.0	1221	2	Q54VR9_DICDI	Q54vr9 dictyosteli		
754	79.5	7.0	2425	2	Q4FX61_LEIMA	Q4fx61 leishmania	827	79	7.0	1266	2	Q4X245_ASPFU	Q4x245 aspergillus		
755	79.5	7.0	5703	1	MUC5B_HUMAN	Q9hc84 homo sapien	828	79	7.0	1368	2	Q52E29_MAGGR	Q52e29 magnaporthe		
756	79	7.0	195	2	Q9W4V3_DROME	Q9w4v3 drosophila	829	79	7.0	1436	2	Q54WY3_DICDI	Q54wy3 dictyosteli		
757	79	7.0	202	2	Q7XLD8_ORYSA	Q7xld8 oryza sativ	830	79	7.0	1689	2	Q8QZF4_9VIRU	Q8qzf4 crimean-con		
758	79	7.0	213	2	Q6ZU27_HUMAN	Q6zu27 homo sapien	831	79	7.0	1689	2	Q8QZF5_9VIRU	Q8qzf5 crimean-con		
759	79	7.0	249	2	Q6BVX5_DEBHA	Q6bvx5 debaryomyce	832	79	7.0	1689	2	Q991H9_9VIRU	Q991h9 crimean-con		
760	79	7.0	249	2	Q9SJQ4_ARATH	Q9sjq4 arabidopsis	833	79	7.0	1752	2	Q9AE52_RUMFL	Q9ae52 ruminococcu		
761	79	7.0	261	2	Q70CC2_EIMTE	Q70cc2 eimeria ten	834	79	7.0	2616	1	NUDEL_DROME	P98159 drosophila		

835	78.5	6.9	94	2	O61030_TRYCR	O61030	trypanosoma
836	78.5	6.9	142	2	Q26943_TRYCR	Q26943	trypanosoma
837	78.5	6.9	164	2	Q14851_HUMAN	Q14851	homo sapien
838	78.5	6.9	215	2	Q4KE04_PSEF5	Q4ke04	pseudomonas
839	78.5	6.9	231	2	Q8EZW6_LEPIN	Q8ezw6	leptospira
840	78.5	6.9	232	2	Q27423_DROVI	Q27423	drosophila
841	78.5	6.9	233	2	Q5DH54_SCHJA	Q5dh54	schistosoma
842	78.5	6.9	252	2	Q80G93_9MONO	Q80g93	avian pneum
843	78.5	6.9	258	2	Q6TV72_9POXV	Q6tv72	bovine papu
844	78.5	6.9	262	2	Q9JMF0_MOUSE	Q9jmf0	mus musculu
845	78.5	6.9	271	2	Q71DD6_DROYA	Q71dd6	drosophila
846	78.5	6.9	283	2	Q6CIR8_KLULA	Q6cir8	kluyveromyc
847	78.5	6.9	285	2	Q86H76_DICDI	Q86h76	dictyosteli
848	78.5	6.9	294	2	Q99322_HUMAN	Q99322	homo sapien
849	78.5	6.9	312	2	Q625S0_CAEBR	Q625s0	caenorhabdi
850	78.5	6.9	322	2	Q62605_RAT	Q62605	rattus norv
851	78.5	6.9	334	2	Q6VAV5_ANOGA	Q6vav5	anopheles g
852	78.5	6.9	334	2	Q6VAV9_ANOGA	Q6vav9	anopheles g
853	78.5	6.9	338	2	Q95Y19_CAEEL	Q95y19	caenorhabdi
854	78.5	6.9	402	2	Q9N503_CAEEL	Q9n503	caenorhabdi
855	78.5	6.9	410	1	GPC5B_MOUSE	Q923z0	mus musculu
856	78.5	6.9	430	2	Q9N4F8_CAEEL	Q9n4f8	caenorhabdi
857	78.5	6.9	497	2	Q58SI7_DROSI	Q58si7	drosophila
858	78.5	6.9	500	2	Q58SI6_DROSI	Q58si6	drosophila
859	78.5	6.9	506	2	Q53QT8_HUMAN	Q53qt8	homo sapien
860	78.5	6.9	522	2	Q4VAS1_HUMAN	Q4vas1	homo sapien
861	78.5	6.9	525	2	Q6CAQ5_YARLI	Q6caq5	yarrowia li
862	78.5	6.9	540	1	CH60_STRAG	Q9ame7	streptococc
863	78.5	6.9	547	2	Q4R5X1_MACFA	Q4r5x1	macaca fasc
864	78.5	6.9	560	2	Q4VAS3_HUMAN	Q4vas3	homo sapien
865	78.5	6.9	562	1	NUPL_HUMAN	P52594	homo sapien
866	78.5	6.9	562	2	Q4VAS0_HUMAN	Q4vas0	homo sapien
867	78.5	6.9	572	2	Q4QGJ6_LEIMA	Q4qgj6	leishmania
868	78.5	6.9	581	2	Q7R0Z5_GIALA	Q7r0z5	giardia lam
869	78.5	6.9	582	2	Q58SG6_DROSI	Q58sg6	drosophila
870	78.5	6.9	585	2	Q58SG4_DROSI	Q58sg4	drosophila
871	78.5	6.9	585	2	Q5SE80_9MONO	Q5se80	avian pneum
872	78.5	6.9	585	2	Q5SE81_9MONO	Q5se81	avian pneum
873	78.5	6.9	589	2	O43419_HUMAN	O43419	homo sapien
874	78.5	6.9	619	2	Q61JP3_CAEBR	Q61jp3	caenorhabdi
875	78.5	6.9	624	2	Q58SF2_DROSI	Q58sf2	drosophila
876	78.5	6.9	624	2	Q58SF4_DROSI	Q58sf4	drosophila
877	78.5	6.9	624	2	Q58SF5_DROSI	Q58sf5	drosophila
878	78.5	6.9	624	2	Q58SF9_DROSI	Q58sf9	drosophila
879	78.5	6.9	624	2	Q5ELN1_DROSI	Q5eln1	drosophila
880	78.5	6.9	624	2	Q5ELN5_DROSI	Q5eln5	drosophila
881	78.5	6.9	624	2	Q5ELN9_DROSI	Q5eln9	drosophila
882	78.5	6.9	627	2	Q8MP19_DICDI	Q8mp19	dictyosteli
883	78.5	6.9	647	2	Q7RYY1_NEUCR	Q7ryy1	neurospora
884	78.5	6.9	681	2	Q555L9_DICDI	Q55519	dictyosteli
885	78.5	6.9	708	2	Q73H41_WOLPM	Q73h41	wolbachia p
886	78.5	6.9	719	2	Q51P83_MAGGR	Q51p83	magnaporthe
887	78.5	6.9	733	2	Q55E25_DICDI	Q55e25	dictyosteli
888	78.5	6.9	763	2	Q965Y7_CAEEL	Q965y7	caenorhabdi
889	78.5	6.9	804	2	Q5RDL3_PONPY	Q5rdl3	pongo pygma
890	78.5	6.9	830	2	Q6CAY0_YARLI	Q6cay0	yarrowia li
891	78.5	6.9	853	2	Q54S28_DICDI	Q54s28	dictyosteli
892	78.5	6.9	858	2	Q9H8D9_HUMAN	Q9h8d9	homo sapien
893	78.5	6.9	889	2	Q4UCE2_THEAN	Q4uce2	theileria a
894	78.5	6.9	915	2	Q4FZU8_RAT	Q4fzu8	rattus norv
895	78.5	6.9	941	2	Q592X0_BRARE	Q592x0	brachydanio
896	78.5	6.9	1159	2	Q55GQ9_DICDI	Q55gq9	dictyosteli
897	78.5	6.9	1236	2	Q9C105_SCHPO	Q9c105	schizosacch
898	78.5	6.9	1487	1	LPHN2_RAT	O88923	rattus norv
899	78.5	6.9	1595	2	Q5SBM3_LACSK	Q5sbm3	lactobacill
900	78.5	6.9	1740	2	Q8ML25_DROME	Q8ml25	drosophila
901	78.5	6.9	1820	2	Q54F55_DICDI	Q54f55	dictyosteli
902	78.5	6.9	1845	2	Q55AX2_DICDI	Q55ax2	dictyosteli
903	78.5	6.9	1983	2	Q9V696_DROME	Q9v696	drosophila
904	78.5	6.9	2378	2	Q7N7Y6_PHOLL	Q7n7y6	photorhabdu
905	78.5	6.9	2381	2	Q54QC0_DICDI	Q54qc0	dictyosteli
906	78.5	6.9	5374	2	Q99ND0_MOUSE	Q99nd0	mus musculu
907	78	6.9	119	2	O61034_TRYCR	O61034	trypanosoma
908	78	6.9	248	2	Q6CFU5_YARLI	Q6cfu5	yarrowia li
909	78	6.9	253	2	P74526_SYNY3	P74526	synechocyst
910	78	6.9	254	2	Q54U47_DICDI	Q54u47	dictyosteli
911	78	6.9	293	2	Q9CCE9_MYCLE	Q9cce9	mycobacteri
912	78	6.9	334	2	Q6VAV4_ANOGA	Q6vav4	anopheles g
913	78	6.9	338	2	Q7WZI1_BACUA	Q7wzi1	bacillus th
914	78	6.9	345	2	Q690V2_ANOSA	Q690v2	anolis sagr
915	78	6.9	345	2	Q690V6_ANOSA	Q690v6	anolis sagr
916	78	6.9	345	2	Q690V7_ANOSA	Q690v7	anolis sagr
917	78	6.9	345	2	Q690X3_ANOSA	Q690x3	anolis sagr
918	78	6.9	345	2	Q692A4_ANOSA	Q692a4	anolis sagr
919	78	6.9	345	2	Q692C2_9SAUR	Q692c2	anolis quad
920	78	6.9	356	2	Q7TFJ3_RHCM6	Q7tfj3	rhesus cyto
921	78	6.9	379	2	Q42763_GOSHI	Q42763	gossypium h
922	78	6.9	397	2	Q55DL3_DICDI	Q55dl3	dictyosteli
923	78	6.9	400	2	Q9SQF7_BRAJU	Q9sqf7	brassica ju
924	78	6.9	405	2	Q95XV0_CAEEL	Q95xv0	caenorhabdi
925	78	6.9	410	2	Q5R5R6_PONPY	Q5r5r6	pongo pygma
926	78	6.9	429	2	Q5KJ46_CRYNE	Q5kj46	cryptococcu
927	78	6.9	434	2	Q9SKN2_ARATH	Q9skn2	arabidopsis
928	78	6.9	444	2	Q5FSE1_GLUOX	Q5fse1	gluconobact
929	78	6.9	453	2	Q870S8_NEUCR	Q870s8	neurospora
930	78	6.9	475	2	Q51JC1_MAGGR	Q51jc1	magnaporthe
931	78	6.9	495	2	Q74847_9HIV1	Q74847	human immun
932	78	6.9	513	2	O43418_HUMAN	O43418	homo sapien
933	78	6.9	526	2	Q5JGD8_PYRKO	Q5jgd8	pyrococcus
934	78	6.9	530	2	Q07701_CHV12	Q07701	cercopithec
935	78	6.9	573	2	Q8T0R9_DROME	Q8t0r9	drosophila
936	78	6.9	578	2	Q50V82_ENTHI	Q50v82	entamoeba h
937	78	6.9	622	2	Q58SH9_DROSI	Q58sh9	drosophila
938	78	6.9	629	2	Q5ELS3_DROME	Q5els3	drosophila
939	78	6.9	629	2	Q5ELS7_DROME	Q5els7	drosophila
940	78	6.9	637	1	CD2AP_MOUSE	Q9jlq0	mus musculu
941	78	6.9	637	2	Q7TSS5_RAT	Q7tss5	rattus norv
942	78	6.9	689	2	Q724Q0_LISMF	Q724q0	listeria mo
943	78	6.9	699	2	Q6CSM7_KLULA	Q6csm7	kluyveromyc
944	78	6.9	753	2	Q54SK9_DICDI	Q54sk9	dictyosteli
945	78	6.9	759	2	O05143_RUMFL	O05143	ruminococcu
946	78	6.9	796	2	Q5CW90_CRYPV	Q5cw90	cryptospori
947	78	6.9	823	2	Q6C159_YARLI	Q6c159	yarrowia li
948	78	6.9	907	2	Q6CTD8_KLULA	Q6ctd8	kluyveromyc
949	78	6.9	916	2	Q9W4A6_DROME	Q9w4a6	drosophila
950	78	6.9	925	2	Q7XFP0_ORYSA	Q7xfp0	oryza sativ
951	78	6.9	984	2	Q4UEB9_THEAN	Q4ueb9	theileria a
952	78	6.9	994	2	Q5KBC7_CRYNE	Q5kbc7	cryptococcu
953	78	6.9	1000	2	Q95QH6_CAEEL	Q95qh6	caenorhabdi
954	78	6.9	1033	2	Q4HYJ6_GIBZE	Q4hyj6	gibberella
955	78	6.9	1046	2	Q4SDR0_TETNG	Q4sdr0	tetraodon n
956	78	6.9	1050	2	O16436_CAEEL	O16436	caenorhabdi
957	78	6.9	1091	1	NCAM1_CHICK	P13590	gallus gall
958	78	6.9	1167	2	Q54CK8_DICDI	Q54ck8	dictyosteli
959	78	6.9	1250	2	Q54GP5_DICDI	Q54gp5	dictyosteli
960	78	6.9	1280	2	Q5BGG9_EMENI	Q5bgg9	aspergillus
961	78	6.9	1589	2	Q54I34_DICDI	Q54i34	dictyosteli
962	78	6.9	1723	1	PMP20_CHLPN	Q9z812	chlamydia p
963	78	6.9	1822	2	Q7R0W4_GIALA	Q7r0w4	giardia lam
964	78	6.9	1955	1	AGRN_CHICK	P31696	gallus gall
965	78	6.9	2119	2	Q4FX59_LEIMA	Q4fx59	leishmania
966	78	6.9	2162	2	Q70PP2_DROME	Q70pp2	drosophila
967	78	6.9	3218	2	Q9W3V6_DROME	Q9w3v6	drosophila
968	78	6.9	3529	2	Q9GP30_THEPA	Q9gp30	theileria p
969	78	6.9	3529	2	Q4N9U4_THEPA	Q4n9u4	theileria p
970	78	6.9	4540	2	Q55EG2_DICDI	Q55eg2	dictyosteli
971	77.5	6.8	215	2	Q6CBZ1_YARLI	Q6cbz1	yarrowia li
972	77.5	6.8	219	2	Q61B16_CAEBR	Q61b16	caenorhabdi
973	77.5	6.8	238	1	SPRR3_MOUSE	O09116	mus musculu
974	77.5	6.8	250	2	Q8FSI6_COREF	Q8fsi6	corynebacte
975	77.5	6.8	260	2	Q6ND60_RHOPA	Q6nd60	rhodopseudo
976	77.5	6.8	270	2	Q82IY9_STRAW	Q82iy9	streptomyce
977	77.5	6.8	278	2	Q4I579_GIBZE	Q4i579	gibberella
978	77.5	6.8	299	2	Q4HYT1_GIBZE	Q4hyt1	gibberella
979	77.5	6.8	302	2	Q4I5S3_GIBZE	Q4i5s3	gibberella
980	77.5	6.8	346	2	Q52J82_9SAUR	Q52j82	heteronotia

981	77.5	6.8	370	2	Q9XWN5_CAEEL	Q9xwn5 caenorhabdi	1054	77	6.8	345	2	Q691Y6_ANOSA	Q691y6 anolis sagr		
982	77.5	6.8	425	2	Q702W3_HHV1	Q702w3 human herpe	1055	77	6.8	345	2	Q691Z2_ANOSA	Q691z2 anolis sagr		
983	77.5	6.8	430	2	Q6K4M7_ORYSA	Q6k4m7 oryza sativ	1056	77	6.8	350	2	Q9RT72_DEIRA	Q9rt72 deinococcus		
984	77.5	6.8	447	2	Q8SBG8_BPSF5	Q8sbg8 bacteriopha	1057	77	6.8	369	2	Q7YUQ4_9TRYP	Q7yuq4 trypanosoma		
985	77.5	6.8	478	2	Q55RT1_CRYNE	Q55rt1 cryptococcu	1058	77	6.8	381	2	Q59MN5_CANAL	Q59mn5 candida alb		
986	77.5	6.8	486	2	Q563C8_AEDAE	Q563c8 aedes aegyp	1059	77	6.8	453	1	MALE_PYRAB	Q9v297 pyrococcus		
987	77.5	6.8	497	2	Q7XHL3_ORYSA	Q7xhl3 oryza sativ	1060	77	6.8	472	2	Q55U45_CRYNE	Q55u45 cryptococcu		
988	77.5	6.8	511	2	Q8UZ62_HHV1	Q8uz62 human herpe	1061	77	6.8	476	2	Q4JQF8_9PEZI	Q4jqf8 chaetomium		
989	77.5	6.8	513	2	Q4U8S8_THEAN	Q4u8s8 theileria a	1062	77	6.8	516	2	Q5CM29_CRYHO	Q5cm29 cryptospori		
990	77.5	6.8	514	1	ACVR2_XENLA	P27039 xenopus lae	1063	77	6.8	521	2	Q54DL6_DICDI	Q54dl6 dictyosteli		
991	77.5	6.8	514	2	Q5D043_XENLA	Q5d043 xenopus lae	1064	77	6.8	540	2	Q4ZZE2_PSESY	Q4zze2 pseudomonas		
992	77.5	6.8	522	2	Q54RY2_DICDI	Q54ry2 dictyosteli	1065	77	6.8	573	2	Q5CWJ4_CRYPV	Q5cwj4 cryptospori		
993	77.5	6.8	540	1	CH60_STRSA	Q8kj16 streptococc	1066	77	6.8	598	2	Q20747_CAEEL	Q20747 caenorhabdi		
994	77.5	6.8	542	2	Q54SA9_DICDI	Q54sa9 dictyosteli	1067	77	6.8	608	2	Q4IK10_GIBZE	Q4ik10 gibberella		
995	77.5	6.8	547	2	Q8IV81_HUMAN	Q8iv81 homo sapien	1068	77	6.8	615	2	Q5AQW3_EMENI	Q5aqw3 aspergillus		
996	77.5	6.8	550	2	Q70KA7_9ACTO	Q70ka7 gordonia we	1069	77	6.8	625	2	Q58SF7_DROSI	Q58sf7 drosophila		
997	77.5	6.8	561	2	Q4KLH5_RAT	Q4klh5 rattus norv	1070	77	6.8	626	2	Q61LN4_CAEBR	Q61ln4 caenorhabdi		
998	77.5	6.8	577	2	Q6FSJ1_CANGA	Q6fsj1 candida gla	1071	77	6.8	632	2	Q5ELU2_DROME	Q5elu2 drosophila		
999	77.5	6.8	592	2	Q23036_CAEEL	Q23036 caenorhabdi	1072	77	6.8	708	2	Q7R9K7_PLAYO	Q7r9k7 plasmodium		
1000	77.5	6.8	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus	1073	77	6.8	713	1	POLH_HUMAN	Q9y253 homo sapien		
1001	77.5	6.8	623	2	O17562_CAEEL	O17562 caenorhabdi	1074	77	6.8	714	2	Q59TK9_CANAL	Q59tk9 candida alb		
1002	77.5	6.8	624	2	Q7SD58_NEUCR	Q7sd58 neurospora	1075	77	6.8	714	2	Q59TP1_CANAL	Q59tp1 candida alb		
1003	77.5	6.8	636	2	Q59H38_HUMAN	Q59h38 homo sapien	1076	77	6.8	717	2	Q8U1H5_PYRFU	Q8u1h5 pyrococcus		
1004	77.5	6.8	668	2	Q5B5D4_EMENI	Q5b5d4 aspergillus	1077	77	6.8	750	2	Q9HFZ4_CANAL	Q9hfz4 candida alb		
1005	77.5	6.8	688	1	SLAP2_CLOTM	Q06853 clostridium	1078	77	6.8	771	1	TMEM8_HUMAN	Q9hcn3 homo sapien		
1006	77.5	6.8	760	2	Q6PJF7_HUMAN	Q6pjf7 homo sapien	1079	77	6.8	771	2	Q4TT35_HUMAN	Q4tt35 homo sapien		
1007	77.5	6.8	806	2	Q9VCQ7_DROME	Q9vcq7 drosophila	1080	77	6.8	772	2	Q82YF8_STRAW	Q82yf8 streptomyce		
1008	77.5	6.8	820	2	Q520Y8_MAGGR	Q520y8 magnaporthe	1081	77	6.8	773	2	Q6IDE4_DROME	Q6ide4 drosophila		
1009	77.5	6.8	839	2	Q614L9_CAEBR	Q61419 caenorhabdi	1082	77	6.8	802	2	Q7YVP9_9TRYP	Q7yvp9 trypanosoma		
1010	77.5	6.8	939	2	Q592X1_BRARE	Q592x1 brachydanio	1083	77	6.8	902	2	Q8Q7H5_9HIV1	Q8q7h5 human immun		
1011	77.5	6.8	941	2	Q592W6_BRARE	Q592w6 brachydanio	1084	77	6.8	941	2	Q7Z5R7_HUMAN	Q7z5r7 homo sapien		
1012	77.5	6.8	941	2	Q592W7_BRARE	Q592w7 brachydanio	1085	77	6.8	948	2	Q8NDA4_HUMAN	Q8nda4 homo sapien		
1013	77.5	6.8	951	1	SFRS8_HUMAN	Q12872 homo sapien	1086	77	6.8	956	2	Q4SFS4_TETNG	Q4sfs4 tetraodon n		
1014	77.5	6.8	982	2	Q6CGV5_YARLI	Q6cgv5 yarrowia li	1087	77	6.8	979	2	Q6C863_YARLI	Q6c863 yarrowia li		
1015	77.5	6.8	1085	2	Q4QHD4_LEIMA	Q4qhd4 leishmania	1088	77	6.8	980	2	Q5TPB2_ANOGA	Q5tpb2 anopheles g		
1016	77.5	6.8	1118	2	Q6CX19_KLULA	Q6cx19 kluyveromyc	1089	77	6.8	1055	2	Q55PJ4_CRYNE	Q55pj4 cryptococcu		
1017	77.5	6.8	1127	2	Q9C608_ARATH	Q9c608 arabidopsis	1090	77	6.8	1072	2	Q4G0A4_HUMAN	Q4g0a4 homo sapien		
1018	77.5	6.8	1258	2	Q4RGJ4_TETNG	Q4rgj4 tetraodon n	1091	77	6.8	1081	2	Q59EA1_HUMAN	Q59ea1 homo sapien		
1019	77.5	6.8	1316	2	Q7Q8U5_ANOGA	Q7q8u5 anopheles g	1092	77	6.8	1092	1	NCA12_XENLA	P36335 xenopus lae		
1020	77.5	6.8	1383	2	Q874K9_CANAL	Q874k9 candida alb	1093	77	6.8	1168	2	Q8S7C7_ORYSA	Q8s7c7 oryza sativ		
1021	77.5	6.8	1390	2	Q54GX9_DICDI	Q54gx9 dictyosteli	1094	77	6.8	1168	2	Q7XC17_ORYSA	Q7xc17 oryza sativ		
1022	77.5	6.8	1765	2	Q54WL2_DICDI	Q54wl2 dictyosteli	1095	77	6.8	1184	2	Q4IHX0_GIBZE	Q4ihx0 gibberella		
1023	77.5	6.8	1842	2	Q4N830_THEPA	Q4n830 theileria p	1096	77	6.8	1205	2	Q6IE70_RAT	Q6ie70 rattus norv		
1024	77.5	6.8	1845	2	Q86JH8_DICDI	Q86jh8 dictyosteli	1097	77	6.8	1223	2	Q6ZS17_HUMAN	Q6zs17 homo sapien		
1025	77.5	6.8	1873	2	Q6S003_DICDI	Q6s003 dictyosteli	1098	77	6.8	1285	2	Q4RXD7_TETNG	Q4rxd7 tetraodon n		
1026	77.5	6.8	1878	2	Q6CPZ4_KLULA	Q6cpz4 kluyveromyc	1099	77	6.8	1346	2	Q54SH1_DICDI	Q54sh1 dictyosteli		
1027	77.5	6.8	2761	2	Q19522_CAEEL	Q19522 caenorhabdi	1100	77	6.8	1404	2	Q59SG9_CANAL	Q59sg9 candida alb		
1028	77.5	6.8	3300	2	Q4N127_THEPA	Q4n127 theileria p	1101	77	6.8	1462	2	Q550D3_DICDI	Q550d3 dictyosteli		
1029	77.5	6.8	4630	2	Q7UWM5_RHOBA	Q7uwm5 rhodopirell	1102	77	6.8	1462	2	Q86AR5_DICDI	Q86ar5 dictyosteli		
1030	77	6.8	178	2	Q5B5J0_EMENI	Q5b5j0 aspergillus	1103	77	6.8	1513	1	MUC2_RAT	Q62635 rattus norv		
1031	77	6.8	187	2	Q4R111_CAEEL	Q4r111 caenorhabdi	1104	77	6.8	1521	2	Q8CHS9_MOUSE	Q8chs9 mus musculu		
1032	77	6.8	187	2	Q77AU9_LYCVW	Q77au9 lymphocytic	1105	77	6.8	1649	2	Q60K37_CAEBR	Q60k37 caenorhabdi		
1033	77	6.8	187	2	Q77AV0_LYCVW	Q77av0 lymphocytic	1106	77	6.8	1706	2	Q7TGF2_9VIRU	Q7tgf2 hepatitis e		
1034	77	6.8	187	2	Q9YJ85_LYCVW	Q9yj85 lymphocytic	1107	77	6.8	1937	2	Q5CY21_CRYPV	Q5cy21 cryptospori		
1035	77	6.8	187	2	Q9YPM0_LYCVW	Q9ypm0 lymphocytic	1108	77	6.8	2112	2	Q80U93_MOUSE	Q80u93 mus musculu		
1036	77	6.8	213	2	Q6M959_NEUCR	Q6m959 neurospora	1109	77	6.8	2176	2	Q54VP0_DICDI	Q54vp0 dictyosteli		
1037	77	6.8	277	2	Q5A5U6_CANAL	Q5a5u6 candida alb	1110	77	6.8	2187	1	NACAM_MOUSE	P70670 mus musculu		
1038	77	6.8	292	2	Q7QJA0_ANOGA	Q7qja0 anopheles g	1111	77	6.8	2300	2	Q7SFP6_NEUCR	Q7sfp6 neurospora		
1039	77	6.8	321	2	Q4IK96_GIBZE	Q4ik96 gibberella	1112	77	6.8	2316	1	PTPRZ_RAT	Q62656 rattus norv		
1040	77	6.8	340	2	Q57HE0_SALCH	Q57he0 salmonella	1113	77	6.8	2566	2	Q8TSE7_METAC	Q8tse7 methanosarc		
1041	77	6.8	340	2	Q8ZKQ1_SALTY	Q8zkq1 salmonella	1114	77	6.8	3443	2	Q8JZM8_MOUSE	Q8jzm8 mus musculu		
1042	77	6.8	345	2	Q690T8_ANOSA	Q690t8 anolis sagr	1115	77	6.8	4782	2	Q8K1G6_MOUSE	Q8k1g6 mus musculu		
1043	77	6.8	345	2	Q690U2_ANOSA	Q690u2 anolis sagr	1116	77	6.8	6011	2	Q4U447_POLCB	Q4u447 polyangium		
1044	77	6.8	345	2	Q690U5_ANOSA	Q690u5 anolis sagr	1117	77	6.8	11696	2	Q5CV09_CRYPV	Q5cv09 cryptospori		
1045	77	6.8	345	2	Q690U6_ANOSA	Q690u6 anolis sagr	1118	76.5	6.7	123	2	O15773_TRYCR	O15773 trypanosoma		
1046	77	6.8	345	2	Q690U8_ANOSA	Q690u8 anolis sagr	1119	76.5	6.7	232	2	Q69EW2_STRBO	Q69ew2 streptococc		
1047	77	6.8	345	2	Q690V1_ANOSA	Q690v1 anolis sagr	1120	76.5	6.7	250	2	Q59UP6_CANAL	Q59up6 candida alb		
1048	77	6.8	345	2	Q690W8_ANOSA	Q690w8 anolis sagr	1121	76.5	6.7	250	2	Q9HFS1_CANAL	Q9hfs1 candida alb		
1049	77	6.8	345	2	Q690X6_ANOSA	Q690x6 anolis sagr	1122	76.5	6.7	266	2	Q4HZD3_GIBZE	Q4hzd3 gibberella		
1050	77	6.8	345	2	Q690X8_ANOSA	Q690x8 anolis sagr	1123	76.5	6.7	299	2	Q825U2_STRAW	Q825u2 streptomyce		
1051	77	6.8	345	2	Q691U6_ANOSA	Q691u6 anolis sagr	1124	76.5	6.7	300	2	Q6CCZ0_YARLI	Q6ccz0 yarrowia li		
1052	77	6.8	345	2	Q691Y0_ANOSA	Q691y0 anolis sagr	1125	76.5	6.7	304	2	Q6AW28_BACTU	Q6aw28 bacillus th		
1053	77	6.8	345	2	Q691Y1_ANOSA	Q691y1 anolis sagr	1126	76.5	6.7	308	2	Q9BRD2_HUMAN	Q9brd2 homo sapien		

1127	76.5	6.7	345	2	Q6UJM5_9SAUR	Q6ujm5	diplodactyl	1200	76	6.7	309	2	Q7S0P9_NEUCR	Q7s0p9	neurospora		
1128	76.5	6.7	346	2	Q52JE0_9SAUR	Q52je0	heteronotia	1201	76	6.7	313	2	Q8BEJ1_9POXV	Q8bej1	skunkpox vi		
1129	76.5	6.7	346	2	Q52JD9_9SAUR	Q52jd9	heteronotia	1202	76	6.7	340	2	Q8Z2X8_SALTI	Q8z2x8	salmonella		
1130	76.5	6.7	346	2	Q52JB6_9SAUR	Q52jb6	heteronotia	1203	76	6.7	345	2	Q690T5_ANOSA	Q690t5	anolis sagr		
1131	76.5	6.7	346	2	Q52J84_9SAUR	Q52j84	heteronotia	1204	76	6.7	345	2	Q690T7_ANOSA	Q690t7	anolis sagr		
1132	76.5	6.7	346	2	Q52J86_9SAUR	Q52j86	heteronotia	1205	76	6.7	345	2	Q690U0_ANOSA	Q690u0	anolis sagr		
1133	76.5	6.7	349	2	Q9UF43_HUMAN	Q9uf43	homo sapien	1206	76	6.7	345	2	Q690U1_ANOSA	Q690u1	anolis sagr		
1134	76.5	6.7	357	2	Q8NJZ0_BIOOC	Q8njz0	bionectria	1207	76	6.7	345	2	Q690U3_ANOSA	Q690u3	anolis sagr		
1135	76.5	6.7	358	2	Q6CCM7_YARLI	Q6ccm7	yarrowia li	1208	76	6.7	345	2	Q690W5_ANOSA	Q690w5	anolis sagr		
1136	76.5	6.7	360	2	Q4HV07_GIBZE	Q4hv07	gibberella	1209	76	6.7	345	2	Q690W9_ANOSA	Q690w9	anolis sagr		
1137	76.5	6.7	385	2	Q9NHU9_DROMI	Q9nhu9	drosophila	1210	76	6.7	345	2	Q691G5_ANOSA	Q691g5	anolis sagr		
1138	76.5	6.7	433	2	Q9K6G1_BACHD	Q9k6g1	bacillus ha	1211	76	6.7	345	2	Q691G8_ANOSA	Q691g8	anolis sagr		
1139	76.5	6.7	452	2	Q6SYY7_CANAL	Q6syy7	candida alb	1212	76	6.7	345	2	Q691Q6_ANOSA	Q691q6	anolis sagr		
1140	76.5	6.7	456	2	Q61PC9_CAEBR	Q61pc9	caenorhabdi	1213	76	6.7	345	2	Q691T7_ANOSA	Q691t7	anolis sagr		
1141	76.5	6.7	457	2	Q86AK1_DICDI	Q86ak1	dictyosteli	1214	76	6.7	345	2	Q691U4_ANOSA	Q691u4	anolis sagr		
1142	76.5	6.7	457	2	Q51DZ6_ENTHI	Q51dz6	entamoeba h	1215	76	6.7	345	2	Q692A0_ANOSA	Q692a0	anolis sagr		
1143	76.5	6.7	459	2	Q55D89_DICDI	Q55d89	dictyosteli	1216	76	6.7	345	2	Q692A2_ANOSA	Q692a2	anolis sagr		
1144	76.5	6.7	490	2	Q753Y1_ASHGO	Q753y1	ashbya goss	1217	76	6.7	345	2	Q692A3_ANOSA	Q692a3	anolis sagr		
1145	76.5	6.7	491	2	Q59ZU0_CANAL	Q59zu0	candida alb	1218	76	6.7	345	2	Q8WDI1_ANOSA	Q8wdi1	anolis sagr		
1146	76.5	6.7	505	2	Q14395_HUMAN	Q14395	homo sapien	1219	76	6.7	360	2	Q4WG94_ASPFU	Q4wg94	aspergillus		
1147	76.5	6.7	514	2	Q5AYH4_EMENI	Q5ayh4	aspergillus	1220	76	6.7	368	1	VE2_HPV45	P36794	human papil		
1148	76.5	6.7	520	2	Q6CTM5_KLULA	Q6ctm5	kluyveromyc	1221	76	6.7	370	2	Q9FN39_ARATH	Q9fn39	arabidopsis		
1149	76.5	6.7	533	2	Q51Z81_MAGGR	Q51z81	magnaporthe	1222	76	6.7	372	2	Q5HS25_STAEQ	Q5hs25	staphylococ		
1150	76.5	6.7	542	2	Q59145_9GAMM	Q59145	aeromonas s	1223	76	6.7	372	2	Q8CQM2_STAEP	Q8cqm2	staphylococ		
1151	76.5	6.7	576	2	Q5CVT9_CRYPV	Q5cvt9	cryptospori	1224	76	6.7	374	2	Q8EC31_SHEON	Q8ec31	shewanella		
1152	76.5	6.7	601	2	Q4JUC4_CORJK	Q4juc4	corynebacte	1225	76	6.7	389	1	ADHA_CLOAB	Q04944	clostridium		
1153	76.5	6.7	634	1	HWP1_CANAL	P46593	candida alb	1226	76	6.7	415	2	Q641C6_XENLA	Q641c6	xenopus lae		
1154	76.5	6.7	634	2	Q59TL7_CANAL	Q59tl7	candida alb	1227	76	6.7	428	2	Q86DA4_CAEEL	Q86da4	caenorhabdi		
1155	76.5	6.7	645	2	Q4H446_HYLJA	Q4h446	hyla japoni	1228	76	6.7	429	2	Q7JMU4_CAEEL	Q7jmu4	caenorhabdi		
1156	76.5	6.7	653	1	LRRC4_HUMAN	Q9hbw1	homo sapien	1229	76	6.7	431	1	YMH7_CAEEL	P34474	caenorhabdi		
1157	76.5	6.7	658	1	SHK1_SCHPO	P50527	schizosacch	1230	76	6.7	441	2	Q72NA6_LEPIC	Q72na6	leptospira		
1158	76.5	6.7	676	2	Q9VB94_DROME	Q9vb94	drosophila	1231	76	6.7	441	2	Q8F895_LEPIN	Q8f895	leptospira		
1159	76.5	6.7	695	2	Q802U4_BRARE	Q802u4	brachydanio	1232	76	6.7	452	2	Q9ADQ9_STAAU	Q9adq9	staphylococ		
1160	76.5	6.7	703	2	Q75YM4_STRPN	Q75ym4	streptococc	1233	76	6.7	457	2	Q524Z4_MAGGR	Q524z4	magnaporthe		
1161	76.5	6.7	718	2	Q23447_CAEEL	Q23447	caenorhabdi	1234	76	6.7	468	2	O55279_ADEGX	O55279	avian adeno		
1162	76.5	6.7	750	2	O39307_9ALPH	O39307	equid herpe	1235	76	6.7	495	2	Q58SI2_DROSI	Q58si2	drosophila		
1163	76.5	6.7	862	2	Q615W4_CAEBR	Q615w4	caenorhabdi	1236	76	6.7	495	2	Q58SK3_DROSI	Q58sk3	drosophila		
1164	76.5	6.7	862	2	Q8K0T1_MOUSE	Q8k0t1	mus musculu	1237	76	6.7	508	2	Q8GYU2_ARATH	Q8gyu2	arabidopsis		
1165	76.5	6.7	912	2	Q54JE2_DICDI	Q54je2	dictyosteli	1238	76	6.7	509	2	Q6UXI9_HUMAN	Q6uxi9	homo sapien		
1166	76.5	6.7	939	2	Q592W8_BRARE	Q592w8	brachydanio	1239	76	6.7	522	2	Q58SM8_DROME	Q58sm8	drosophila		
1167	76.5	6.7	943	1	YL61_SCHPO	Q8tfg9	schizosacch	1240	76	6.7	522	2	Q58SN0_DROME	Q58sn0	drosophila		
1168	76.5	6.7	948	2	Q54KH7_DICDI	Q54kh7	dictyosteli	1241	76	6.7	522	2	Q58SN3_DROME	Q58sn3	drosophila		
1169	76.5	6.7	954	2	Q610Z8_CAEBR	Q610z8	caenorhabdi	1242	76	6.7	522	2	Q58SN4_DROME	Q58sn4	drosophila		
1170	76.5	6.7	1011	2	Q9NHZ9_HELPN	Q9nhz9	helicoverpa	1243	76	6.7	532	2	O01972_CAEEL	O01972	caenorhabdi		
1171	76.5	6.7	1023	2	Q7M009_SCMVC	Q7m009	simian cyto	1244	76	6.7	534	2	Q7PAE0_RICSI	Q7pae0	rickettsia		
1172	76.5	6.7	1201	2	Q8EZH2_LEPIN	Q8ezh2	leptospira	1245	76	6.7	544	2	Q5Y9C0_LACPA	Q5y9c0	lactobacill		
1173	76.5	6.7	1223	2	Q68FE6_MOUSE	Q68fe6	mus musculu	1246	76	6.7	545	2	Q4PFW4_USTMA	Q4pfw4	ustilago ma		
1174	76.5	6.7	1230	2	Q54JY4_DICDI	Q54jy4	dictyosteli	1247	76	6.7	549	2	Q9M1B1_ARATH	Q9m1b1	arabidopsis		
1175	76.5	6.7	1259	2	Q72MU1_LEPIC	Q72mu1	leptospira	1248	76	6.7	563	2	Q7PMB9_ANOGA	Q7pmb9	anopheles g		
1176	76.5	6.7	1262	2	Q80T73_MOUSE	Q80t73	mus musculu	1249	76	6.7	565	2	Q5B4U2_EMENI	Q5b4u2	aspergillus		
1177	76.5	6.7	1284	2	Q8RQU9_BACGO	Q8rqu9	bacillus gl	1250	76	6.7	569	2	Q9SL10_ARATH	Q9sl10	arabidopsis		
1178	76.5	6.7	1326	2	Q6FR84_CANGA	Q6fr84	candida gla	1251	76	6.7	570	2	Q61N12_CAEBR	Q61n12	caenorhabdi		
1179	76.5	6.7	1401	2	Q54MH9_DICDI	Q54mh9	dictyosteli	1252	76	6.7	576	2	Q06604_YEAST	Q06604	saccharomyc		
1180	76.5	6.7	1414	2	Q53MF8_ORYSA	Q53mf8	oryza sativ	1253	76	6.7	582	2	Q58SG7_DROSI	Q58sg7	drosophila		
1181	76.5	6.7	1420	2	Q4FWR7_LEIMA	Q4fwr7	leishmania	1254	76	6.7	582	2	Q58SG8_DROSI	Q58sg8	drosophila		
1182	76.5	6.7	1578	2	Q55C84_DICDI	Q55c84	dictyosteli	1255	76	6.7	582	2	Q58SG9_DROSI	Q58sg9	drosophila		
1183	76.5	6.7	1672	1	PMPB_CHLMU	Q9pjy2	chlamydia m	1256	76	6.7	582	2	Q58SH3_DROSI	Q58sh3	drosophila		
1184	76.5	6.7	1674	2	Q80Z18_MOUSE	Q80z18	mus musculu	1257	76	6.7	585	2	Q58SH0_DROSI	Q58sh0	drosophila		
1185	76.5	6.7	1696	2	Q69Q09_ORYSA	Q69q09	oryza sativ	1258	76	6.7	586	2	Q50PH5_ENTHI	Q50ph5	entamoeba h		
1186	76.5	6.7	1704	2	Q54H52_DICDI	Q54h52	dictyosteli	1259	76	6.7	595	2	Q7R2J1_GIALA	Q7r2j1	giardia lam		
1187	76.5	6.7	2269	2	Q5CWU1_CRYPV	Q5cwu1	cryptospori	1260	76	6.7	598	2	Q5ELV4_DROSI	Q5elv4	drosophila		
1188	76.5	6.7	2306	2	Q4WYG2_ASPFU	Q4wyg2	aspergillus	1261	76	6.7	598	2	Q5ELV5_DROSI	Q5elv5	drosophila		
1189	76.5	6.7	2335	2	Q7YYR5_CRYPV	Q7yyr5	cryptospori	1262	76	6.7	598	2	Q5ELV8_DROSI	Q5elv8	drosophila		
1190	76.5	6.7	3088	2	Q68CH7_STRCZ	Q68ch7	streptomyce	1263	76	6.7	598	2	Q5ELW0_DROSI	Q5elw0	drosophila		
1191	76.5	6.7	3176	2	Q6V7I2_EAV	Q6v7i2	equine arte	1264	76	6.7	607	2	Q4V8G0_RAT	Q4v8g0	rattus norv		
1192	76.5	6.7	3176	2	Q6V7J1_EAV	Q6v7j1	equine arte	1265	76	6.7	612	2	Q7NY06_CHRVO	Q7ny06	chromobacte		
1193	76.5	6.7	4015	2	Q4YTY6_PLABE	Q4yty6	plasmodium	1266	76	6.7	622	2	Q6V6D8_DROSI	Q6v6d8	drosophila		
1194	76.5	6.7	4736	2	Q7YT99_MYTGA	Q7yt99	mytilus gal	1267	76	6.7	622	2	Q6V6E2_DROSI	Q6v6e2	drosophila		
1195	76	6.7	162	2	Q4X239_ASPFU	Q4x239	aspergillus	1268	76	6.7	622	2	Q6V6E4_DROSI	Q6v6e4	drosophila		
1196	76	6.7	167	2	Q14883_HUMAN	Q14883	homo sapien	1269	76	6.7	622	2	Q58SF6_DROSI	Q58sf6	drosophila		
1197	76	6.7	243	2	Q25335_LEIMA	Q25335	leishmania	1270	76	6.7	622	2	Q58SG2_DROSI	Q58sg2	drosophila		
1198	76	6.7	269	2	Q9VLN8_DROME	Q9vln8	drosophila	1271	76	6.7	622	2	Q5ELQ5_DROSI	Q5elq5	drosophila		
1199	76	6.7	301	2	Q924F9_GEOBU	Q924f9	geomys burs	1272	76	6.7	622	2	Q5ELQ9_DROSI	Q5elq9	drosophila		

1273	76	6.7	625	2	Q58SF3_DROSI	Q58sf3	drosophila
1274	76	6.7	625	2	Q58SH8_DROSI	Q58sh8	drosophila
1275	76	6.7	625	2	Q5ELN3_DROSI	Q5eln3	drosophila
1276	76	6.7	625	2	Q6V6E1_DROSI	Q6v6e1	drosophila
1277	76	6.7	653	2	Q73TB8_MYCPA	Q73tb8	mycobacteri
1278	76	6.7	676	2	Q54PX8_DICDI	Q54px8	dictyosteli
1279	76	6.7	679	2	Q69HN9_CIOIN	Q69hn9	ciona intes
1280	76	6.7	686	2	Q61XJ6_CAEBR	Q61xj6	caenorhabdi
1281	76	6.7	686	2	Q50194_MYCLE	Q50194	mycobacteri
1282	76	6.7	725	2	Q6JAD6_MAIZE	Q6jad6	zea mays (m
1283	76	6.7	729	2	Q51WE3_MAGGR	Q51we3	magnaporthe
1284	76	6.7	768	2	Q8J2T4_GRIFR	Q8j2t4	grifola fro
1285	76	6.7	812	2	Q86AW3_DICDI	Q86aw3	dictyosteli
1286	76	6.7	822	2	Q54Z52_DICDI	Q54z52	dictyosteli
1287	76	6.7	823	2	Q54Y28_DICDI	Q54y28	dictyosteli
1288	76	6.7	858	2	Q5TYT7_BRARE	Q5tyt7	brachydanio
1289	76	6.7	922	2	Q95U05_DROME	Q95u05	drosophila
1290	76	6.7	927	2	Q52F88_MAGGR	Q52f88	magnaporthe
1291	76	6.7	937	2	Q4Q7L1_LEIMA	Q4q7l1	leishmania
1292	76	6.7	962	2	Q4K4X8_PSEF5	Q4k4x8	pseudomonas
1293	76	6.7	981	2	Q54SW0_DICDI	Q54sw0	dictyosteli
1294	76	6.7	981	2	Q6GQI9_XENLA	Q6gqi9	xenopus lae
1295	76	6.7	1016	1	ENG1_SCHPO	Q9ut45	schizosacch
1296	76	6.7	1067	2	Q6BUL7_DEBHA	Q6bul7	debaryomyce
1297	76	6.7	1094	2	Q4P201_USTMA	Q4p201	ustilago ma
1298	76	6.7	1154	2	Q54PP7_DICDI	Q54pp7	dictyosteli
1299	76	6.7	1194	2	Q6C4Z0_YARLI	Q6c4z0	yarrowia li
1300	76	6.7	1216	2	Q527R4_MAGGR	Q527r4	magnaporthe
1301	76	6.7	1228	2	Q44334_9RHIZ	Q44334	agrobacteri
1302	76	6.7	1263	2	Q8T0M2_DROME	Q8t0m2	drosophila
1303	76	6.7	1267	2	Q54TJ5_DICDI	Q54tj5	dictyosteli
1304	76	6.7	1269	2	Q54CA1_DICDI	Q54ca1	dictyosteli
1305	76	6.7	1360	2	Q9TYK4_CAEEL	Q9tyk4	caenorhabdi
1306	76	6.7	1423	2	Q6CRU1_KLULA	Q6cru1	kluyveromyc
1307	76	6.7	1426	2	Q9X3P6_9FIRM	Q9x3p6	caldicellul
1308	76	6.7	1462	2	Q9V5Q8_DROME	Q9v5q8	drosophila
1309	76	6.7	1489	2	O23302_ARATH	O23302	arabidopsis
1310	76	6.7	1505	2	Q55DJ9_DICDI	Q55dj9	dictyosteli
1311	76	6.7	1586	2	Q59SN8_CANAL	Q59sn8	candida alb
1312	76	6.7	1588	2	Q59SR0_CANAL	Q59sr0	candida alb
1313	76	6.7	1689	2	Q911R1_9VIRU	Q911r1	crimean-con
1314	76	6.7	1789	2	Q8T145_DICDI	Q8t145	dictyosteli
1315	76	6.7	1828	2	Q54VB5_DICDI	Q54vb5	dictyosteli
1316	76	6.7	2957	2	Q4REV8_TETNG	Q4rev8	tetraodon n
1317	76	6.7	5376	1	ZAN_MOUSE	O88799	mus musculu
1318	75.5	6.6	127	2	O61035_TRYCR	O61035	trypanosoma
1319	75.5	6.6	154	2	Q4VT13_9CONI	Q4vt13	pinus chiap
1320	75.5	6.6	161	2	Q522F4_MAGGR	Q522f4	magnaporthe
1321	75.5	6.6	169	2	Q870Y2_NEUCR	Q870y2	neurospora
1322	75.5	6.6	193	2	Q8XTI3_RALSO	Q8xti3	ralstonia s
1323	75.5	6.6	194	2	Q9Y9W0_AERPE	Q9y9w0	aeropyrum p
1324	75.5	6.6	198	2	Q4WAE1_ASPFU	Q4wae1	aspergillus
1325	75.5	6.6	228	2	Q8HZB6_9PRIM	Q8hzb6	gorilla gor
1326	75.5	6.6	232	2	Q69EV5_STRBO	Q69ev5	streptococc
1327	75.5	6.6	232	2	Q69EV7_STRBO	Q69ev7	streptococc
1328	75.5	6.6	232	2	Q69EV8_STRBO	Q69ev8	streptococc
1329	75.5	6.6	232	2	Q69EX1_STRBO	Q69ex1	streptococc
1330	75.5	6.6	260	2	O27007_METTH	O27007	methanobact
1331	75.5	6.6	266	2	Q5A0C8_CANAL	Q5a0c8	candida alb
1332	75.5	6.6	273	2	P87519_BHV4	P87519	bovine herp
1333	75.5	6.6	273	2	Q99CZ0_BHV4	Q99cz0	bovine herp
1334	75.5	6.6	275	2	Q55K40_CRYNE	Q55k40	cryptococcu
1335	75.5	6.6	275	2	Q5K9F9_CRYNE	Q5k9f9	cryptococcu
1336	75.5	6.6	275	2	Q8DLY5_SYNEL	Q8dly5	synechococc
1337	75.5	6.6	282	2	Q8L8N4_ARATH	Q8l8n4	arabidopsis
1338	75.5	6.6	299	2	Q8ZZP6_PYRAE	Q8zzp6	pyrobaculum
1339	75.5	6.6	300	2	Q95XH5_CAEEL	Q95xh5	caenorhabdi
1340	75.5	6.6	301	2	Q4I1K5_GIBZE	Q4i1k5	gibberella
1341	75.5	6.6	306	2	Q5BFA2_EMENI	Q5bfa2	aspergillus
1342	75.5	6.6	306	2	Q88V34_LACPL	Q88v34	lactobacill
1343	75.5	6.6	313	2	Q57LA1_SALCH	Q57la1	salmonella
1344	75.5	6.6	321	2	Q9XUL7_CAEEL	Q9xul7	caenorhabdi
1345	75.5	6.6	329	2	Q6FIA0_HUMAN	Q6fia0	homo sapien
1346	75.5	6.6	329	2	Q9NWV8_HUMAN	Q9nwv8	homo sapien
1347	75.5	6.6	329	2	Q5R7L2_PONPY	Q5r7l2	pongo pygma
1348	75.5	6.6	330	2	Q86AR7_DICDI	Q86ar7	dictyosteli
1349	75.5	6.6	346	2	Q9TFU7_9SAUR	Q9tfu7	teratoscinc
1350	75.5	6.6	346	2	Q52J83_9SAUR	Q52j83	heteronotia
1351	75.5	6.6	346	2	Q52J75_9SAUR	Q52j75	heteronotia
1352	75.5	6.6	346	2	Q52J73_9SAUR	Q52j73	heteronotia
1353	75.5	6.6	355	2	Q554K2_DICDI	Q554k2	dictyosteli
1354	75.5	6.6	360	2	Q4SSY6_TETNG	Q4ssy6	tetraodon n
1355	75.5	6.6	385	2	Q8T8L4_DROMI	Q8t8l4	drosophila
1356	75.5	6.6	385	2	Q9N666_DROMI	Q9n666	drosophila
1357	75.5	6.6	385	2	Q9NHU6_DROMI	Q9nhu6	drosophila
1358	75.5	6.6	385	2	Q9NHU7_DROMI	Q9nhu7	drosophila
1359	75.5	6.6	395	2	Q4HAL0_9DEIO	Q4hal0	deinococcus
1360	75.5	6.6	397	2	Q702W7_HHV1	Q702w7	human herpe
1361	75.5	6.6	397	2	Q702X1_HHV1	Q702x1	human herpe
1362	75.5	6.6	420	2	Q8N7W9_HUMAN	Q8n7w9	homo sapien
1363	75.5	6.6	430	1	PO2F3_RAT	P42571	rattus norv
1364	75.5	6.6	445	2	Q4NLM7_9MICC	Q4nlm7	arthrobacte
1365	75.5	6.6	456	2	Q584V6_9TRYP	Q584v6	trypanosoma
1366	75.5	6.6	459	2	Q54G90_DICDI	Q54g90	dictyosteli
1367	75.5	6.6	464	2	Q90WQ6_ONCMY	Q90wq6	oncorhynchu
1368	75.5	6.6	468	1	VAS1_BOVIN	P40682	bos taurus
1369	75.5	6.6	469	2	Q54P62_DICDI	Q54p62	dictyosteli
1370	75.5	6.6	469	2	Q82S40_NITEU	Q82s40	nitrosomona
1371	75.5	6.6	476	2	Q9C1S9_HUMIN	Q9c1s9	humicola in
1372	75.5	6.6	478	2	Q5KG84_CRYNE	Q5kg84	cryptococcu
1373	75.5	6.6	478	2	O61122_DICDI	O61122	dictyosteli
1374	75.5	6.6	481	2	Q9VWK3_DROME	Q9vwk3	drosophila
1375	75.5	6.6	492	2	Q94HR9_ARATH	Q94hr9	arabidopsis
1376	75.5	6.6	496	1	CWLB_BACSU	Q02114	bacillus su
1377	75.5	6.6	496	2	Q54PX0_DICDI	Q54px0	dictyosteli
1378	75.5	6.6	500	2	Q54L47_DICDI	Q54l47	dictyosteli
1379	75.5	6.6	505	2	Q61PF3_CAEBR	Q61pf3	caenorhabdi
1380	75.5	6.6	511	1	VGLC_HHV11	P10228	human herpe
1381	75.5	6.6	511	2	Q8UYA4_HHV1	Q8uya4	human herpe
1382	75.5	6.6	511	2	Q8UYE2_HHV1	Q8uye2	human herpe
1383	75.5	6.6	511	2	Q8UYF2_HHV1	Q8uyf2	human herpe
1384	75.5	6.6	511	2	Q8UZ65_HHV1	Q8uz65	human herpe
1385	75.5	6.6	511	2	Q8UZ68_HHV1	Q8uz68	human herpe
1386	75.5	6.6	511	2	Q8UZ69_HHV1	Q8uz69	human herpe
1387	75.5	6.6	511	2	Q8UZ70_HHV1	Q8uz70	human herpe
1388	75.5	6.6	511	2	Q8UZ71_HHV1	Q8uz71	human herpe
1389	75.5	6.6	511	2	Q9WIW3_HHV1	Q9wiw3	human herpe
1390	75.5	6.6	534	2	Q72BB2_DESVH	Q72bb2	desulfovibr
1391	75.5	6.6	541	2	Q51UA3_MAGGR	Q51ua3	magnaporthe
1392	75.5	6.6	547	1	MUC13_RAT	P97881	rattus norv
1393	75.5	6.6	559	1	NUPL_MOUSE	Q8k2k6	mus musculu
1394	75.5	6.6	560	2	Q4N7W3_THEPA	Q4n7w3	theileria p
1395	75.5	6.6	609	2	Q9A6T7_CAUCR	Q9a6t7	caulobacter
1396	75.5	6.6	610	2	Q52FM4_MAGGR	Q52fm4	magnaporthe
1397	75.5	6.6	613	2	Q51TE4_MAGGR	Q51te4	magnaporthe
1398	75.5	6.6	633	2	Q519D6_ENTHI	Q519d6	entamoeba h
1399	75.5	6.6	639	2	Q8TPL3_METAC	Q8tpl3	methanosarc
1400	75.5	6.6	650	2	Q8EYE4_LEPIN	Q8eye4	leptospira
1401	75.5	6.6	665	2	Q97G25_CLOAB	Q97g25	clostridium
1402	75.5	6.6	696	2	Q5F2D4_MOUSE	Q5f2d4	mus musculu
1403	75.5	6.6	736	2	Q8C0R7_MOUSE	Q8c0r7	mus musculu
1404	75.5	6.6	737	1	KNS1_YEAST	P32350	saccharomyc
1405	75.5	6.6	759	2	Q5HY92_HUMAN	Q5hy92	homo sapien
1406	75.5	6.6	782	2	Q54WL9_DICDI	Q54wl9	dictyosteli
1407	75.5	6.6	783	2	Q63158_RAT	Q63158	rattus norv
1408	75.5	6.6	784	2	Q6CI85_YARLI	Q6ci85	yarrowia li
1409	75.5	6.6	795	2	Q7Q7F0_ANOGA	Q7q7f0	anopheles g
1410	75.5	6.6	817	2	Q6PGX9_BRARE	Q6pgx9	brachydanio
1411	75.5	6.6	859	2	Q5VYE4_HUMAN	Q5vye4	homo sapien
1412	75.5	6.6	864	1	AT7L1_HUMAN	Q9ulk2	homo sapien
1413	75.5	6.6	864	2	Q5B9X1_EMENI	Q5b9x1	aspergillus
1414	75.5	6.6	864	2	Q5MYY2_SIVCZ	Q5myy2	chimpanzee
1415	75.5	6.6	877	2	Q9H3Q6_HUMAN	Q9h3q6	homo sapien
1416	75.5	6.6	877	2	Q8Q7I5_9HIV1	Q8q7i5	human immun
1417	75.5	6.6	878	2	Q9H3Q7_HUMAN	Q9h3q7	homo sapien
1418	75.5	6.6	932	1	RBM12_MACMU	Q8sq27	macaca mula

1419	75.5	6.6	935	2	Q4N3A6_THEPA	Q4n3a6	theileria p
1420	75.5	6.6	942	2	Q7WYN3_9CLOT	Q7wyn3	acetivibrio
1421	75.5	6.6	957	2	O14651_HUMAN	O14651	homo sapien
1422	75.5	6.6	964	2	Q6CDQ6_YARLI	Q6cdq6	yarrowia li
1423	75.5	6.6	1012	2	Q4P4L4_USTMA	Q4p4l4	ustilago ma
1424	75.5	6.6	1020	2	Q688J1_ORYSA	Q688j1	oryza sativ
1425	75.5	6.6	1045	2	Q86T37_HUMAN	Q86t37	homo sapien
1426	75.5	6.6	1045	2	Q5VV36_HUMAN	Q5vv36	homo sapien
1427	75.5	6.6	1206	1	BUN2_DROME	Q24523	drosophila
1428	75.5	6.6	1217	2	Q9UKW9_HUMAN	Q9ukw9	homo sapien
1429	75.5	6.6	1224	2	Q5B1R5_EMENI	Q5b1r5	aspergillus
1430	75.5	6.6	1236	2	Q54WQ2_DICDI	Q54wq2	dictyosteli
1431	75.5	6.6	1246	2	Q51FG7_ENTHI	Q51fg7	entamoeba h
1432	75.5	6.6	1293	2	Q4Q6D9_LEIMA	Q4q6d9	leishmania
1433	75.5	6.6	1320	2	Q86TC9_HUMAN	Q86tc9	homo sapien
1434	75.5	6.6	1320	2	Q5VV35_HUMAN	Q5vv35	homo sapien
1435	75.5	6.6	1388	1	COFA1_HUMAN	P39059	homo sapien
1436	75.5	6.6	1391	2	Q8N3L4_HUMAN	Q8n3l4	homo sapien
1437	75.5	6.6	1414	2	Q80Z22_MOUSE	Q80z22	mus musculu
1438	75.5	6.6	1444	2	Q94KE2_ARATH	Q94ke2	arabidopsis
1439	75.5	6.6	1452	2	Q55DV2_DICDI	Q55dv2	dictyosteli
1440	75.5	6.6	1464	2	Q871F7_NEUCR	Q871f7	neurospora
1441	75.5	6.6	1532	2	Q9LUW1_ARATH	Q9luw1	arabidopsis
1442	75.5	6.6	1825	2	Q748I6_GEOSL	Q748i6	geobacter s
1443	75.5	6.6	2055	2	Q7S659_NEUCR	Q7s659	neurospora
1444	75.5	6.6	2151	2	Q9Y1L3_DROME	Q9y1l3	drosophila
1445	75.5	6.6	2151	2	Q9VPL6_DROME	Q9vpl6	drosophila
1446	75.5	6.6	2850	2	Q80T03_MOUSE	Q80t03	mus musculu
1447	75.5	6.6	5322	2	Q9VPL9_DROME	Q9vpl9	drosophila
1448	75	6.6	94	2	Q14886_HUMAN	Q14886	homo sapien
1449	75	6.6	166	2	Q5IDY2_PINTA	Q5idy2	pinus taeda
1450	75	6.6	168	2	Q9NL63_SARPE	Q9nl63	sarcophaga
1451	75	6.6	201	2	Q6WAZ6_TRYCR	Q6waz6	trypanosoma
1452	75	6.6	249	2	Q4SF86_TETNG	Q4sf86	tetraodon n
1453	75	6.6	253	2	Q6DT07_HELPY	Q6dt07	helicobacte
1454	75	6.6	255	2	Q4IP33_GIBZE	Q4ip33	gibberella
1455	75	6.6	275	2	Q8T4R0_AEDAE	Q8t4r0	aedes aegyp
1456	75	6.6	276	2	Q52BL6_MAGGR	Q52bl6	magnaporthe
1457	75	6.6	278	2	Q4H3L9_CIOIN	Q4h319	ciona intes
1458	75	6.6	310	2	O58861_PYRHO	O58861	pyrococcus
1459	75	6.6	314	2	Q61WW6_CAEBR	Q61ww6	caenorhabdi
1460	75	6.6	315	2	Q6DST9_ARATH	Q6dst9	arabidopsis
1461	75	6.6	318	2	Q96B22_HUMAN	Q96b22	homo sapien
1462	75	6.6	319	2	Q7ZXM3_XENLA	Q7zxm3	xenopus lae
1463	75	6.6	321	2	Q5TPB1_ANOGA	Q5tpb1	anopheles g
1464	75	6.6	328	2	O00446_HUMAN	O00446	homo sapien
1465	75	6.6	333	2	Q92K36_RHIME	Q92k36	rhizobium m
1466	75	6.6	337	2	Q6FUQ8_CANGA	Q6fuq8	candida gla
1467	75	6.6	344	2	Q691Z8_ANOSA	Q691z8	anolis sagr
1468	75	6.6	345	2	Q690W1_ANOSA	Q690w1	anolis sagr
1469	75	6.6	345	2	Q690X0_ANOSA	Q690x0	anolis sagr
1470	75	6.6	345	2	Q691G9_ANOSA	Q691g9	anolis sagr
1471	75	6.6	345	2	Q691M1_ANOSA	Q691m1	anolis sagr
1472	75	6.6	345	2	Q691R1_ANOSA	Q691r1	anolis sagr
1473	75	6.6	345	2	Q691U7_ANOSA	Q691u7	anolis sagr
1474	75	6.6	345	2	Q692A8_ANOSA	Q692a8	anolis sagr
1475	75	6.6	355	2	Q51HS7_MAGGR	Q51hs7	magnaporthe
1476	75	6.6	370	2	Q9N4A9_CAEEL	Q9n4a9	caenorhabdi
1477	75	6.6	382	2	Q4PHJ5_USTMA	Q4phj5	ustilago ma
1478	75	6.6	402	2	Q60JK0_CAEBR	Q60jk0	caenorhabdi
1479	75	6.6	420	2	Q5RAU1_PONPY	Q5rau1	pongo pygma
1480	75	6.6	424	2	Q8ZT35_PYRAE	Q8zt35	pyrobaculum
1481	75	6.6	427	2	Q54RN1_DICDI	Q54rn1	dictyosteli
1482	75	6.6	429	2	Q55T95_CRYNE	Q55t95	cryptococcu
1483	75	6.6	430	2	Q5CF57_CRYHO	Q5cf57	cryptospori
1484	75	6.6	435	2	Q5A792_CANAL	Q5a792	candida alb
1485	75	6.6	439	2	Q5TWJ2_ANOGA	Q5twj2	anopheles g
1486	75	6.6	440	2	Q4HUF2_GIBZE	Q4huf2	gibberella
1487	75	6.6	468	1	ALS2_CANAL	O74657	candida alb
1488	75	6.6	468	2	Q9URQ0_CANAL	Q9urq0	candida alb
1489	75	6.6	469	2	Q7JJ48_CERAE	Q7jj48	cercopithec
1490	75	6.6	474	2	O46597_CERAE	O46597	cercopithec
1491	75	6.6	475	2	O22794_ARATH	O22794	arabidopsis
1492	75	6.6	491	1	Y1270_CORGL	P42531	corynebacte
1493	75	6.6	532	2	Q6P7V2_MOUSE	Q6p7v2	mus musculu
1494	75	6.6	542	2	Q8PF22_XANAC	Q8pf22	xanthomonas
1495	75	6.6	544	1	CH60_LACZE	O32847	lactobacill
1496	75	6.6	554	1	CHIT_MANSE	P36362	manduca sex
1497	75	6.6	554	2	Q8CCJ9_MOUSE	Q8ccj9	mus musculu
1498	75	6.6	574	2	Q5CME1_CRYHO	Q5cme1	cryptospori
1499	75	6.6	590	2	Q5GSE0_WOLTR	Q5gse0	wolbachia s
1500	75	6.6	604	2	O13845_SCHPO	O13845	schizosacch

ALIGNMENTS

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RESULT 1
Q9UNF4_HUMAN
ID   Q9UNF4_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q9UNF4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hyaluronic acid receptor (XLKD1).
GN   Name=HAR; ORFNames=UNQ230;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AF127670; AAD49220.2; -; mRNA.
DR   EMBL; AY358925; AAQ89284.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSG00000133800; Homo sapiens.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
SQ   SEQUENCE   322 AA;  35213 MW;  8B4D6D623F52D559 CRC64;

  Query Match           100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-90;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 235


RESULT 2
Q8TC18_HUMAN
ID   Q8TC18_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q8TC18;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Extracellular link domain containing 1.
GN   Name=XLKD1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026231; AAH26231.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSG00000133800; Homo sapiens.
DR   HGNC; HGNC:14687; XLKD1.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35183 MW;  0B1EDBD76CE4610A CRC64;

  Query Match             98.8%;  Score 1122;  DB 2;  Length 322;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-88;
  Matches  219;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIRKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 235


RESULT 3
Q9Y5Y7_HUMAN
ID   Q9Y5Y7_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q9Y5Y7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA   Jackson D.G.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
DR   EMBL; AF118108; AAD42764.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006928; P:cell motility; TAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
SQ   SEQUENCE   322 AA;  35238 MW;  0EBEA56729CEFFF7 CRC64;

  Query Match             98.3%;  Score 1117;  DB 2;  Length 322;
  Best Local Similarity   98.6%;  Pred. No. 3.2e-88;
  Matches  217;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVD 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFGAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSRIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||||
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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 4
Q6UC88_BOVIN
ID   Q6UC88_BOVIN PRELIMINARY;      PRT;   322 AA.
AC   Q6UC88;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cell surface retention sequence binding protein-1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA   Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA   Huang J.S.;
RT   "Cloning, expression, characterization and role in autocrine cell
RT   growth of cell surface retention sequence binding protein-1.";
RL   J. Biol. Chem. 278:43855-43869(2003).
DR   EMBL; AY372937; AAQ85130.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35561 MW;  4901DA1BF92648AE CRC64;

  Query Match             64.3%;  Score 730;  DB 2;  Length 322;
  Best Local Similarity   63.6%;  Pred. No. 9.5e-55;
  Matches  140;  Conservative   31;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              |||||||||||:||:||   |||||:|||:||    ||||||:|||||:||:|| :||||
Db         16 TTRLLVQGSLRSEEISILGPCRIMGVTLVTKKTQPLLNFTEAQEACRLVGLTLASQDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
               | |  ||||||||| : |||| ||  ||||||:||||:||:  :| :  :||:|||| |
Db         76 EARKFGFETCSYGWVKNQFVVIPRIISNPKCGKSGVGVVIWRSSLSSRHRSYCHNSSDIW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              |||:|||||| ||:|||:||| ||: :|||||:|  |         ||  |  |||| ||
Db        136 INSCLPEIITTDDPLFNTETATYTTKLMVSDSTHSELSTDGPDYVTTTVAPPLASTSTPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              ::||||:|| ||:|| ::|| |  ::|: |||||| ||||
Db        196 KRKLICITEAFMDTSAVATERESDIQNRPAFKNEAVGFGG 235


RESULT 5
Q8BHC0_MOUSE
ID   Q8BHC0_MOUSE PRELIMINARY;      PRT;   318 AA.
AC   Q8BHC0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE   cDNA, RIKEN full-length enriched library, clone:1200012G08
DE   product:extra cellular link domain-containing 1, full insert
DE   sequence).
GN   Name=Xlkd1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
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RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC038653; AAH38653.1; -; mRNA.
DR   EMBL; BC038892; AAH38892.1; -; mRNA.
DR   EMBL; AK004726; BAC25094.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSMUSG00000030787; Mus musculus.
DR   MGI; MGI:2136348; Xlkd1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR   GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   318 AA;  34573 MW;  34AA31AEF5430B08 CRC64;

  Query Match             59.9%;  Score 680;  DB 2;  Length 318;
  Best Local Similarity   61.4%;  Pred. No. 2e-50;
  Matches  135;  Conservative   28;  Mismatches   53;  Indels    4;  Gaps    3;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              |||  |||:   ::|||  :|||||: || :  | |:|||||  |||::|||:|| :||||
Db         16 TTRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLGLTLASRDQVE 74

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              :| |: ||||||||||: | || ||  ||:|||| ||||  | |::| |||:||||||
Db         75 SAQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFKAYCHNSSDTW 134

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEPIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              |||||||:||  |: :||  |  ||| || | |  :|| || |   ||  ||  ||: |
Db        135 VNSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT-RAPPLTSMAR 191

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              : | ||:|||: |  ||:|||| || : ||||||||||
Db        192 KTKKICITEVYTEPITMATETEAFVASGAAFKNEAAGFGG 231


RESULT 6
Q99NE4_MOUSE
ID   Q99NE4_MOUSE PRELIMINARY;      PRT;   318 AA.
AC   Q99NE4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hyaluronan receptor precursor.
GN   Name=Xlkd1; Synonyms=LYVE-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;
RA   Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT   "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT   endothelium.";
RL   J. Biol. Chem. 276:19420-19430(2001).
DR   EMBL; AJ311501; CAC33082.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   MGI; MGI:2136348; Xlkd1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR   GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor; Signal.
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FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    318       LYVE-1.
SQ   SEQUENCE   318 AA;  34641 MW;  1248974A16113330 CRC64;

  Query Match             59.9%;  Score 680;  DB 2;  Length 318;
  Best Local Similarity   61.4%;  Pred. No. 2e-50;
  Matches  135;  Conservative   28;  Mismatches   53;  Indels    4;  Gaps    3;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              |||  |||:   ::|||  :|||||: || :  | |:||||| |||::|||:|| :|||| 
Db         16 TTRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLGLTLASRDQVE 74

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              :| |: |||||||||||: | || ||  ||:||||| |||||  | |::| |||:|||||| 
Db         75 SAQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFKAYCHNSSDTW 134

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              |||||||:||  |: :||  |  ||| || | |  :|| || |   ||  ||  ||: | 
Db        135 VNSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT-RAPPLTSMAR 191

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              : | ||:|||: |  ||:|||| || : ||||||||||| 
Db        192 KTKKICITEVYTEPITMATETEAFVASGAAFKNEAAGFGG 231


RESULT 7
Q7YS22_PIG
ID   Q7YS22_PIG  PRELIMINARY;      PRT;   201 AA.
AC   Q7YS22;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA   Sellke F.W., Bianchi C.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY304537; AAP69946.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     201    201
SQ   SEQUENCE   201 AA;  22219 MW;  BAAF34E7EACBBAE3 CRC64;

  Query Match             46.3%;  Score 526.5;  DB 2;  Length 201;
  Best Local Similarity   64.6%;  Pred. No. 2.1e-37;
  Matches  102;  Conservative   20;  Mismatches   33;  Indels    3;  Gaps    2;

Qy         66 SFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI 125
              |||||||||| | |:|| || ||||||||| |||:|:  :|::| |||:||||| |||||
Db          1 SFETCSYGWVKDQFLVIPRIYPNPKCGKNGKGVLVWRHSLSQKFEAYCHNSSDTRTNSCI 60

Qy        126 PEIITTKDPIFNTQTATQTTEFIVSDSTYSVAS--PYSTI-PAPTTTPPAPASTSIPRRK 182
              ||||  | || ||| ||  |||  |:| | | ::  | |::  |   ||    |:|| ||::
Db         61 PEIIPTNDPTFNTNTAPYTTEMTVNDRTSSSSTNGPSSSVMPTVVTTSLPLATTSTPRKR 120

Qy        183 KLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              ||||:|| |||||:|||| ::||: |||||| ||||
Db        121 KLICITEAFMETSTISTETELYIENRTAFKNEAIGFGG 158


RESULT 8
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Q58E15_XENLA
ID   Q58E15_XENLA PRELIMINARY;      PRT;   392 AA.
AC   Q58E15;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092113; AAH92113.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER     392    392
SQ   SEQUENCE   392 AA;  43658 MW;  AF47C05AC550C6A1 CRC64;

  Query Match             21.6%;  Score 245;  DB 2;  Length 392;
  Best Local Similarity   34.9%;  Pred. No. 1.1e-12;
  Matches   58;  Conservative   18;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         19 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 78
              :|||  |:  | |       ||  :| : | :|  |:|   |:| ||   |||| |||: |
Db         33 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTSIANYTQLEIALDFGFETCRYGWIEDR 92

Qy         79 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 128
                |:| || ||| |  |  |:       | ::  ||||:|:|   ||:| :
Db         93 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 151

Qy        129 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 173
               | : ||  :||           ||         | |||    | |
Db        152 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 189
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RESULT 9
Q6GM56_XENLA
ID   Q6GM56_XENLA PRELIMINARY;      PRT;   441 AA.
AC   Q6GM56;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC443701 protein (Fragment).
GN   Name=LOC443701;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC074228; AAH74228.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   441 AA;  49207 MW;  DF9AA596D506D1A1 CRC64;

  Query Match             21.2%;  Score 241;  DB 2;  Length 441;
  Best Local Similarity   34.3%;  Pred. No. 2.7e-12;
  Matches   57;  Conservative   19;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         19 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 78
              :|||  |:  | |     ||  :| : | :|  ::|   |:| ||   |||| |||: |
Db         32 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTTIASYAQLEIALDFGFETCRYGWIEDR 91

Qy         79 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 128
               |:| || ||| | | |:       | ::  ||||:|:|   ||:| :
Db         92 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 150

Qy        129 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 173
               | : ||  :||           ||       | |||    | |
Db        151 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 188


RESULT 10
Q6P8A2_XENTR
ID   Q6P8A2_XENTR PRELIMINARY;      PRT;   437 AA.
AC   Q6P8A2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75816.
GN   Name=MGC75816;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061327; AAH61327.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Hypothetical protein.
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SQ   SEQUENCE   437 AA;  49108 MW;  7088441D0E138C10 CRC64;

  Query Match             19.9%;  Score 226;  DB 2;  Length 437;
  Best Local Similarity   34.1%;  Pred. No. 5.3e-11;
  Matches   61;  Conservative   18;  Mismatches   78;  Indels   22;  Gaps    4;

Qy         19 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 78
              :|||  |: | |      || :| : |  | ::|    :| |    |||| |||: |
Db         24 ISCRFKGVFHVEKYDRYALNREDAIKLCHELNTTIANLTLMEIAQDIGFETCRYGWIEDR 83

Qy         79 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIP----------E 127
               ||| || ||| |  |  |:       | :: |||||:|:|   || |          :
Db         84 -VVIPRIKPNPICAANYTGIFTLGNNDSLRYDAYCYNASETEDKSCEPVLLLNETDLSHK 142

Qy        128 IITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAP---------TTTPPA-PAST 176
               | : ||  :||   :|      |  | :   |    | ||             || |   | ||
Db        143 TIDSYDPTLDTQNPFRTQNSDKSGDTVTDPGPAMITPDPGQDWDDIQGTTDPHGDPFST 201


RESULT 11
CD44_RAT
ID   CD44_RAT       STANDARD;      PRT;   503 AA.
AC   P26051; Q99021;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE   24).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC   STRAIN=BDIX; TISSUE=Pancreas;
RX   MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA   Guenthert U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA   Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT   "A new variant of glycoprotein CD44 confers metastatic potential to
RT   rat carcinoma cells.";
RL   Cell 65:13-24(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RA   Stevens J.W., Midura R.J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SULFATION OF TYR-288.
RX   PubMed=9692903;
RA   Sleeman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT   "CD44 variant exon v5 encodes a tyrosine that is sulphated.";
RL   Eur. J. Biochem. 255:74-80(1998).
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=2; Synonyms=Long, Meta-1;
CC         IsoId=P26051-1; Sequence=Displayed;
CC       Name=1; Synonyms=Short;
CC         IsoId=P26051-2; Sequence=VSP_005330;
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC       can be more or less sulfated (By similarity).
CC   -!- PTM: Phosphorylated; activation of PKC results in the
CC       dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC       and the phosphorylation of Ser-433 (By similarity).
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M61875; AAA53532.1; -; mRNA.
DR   EMBL; M61874; AAA53534.1; -; mRNA.
DR   EMBL; U52179; AAA97915.1; -; mRNA.
DR   EMBL; U46957; AAA92920.1; -; mRNA.
DR   PIR; B38745; B38745.
DR   HSSP; P98066; 1TSG.
DR   SMR; P26051; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0007155; P:cell adhesion; NAS.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW   Sulfation; Transmembrane.
FT   SIGNAL        1     21
FT   CHAIN        22    503       CD44 antigen.
FT   TOPO_DOM     22    410       Extracellular (Potential).
FT   TRANSMEM    411    431       Potential.
FT   TOPO_DOM    432    503       Cytoplasmic (Potential).
FT   DOMAIN       35    124       Link.
FT   REGION      228    410       Stem.
FT   COMPBIAS    154    162       Arg/Lys-rich (basic).
FT   MOD_RES      22     22       Pyrrolidone carboxylic acid (Probable).
FT   MOD_RES     288    288       Sulfotyrosine (in isoform 2).
FT   MOD_RES     433    433       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES     467    467       Phosphoserine (By similarity).
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     60     60       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    114    114       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    124    124       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    266    266       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     56    122       By similarity.
FT   DISULFID     80    100       By similarity.
FT   VARSPLIC    224    385       IATTPWVSAHTKQNQERTQWNPIHSNPEVLLQTTTRMTDID
FT                                RNSTSAHGENWTQEPQPPFNNHEYQDEEETPHATSTTWADP
FT                                NSTTEEAATQKEKWFENEWQGKNPPTPSEDSHVTEGTTASA
FT                                HNNHPSQRMTTQSQEDVSWTDFFDPISHPMGQGHQTESK
FT                                -> SDGDSSMDPRGGFDTVTHGSELA (in isoform
FT                                1).
FT                                /FTId=VSP_005330.
FT   CONFLICT     74     74       R -> S (in Ref. 2).
SQ   SEQUENCE   503 AA;  55946 MW;  FB489D009BD4EE22 CRC64;

  Query Match             18.8%;  Score 213.5;  DB 1;  Length 503;
  Best Local Similarity   32.1%;  Pred. No. 7.6e-10;
  Matches   51;  Conservative   25;  Mismatches   76;  Indels    7;  Gaps    3;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  | || |     :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST 162
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                    |:   : |:     |   :  | | ||    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 167


RESULT 12
O08779_RAT
ID   O08779_RAT  PRELIMINARY;      PRT;   780 AA.
AC   O08779;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD44 protein.
GN   Name=CD44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BDX; TISSUE=Pancreas;
RA   Hofmann M.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U96138; AAB54002.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O08779; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   780 AA;  85917 MW;  CC4D35AB1EA7377C CRC64;

  Query Match             18.8%;  Score 213.5;  DB 2;  Length 780;
  Best Local Similarity   32.1%;  Pred. No. 1.3e-09;
  Matches   51;  Conservative   25;  Mismatches   76;  Indels    7;  Gaps    3;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST 162
                    |:   : |:     |   :  | | ||    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 167


RESULT 13
O70509_RAT
ID   O70509_RAT  PRELIMINARY;      PRT;   364 AA.
AC   O70509;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Glycoprotein CD44s (Cd44 protein).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA   Stevens J.W.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney, and Pituitary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065147; AAC17117.1; -; mRNA.
DR   EMBL; BC061531; AAH61531.1; -; mRNA.
DR   EMBL; BC085703; AAH85703.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O70509; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   364 AA;  39725 MW;  BA249776C4419AA7 CRC64;

  Query Match             18.6%;  Score 211.5;  DB 2;  Length 364;
  Best Local Similarity   32.1%;  Pred. No. 7.7e-10;
  Matches   51;  Conservative   24;  Mismatches   77;  Indels    7;  Gaps    3;

Qy          5 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 64
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALS 74

Qy         65 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 124
                |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
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Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        125 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST 162
                |:   : |:      |   :  | | ||    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRT 167


RESULT 14
Q98SR5_ANAPL
ID   Q98SR5_ANAPL PRELIMINARY;      PRT;   265 AA.
AC   Q98SR5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   T cell antigen CD44 isoform b.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=White Pekin;
RA   Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332869; AAK18277.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   265 AA;  29215 MW;  77C176E0A898D081 CRC64;

  Query Match             18.6%;  Score 211;  DB 2;  Length 265;
  Best Local Similarity   28.4%;  Pred. No. 5.8e-10;
  Matches   62;  Conservative   31;  Mismatches   93;  Indels   32;  Gaps    5;

Qy         14 ELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYG 73
              |    ||||  |:  | |      |  ||| : || |  :|:  :|:| | :  |||| ||
Db         21 ETQFNVSCRYRGVFHVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

Qy         74 WVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIP------- 126
              :|  |::|| ||:|   |  |  |:       : :: |||||:::|   :| |
Db         81 FV-VGYIVIPRINPYHLCAANHTGIYKLSANTTGRYDAYCYNATETRDKACEPIERIDTS 139

Qy        127 ------EIITTKDP-----IFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPAS 175
                   ||:   :         |: :  ::   | |      | : | |  |:   :  |
Db        140 FLSNQGEIVIDNEDGSRYNADGTRHSGDSSTSGVDDENVGSGSSHDTTPVDTSIRRSSPS 199

Qy        176 -----TSIPR--------RKKLICVTEVFMETSTMSTE 200
                  | :|           :|   ||    | |  ||:
Db        200 YYGSVTPVPHLSDHSSGGGEKEFPVTNSDDEISPTSTD 237


RESULT 15
Q90ZL8_ANAPL
ID   Q90ZL8_ANAPL PRELIMINARY;      PRT;   398 AA.
AC   Q90ZL8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   T cell antigen CD44 isoform a.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=White Pekin;
RA   Chan S.W.S., Middleton D.L., Warr G.W., Higgins D.A.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY029553; AAK40246.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   398 AA;  43673 MW;  25A944EE2F4AED6D CRC64;

  Query Match             18.4%;  Score 209.5;  DB 2;  Length 398;
  Best Local Similarity   30.1%;  Pred. No. 1.3e-09;
  Matches   52;  Conservative   27;  Mismatches   75;  Indels   19;  Gaps    3;

Qy         14 ELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYG 73
              |    ||||  |:  | |      |  ||| : || |  :|:  :|:| | :  |||| ||
Db         21 ETQFNVSCRYRGVFHVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

Qy         74 WVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIP------- 126
              :|  |::|| ||:|   |  |  |:       : :: |||||:::|   :| |
Db         81 FV-VGYIVIPRINPYHLCAANHTGIYKLSANTTGRYDAYCYNATETRDKACEPIERIDTS 139

Qy        127 ------EIITTKDP-----IFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTT 168
                   ||:   :         |: :  ::   | |      | : | |  |:
Db        140 FLSNQGEIVIDNEDGSRYNADGTRHSGDSSTSGVDDENVGSGSSHDTTPVDTS 192


Search completed: March 20, 2006, 14:13:19
Job time : 70.4764 secs
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OM protein - protein search, using sw model
Run on:          March 20, 2006, 14:17:31 ; Search time 44.1038 Seconds
                                            (without alignments)
                                            2191.725 Million cell updates/sec
Title:           US-10-063-510-6_COPY_16_235
Perfect score:   1136
Sequence:        1 TTRLLVQGSLRAEELSIQVS.........TEPFVENKAAFKNEAAGFGG 220
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:      2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       A_Geneseq_21:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                SUMMARIES
  No.   Score  Match Length DB  ID                          Description
RESULT 1
ID   AAB34702 standard; protein; 250 AA.
DE   Human secreted protein encoded by DNA clone vb28 1.
PN   WO200055375-A1.
PD   21-SEP-2000.
PA   (ALPH-) ALPHAGENE INC.
  Query Match             100.0%;  Score 1136;  DB 3;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-103;
RESULT 2
ID   AAY13379 standard; protein; 322 AA.
DE   Amino acid sequence of protein PRO263.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 3
ID   AAY87287 standard; protein; 322 AA.
DE   Human signal peptide containing protein HSPP-64 SEQ ID NO:64.
PN   WO200000610-A2.
PD   06-JAN-2000.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             100.0%;  Score 1136;  DB 3;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 4
ID   ADC78521 standard; protein; 322 AA.
DE   Human PRO263 protein.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 3;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 5
ID   AAB80247 standard; protein; 322 AA.
DE   Human PRO263 protein.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 6
ID   AAB87528 standard; protein; 322 AA.
DE   Human PRO263.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 7
ID   AAB88391 standard; protein; 322 AA.
DE   Human membrane or secretory protein clone PSEC0135.
PN   EP1067182-A2.
PD   10-JAN-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             100.0%;  Score 1136;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 8
ID   ABG95853 standard; protein; 322 AA.
DE   Human secreted/transmembrane protein PRO263.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 9
ID   ABB84832 standard; protein; 322 AA.
DE   Human PRO263 protein sequence SEQ ID NO:32.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 10
ID   ABB95438 standard; protein; 322 AA.
DE   Human angiogenesis related protein PRO263 SEQ ID NO: 32.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 1136;  DB 5;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 11
ID   ABU71625 standard; protein; 322 AA.
DE   Human PRO polypeptide #36.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 6;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 12
ID   ABU71480 standard; protein; 322 AA.
DE   Human PRO polypeptide #36.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1136;  DB 6;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
RESULT 13
ID   ABU71926 standard; protein; 322 AA.
DE   Human secreted/transmembrane protein PRO263.
PN   US2003003530-A1.
PD   02-JAN-2003.
```

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 14
ID ABO01809 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 15
ID ABU90878 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 16
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 17
ID ABU71954 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 18
ID ABU54382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 19
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 20
ID ABU71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 21
ID ABU72289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 22
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 23
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 24
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 25
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 26
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 27
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 28
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 29
ID ABO53263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 30
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 31
ID ABU89270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;

Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 32
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 33
ID ABU69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 34
ID ABU96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 35
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 36
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 37
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 38
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 39
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 40
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 41
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 42
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 43
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 44
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 45
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 46
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 47
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 48
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 49
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 50

ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 51
ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 52
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 53
ID ADA41958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 54
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 55
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 56
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 57
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 58
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 59
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 60
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 61
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 62
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 63
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 64
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 65
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 66
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 67
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 68
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 69
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 70
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 71
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 72
ID ADC06962 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 73
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 74
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 75
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 76
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 77
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 78
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 79
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 80
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 81
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 82
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 83
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 84
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 85
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 86
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 87
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 88
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 89
ID ADF95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 90
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 91
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 92
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 93
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 94
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 95
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 96
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 97
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 98
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 99
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 100
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 101
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 102
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 103
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 104
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;

Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 105
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 106
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 107
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 108
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 109
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 110
ID ADH53653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 111
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 112
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 113
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 114
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 115
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 116
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 117
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 118
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 119
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 120
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 121
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 122
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 123

ID ADI11563 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 124
ID ADH98208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 125
ID ADH98548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 126
ID ADH98038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 127
ID ADI05026 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 128
ID ADI03376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 129
ID ADI04771 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 130
ID ADH78225 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 131
ID ADI19569 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 132
ID ADH90317 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 133
ID ADI03036 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 134
ID ADH77885 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 135
ID ADH97868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 136
ID ADI01253 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 137
ID ADI01948 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 138
ID ADI03206 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 139
ID ADI11393 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 140
ID ADI02295 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 141
ID ADI11733 standard; protein; 322 AA.
DE Human PRO polypeptide #3.

PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 142
ID ADI05370 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 143
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 144
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 145
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 146
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 147
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 148
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 149
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 150
ID ADH79782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 151
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 152
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 153
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 154
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 155
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 156
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 157
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 158
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 159
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 160
ID ADL93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 161
ID ADC52144 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 162
ID ADE79279 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 163
ID ADE79703 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 164
ID ADE73379 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 165
ID ADE41282 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 166
ID ADE71444 standard; protein; 322 AA.
DE Human PDEBC Incyte 3044710CD1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 167
ID ADE73914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 168
ID ADE99468 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 169
ID ADE98587 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 170
ID ADE99014 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 171
ID ADG40484 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 172
ID ADF73878 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 173
ID ADF73454 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 174
ID ADH06576 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 175
ID ADH06406 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 176
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;

RESULT 177
ID ADH27717 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 178
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 179
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 180
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 181
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 182
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 183
ID ADG69337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 184
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 185
ID ADG92724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 186
ID ADG83898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 187
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 188
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 189
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 190
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 191
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 192
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 193
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 194
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 195
ID ADH33520 standard; protein; 322 AA.

DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 196
ID ADH33860 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 197
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 198
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 199
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 200
ID ADG69167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 201
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 202
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 203
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 204
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 205
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 206
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 207
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 208
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 209
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 210
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 211
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 212
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 213
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.

PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 214
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 215
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 216
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 217
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 218
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 219
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 220
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 221
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 222
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 223
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 224
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 225
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 226
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 227
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 228
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 229
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 230
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 231
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 232
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 233
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 234
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 235
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 236
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 237
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 238
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 239
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 240
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 241
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 242
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 243
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 244
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 245
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 246
ID ADR11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 247
ID ADR17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.

PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 248
ID ADS74636 standard; protein; 322 AA.
DE Human secreted/transmembrane protein #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 249
ID ADT03673 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 250
ID ADY77701 standard; protein; 322 AA.
DE Neoplastic disease detection protein PRO263.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1136; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 251
ID ADY63147 standard; protein; 322 AA.
DE Human clone PSEC0135 protein, SEQ ID 150.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1136; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 252
ID AEA37911 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 253
ID ABB11979 standard; peptide; 344 AA.
DE Human PRO263 homologue, SEQ ID NO:2349.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1136; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.6e-103;
RESULT 254
ID ADR41495 standard; protein; 344 AA.
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1136; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.6e-103;
RESULT 255
ID AAW56249 standard; protein; 322 AA.
DE Amino acid sequence of a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1130; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 1.3e-102;
RESULT 256
ID ABB90289 standard; protein; 322 AA.
DE Human polypeptide SEQ ID NO 2665.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1130; DB 5; Length 322;
Best Local Similarity 99.5%; Pred. No. 1.3e-102;
RESULT 257
ID ADN05866 standard; protein; 322 AA.
DE Antipsoriatic protein sequence #1096.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.3%; Score 1117; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 2.5e-101;
RESULT 258
ID ADQ21089 standard; protein; 322 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 98.3%; Score 1117; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 2.5e-101;
RESULT 259
ID ABU69126 standard; protein; 297 AA.

DE Human NOVX polypeptide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 87.2%; Score 990.5; DB 6; Length 297;
Best Local Similarity 88.6%; Pred. No. 6.7e-89;
RESULT 260
ID ADO08255 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 87.2%; Score 990.5; DB 8; Length 297;
Best Local Similarity 88.6%; Pred. No. 6.7e-89;
RESULT 261
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.9%; Score 680; DB 5; Length 255;
Best Local Similarity 61.4%; Pred. No. 2.3e-58;
RESULT 262
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.9%; Score 680; DB 4; Length 318;
Best Local Similarity 61.4%; Pred. No. 3.1e-58;
RESULT 263
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 45.3%; Score 515; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
RESULT 264
ID ADW24431 standard; protein; 364 AA.
DE Rat CD44.
PN WO200024869-A2.
PD 04-MAY-2000.
PA (UYYA) UNIV YALE.
PA (VIGN/) VIGNERY A.
Query Match 18.8%; Score 213.5; DB 3; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.8e-12;
RESULT 265
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 18.8%; Score 213.5; DB 5; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.8e-12;
RESULT 266
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 18.8%; Score 213.5; DB 2; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.9e-12;
RESULT 267
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 18.8%; Score 213.5; DB 7; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.9e-12;
RESULT 268
ID ADZ51063 standard; protein; 778 AA.
DE Amino acid sequence of murine CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 18.4%; Score 209.5; DB 9; Length 778;
Best Local Similarity 32.7%; Pred. No. 2.6e-11;
RESULT 269
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.4%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.7e-11;
RESULT 270
ID ADQ39384 standard; protein; 668 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.4%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.7e-11;
RESULT 271
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 17.9%; Score 203.5; DB 2; Length 362;
Best Local Similarity 27.3%; Pred. No. 3.7e-11;
RESULT 272
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.9%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 273
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.

PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.9%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 274
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 17.9%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 275
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 17.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 276
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 277
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 17.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 278
ID ADU06304 standard; protein; 742 AA.
DE Novel bronchial cancer-associated human protein SeqID528.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 17.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 279
ID ADY15336 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1142.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 280
ID ADY15338 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1144.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 281
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 282
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 283
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.8%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 284
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 285
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 286
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 17.8%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 287
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 17.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 288
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 17.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 289
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 290
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.
Query Match 17.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 291
ID ADW72142 standard; protein; 742 AA.
DE Human CD44 protein as biomarker for colorectal cancer.
PN US2005014165-A1.
PD 20-JAN-2005.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 17.8%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 292
ID ADZ51062 standard; protein; 742 AA.
DE Amino acid sequence of human CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 17.8%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.4e-10;
RESULT 293
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.6%; Score 200.5; DB 6; Length 608;
Best Local Similarity 25.2%; Pred. No. 1.5e-10;
RESULT 294
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.6%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 295
ID ADW43570 standard; protein; 699 AA.
DE CD44v3-v10.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.6%; Score 200.5; DB 9; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 296
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 17.6%; Score 200.5; DB 4; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 297
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 200.5; DB 6; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 298
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.6%; Score 200.5; DB 7; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 299
ID ADW43568 standard; protein; 700 AA.
DE CD44vRA.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.6%; Score 200.5; DB 9; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.8e-10;
RESULT 300
ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 17.6%; Score 200; DB 2; Length 58;
Best Local Similarity 97.7%; Pred. No. 7.1e-12;
RESULT 301
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 302
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 303
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 304
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 305
ID AAY96140 standard; protein; 493 AA.
DE Human epithelial CD44.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 3; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 306
ID AAU02449 standard; protein; 493 AA.
DE Human epithelial antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.6%; Score 199.5; DB 4; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 307
ID ABU04637 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1303.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 308
ID ABU04627 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1293.
PN WO200278524-A2.
PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 309
ID ABU04639 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1305.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 310
ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 311
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 312
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 313
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.6%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 314
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 17.6%; Score 199.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 315
ID AEB87764 standard; protein; 493 AA.
DE Human CD44, breast tumor marker.
PN WO2005071419-A2.
PD 04-AUG-2005.
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES.
Query Match 17.6%; Score 199.5; DB 9; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.4e-10;
RESULT 316
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 17.5%; Score 198.5; DB 6; Length 365;
Best Local Similarity 31.8%; Pred. No. 1.2e-10;
RESULT 317
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 17.5%; Score 198.5; DB 7; Length 365;
Best Local Similarity 31.8%; Pred. No. 1.2e-10;
RESULT 318
ID AEA03024 standard; protein; 365 AA.
DE CD14 receptor amino acid sequence SEQ ID NO:50.
PN US2005112141-A1.
PD 26-MAY-2005.
PA (TERM/) TERMAN D S.
Query Match 17.5%; Score 198.5; DB 9; Length 365;
Best Local Similarity 31.8%; Pred. No. 1.2e-10;
RESULT 319
ID AAU99123 standard; protein; 493 AA.
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN WO200244342-A2.
PD 06-JUN-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 17.5%; Score 198.5; DB 5; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.7e-10;
RESULT 320
ID ABU04623 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1289.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 198.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.7e-10;
RESULT 321
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 198.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.7e-10;
RESULT 322
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 17.5%; Score 198.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.7e-10;
RESULT 323
ID ABU04617 standard; protein; 425 AA.
DE Human expressed protein tag (EPT) #1283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 198; DB 6; Length 425;
Best Local Similarity 24.4%; Pred. No. 1.6e-10;
RESULT 324
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 325
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.

PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 326
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 327
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 328
ID AAY99851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 17.3%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 329
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 330
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.3%; Score 197; DB 4; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 331
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 332
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 333
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 334
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 335
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 336
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 337
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 338
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 339
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 340
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 341
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 17.3%; Score 197; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 342
ID ADV70207 standard; protein; 361 AA.
DE Tumor-associated antigenic target polypeptide TAT449.
PN WO2004112829-A2.
PD 29-DEC-2004.

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 197; DB 9; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 343
ID ADY19504 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 5310.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 197; DB 9; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 344
ID AEA63870 standard; protein; 361 AA.
DE Protein of human anti-CD44 antibody.
PN JP2005154389-A.
PD 16-JUN-2005.
PA (UYTY) UNIV TOKYO.
PA (FUJY) FUJI PHARM IND CO LTD.
Query Match 17.3%; Score 197; DB 9; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.6e-10;
RESULT 345
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFAStm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.3%; Score 197; DB 4; Length 431;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 346
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 431;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 347
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/tmFAScyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.3%; Score 197; DB 4; Length 436;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 348
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 436;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 349
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 4e-10;
RESULT 350
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 4e-10;
RESULT 351
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 17.3%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 3.1e-10;
RESULT 352
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.3%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 3.1e-10;
RESULT 353
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 17.3%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 354
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 355
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 356
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 357
ID ADV73230 standard; protein; 699 AA.
DE Human colon tumor cell upregulated protein SEQ ID NO 71.
PN WO2004110345-A2.
PD 23-DEC-2004.
PA (PHAA) PHARMACIA CORP.
Query Match 17.3%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 358
ID ADY16689 standard; protein; 699 AA.
DE PRO polypeptide SEQ ID NO 2495.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.4e-10;
RESULT 359
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 17.3%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 1.3e-10;
RESULT 360
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 17.3%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 361
ID ABU04624 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 362
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 363
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 17.3%; Score 196; DB 8; Length 330;
Best Local Similarity 30.9%; Pred. No. 1.8e-10;
RESULT 364
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 365
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 17.3%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 366
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.3%; Score 196; DB 7; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 367
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 17.3%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 368
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.3%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 369
ID ADW43572 standard; protein; 361 AA.
DE CD44s.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.3%; Score 196; DB 9; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 370
ID ADY16699 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 2505.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 196; DB 9; Length 361;
Best Local Similarity 30.9%; Pred. No. 2e-10;
RESULT 371
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.3%; Score 196; DB 6; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.3e-10;
RESULT 372
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.3%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.3e-10;
RESULT 373
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.3%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 2.5e-10;
RESULT 374
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.3%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 3.1e-10;
RESULT 375
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.1%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 7.4e-10;
RESULT 376
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.1%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 1.4e-10;
RESULT 377
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.1%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 1.5e-10;
RESULT 378
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.1%; Score 194; DB 5; Length 273;

Best Local Similarity 30.8%; Pred. No. 2.2e-10;
RESULT 379
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.1%; Score 194; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 3.2e-10;
RESULT 380
ID ADS75483 standard; protein; 361 AA.
DE Human cell surface glycoprotein CD44 amino acid sequence.
PN JP2004275060-A.
PD 07-OCT-2004.
PA (SANY) SANKYO CO LTD.
Query Match 17.1%; Score 194; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 3.2e-10;
RESULT 381
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.9%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.3e-09;
RESULT 382
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.9%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.3e-09;
RESULT 383
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4.3e-10;
RESULT 384
ID ABU04606 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4.3e-10;
RESULT 385
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.8e-10;
RESULT 386
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.8e-10;
RESULT 387
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 9e-10;
RESULT 388
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 16.8%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 9e-10;
RESULT 389
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 16.5%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 4.6e-10;
RESULT 390
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.5%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 3.3e-10;
RESULT 391
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.4%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.3%; Pred. No. 3.7e-10;
RESULT 392
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.3%; Score 185; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 5.2e-10;
RESULT 393
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 16.2%; Score 184; DB 2; Length 69;
Best Local Similarity 95.1%; Pred. No. 3.4e-10;
RESULT 394
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.1%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 8.1e-10;
RESULT 395
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.0%; Score 182; DB 6; Length 112;

Best Local Similarity 34.2%; Pred. No. 1e-09;
RESULT 396
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 15.9%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 1.3e-09;
RESULT 397
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.4%; Score 175.5; DB 4; Length 920;
Best Local Similarity 25.9%; Pred. No. 7.4e-08;
RESULT 398
ID ADI60410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.4%; Score 175.5; DB 7; Length 920;
Best Local Similarity 25.9%; Pred. No. 7.4e-08;
RESULT 399
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.0%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
RESULT 400
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.0%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
RESULT 401
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.2%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 1.1e-05;
RESULT 402
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 13.1%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 1.3e-06;
RESULT 403
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 7.5e-06;
RESULT 404
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.8%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 1.2e-05;
RESULT 405
ID AAR26044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 12.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 406
ID AAW13654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 12.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 407
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 12.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 408
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 12.8%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 409
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 12.8%; Score 145; DB 5; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 410
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 411
ID ABU56653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 412
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 413
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.

PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 414
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 415
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 416
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 12.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 417
ID ADW38508 standard; protein; 277 AA.
DE Immunomodulatory gene TNFa induced protein 6.
PN WO2005000099-A2.
PD 06-JAN-2005.
PA (GENZ) GENZYME CORP.
Query Match 12.8%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 418
ID AEA23596 standard; protein; 277 AA.
DE Human PRO polypeptide SEQ ID NO 138.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
RESULT 419
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 12.8%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.00031;
RESULT 420
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 12.7%; Score 144; DB 8; Length 275;
Best Local Similarity 33.0%; Pred. No. 1.9e-05;
RESULT 421
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.0044;
RESULT 422
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.0046;
RESULT 423
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 11.6%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0015;
RESULT 424
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 11.6%; Score 131.5; DB 8; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0015;
RESULT 425
ID AEB34752 standard; protein; 883 AA.
DE Mammalian mutant BEHAB protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 11.6%; Score 131.5; DB 9; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0015;
RESULT 426
ID AAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.5%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0019;
RESULT 427
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.5%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0019;
RESULT 428
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevican protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.5%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0019;
RESULT 429
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.5%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0019;
RESULT 430

ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.5%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0019;
RESULT 431
ID ADX15811 standard; protein; 2316 AA.
DE Human aggrecan.
PN WO2005012512-A1.
PD 10-FEB-2005.
PA (NAKA/) NAKAMURA N.
Query Match 11.5%; Score 130.5; DB 9; Length 2316;
Best Local Similarity 27.4%; Pred. No. 0.007;
RESULT 432
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 11.4%; Score 129; DB 5; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0052;
RESULT 433
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 11.4%; Score 129; DB 6; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0052;
RESULT 434
ID AAB08023 standard; protein; 95 AA.
DE The domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 11.3%; Score 128.5; DB 3; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00016;
RESULT 435
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.3%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00016;
RESULT 436
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 4; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0025;
RESULT 437
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.2%; Score 127.5; DB 6; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0025;
RESULT 438
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0025;
RESULT 439
ID ADF71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0025;
RESULT 440
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 8; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0025;
RESULT 441
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 4; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 442
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.2%; Score 127.5; DB 6; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 443
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 444
ID ADF71511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 445
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.

PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.2%; Score 127.5; DB 8; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 446
ID ADV70173 standard; protein; 671 AA.
DE Tumor-associated antigenic target polypeptide TAT152.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 447
ID AEA00138 standard; protein; 671 AA.
DE Human TAT152 protein SEQ ID NO:90.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 448
ID AEA00658 standard; protein; 671 AA.
DE Human TAT152 protein sequence SeqID90.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0026;
RESULT 449
ID ABM83434 standard; protein; 761 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.2%; Score 127.5; DB 8; Length 761;
Best Local Similarity 24.7%; Pred. No. 0.0031;
RESULT 450
ID ADH18892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 11.2%; Score 127.5; DB 8; Length 806;
Best Local Similarity 24.7%; Pred. No. 0.0034;
RESULT 451
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.2%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.0035;
RESULT 452
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.2%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.0037;
RESULT 453
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 11.2%; Score 127.5; DB 6; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0038;
RESULT 454
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.2%; Score 127.5; DB 7; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0038;
RESULT 455
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 11.2%; Score 127.5; DB 8; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0038;
RESULT 456
ID AEB34755 standard; protein; 883 AA.
DE Rat poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 11.2%; Score 127.5; DB 9; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0038;
RESULT 457
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 4; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 458
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 459
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.2%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 460
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 461
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 462
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 463
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.

PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 464
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 465
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 466
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 467
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 468
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 469
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 470
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 471
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 472
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 473
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 474
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 475
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 476
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 477
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 478
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 479
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 480
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 481
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 482
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 483
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 484
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 485
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 486
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 487
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 488
ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 489
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 490
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 491
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 492
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 493
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 494
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 495
ID ADD95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 496
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 497
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 498
ID ADE39444 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 499
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 500
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 501
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 502
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 503
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 504
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 505
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 506
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 507
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 508
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 509
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 510
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 511
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 512
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 513
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 514
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 515
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 516
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 517
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;

RESULT 518
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 519
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 520
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 521
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 522
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 523
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 524
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 525
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 526
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 527.

ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 528
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 529
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 530
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 531
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 532
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 533
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 534
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 535
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 536
ID ADH40040 standard; protein; 911 AA.

DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 537
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 538
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 539
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 540
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 541
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 542
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 543
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 544
ID ADH58488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 545
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 546
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 547
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 548
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 549
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 550
ID ADK67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 551
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 552
ID AEA00137 standard; protein; 911 AA.
DE Human TAT145 protein SEQ ID NO:89.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 553
ID AEA00657 standard; protein; 911 AA.
DE Human TAT145 protein sequence SeqID89.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 554
ID AEB34757 standard; protein; 911 AA.
DE Human poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.

PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 11.2%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 555
ID ABR58557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.2%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00091;
RESULT 556
ID ABU56654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.2%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00091;
RESULT 557
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.2%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00091;
RESULT 558
ID ADO24439 standard; protein; 277 AA.
DE Human PRO87335 protein SEQ ID NO:78.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00091;
RESULT 559
ID ADR14117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 11.2%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00091;
RESULT 560
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.1%; Score 126; DB 8; Length 277;
Best Local Similarity 34.1%; Pred. No. 0.0011;
RESULT 561
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.9%; Score 124; DB 7; Length 482;
Best Local Similarity 34.5%; Pred. No. 0.0038;
RESULT 562
ID ABR82200 standard; protein; 2570 AA.
DE Human CLEVER-1 protein SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Query Match 10.9%; Score 124; DB 6; Length 2570;
Best Local Similarity 34.5%; Pred. No. 0.035;
RESULT 563
ID AAY93911 standard; protein; 457 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.8%; Score 123; DB 3; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.0044;
RESULT 564
ID ABB90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 123; DB 5; Length 1082;
Best Local Similarity 33.3%; Pred. No. 0.014;
RESULT 565
ID AAY93910 standard; protein; 2157 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.8%; Score 123; DB 3; Length 2157;
Best Local Similarity 33.3%; Pred. No. 0.035;
RESULT 566
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 123; DB 8; Length 2570;
Best Local Similarity 33.3%; Pred. No. 0.044;
RESULT 567
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.7%; Score 121.5; DB 8; Length 259;
Best Local Similarity 34.9%; Pred. No. 0.0029;
RESULT 568
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 2; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 569
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 3; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 570
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 571
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 572

ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 573
ID ABU58413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 574
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 575
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 576
ID ABU84276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 577
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 578
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 579
ID ABU99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 580
ID ABU82719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 581
ID ABU89840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 582
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 583
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 584
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 585
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 586
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 587
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 588
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 589
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 590
ID ABU85591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 591
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 592
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 593
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 594
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 595
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 596
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 597
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 598
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 599
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 600
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 601
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 602
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 603
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 604
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 605
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 606
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 607
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 608
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 609
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 610
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 611
ID ABU88666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 612
ID ABU83361 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 613
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 614
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 615
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 616
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 617
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 618
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 619
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 620
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 621
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 622
ID ABU65582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 623
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 624
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 625
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 626
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 627
ID ABU55949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 628
ID ABU65277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 629
ID ABU95222 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 630
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 631
ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 632
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 633
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 634
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 635
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 636
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 637
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 638
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 639
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 640
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 641
ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 642
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 643
ID ABU83056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 644
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 645
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 646
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 647
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 648
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 649
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 650
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 651
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 652
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;

RESULT 653
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 654
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 655
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 656
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 657
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 658
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 659
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 660
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 661
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 662
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 663
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 664
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 665
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 666
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 667
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 668
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 669
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 670
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 671
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 672
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 673
ID ABO04532 standard; protein; 360 AA.

DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 674
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 675
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 676
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 677
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 678
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 679
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 680
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 681
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 682
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 683
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 684
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 685
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 686
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 687
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 688
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 689
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 690
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 691
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 692
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 693
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 694
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 695
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 696
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 697
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 698
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 699
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 700
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 701
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 702
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 703
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 704
ID ABR95533 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 705
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 706
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 707
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 708
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 709
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 710
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 711
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 712
ID ABM07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 713
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 714
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 715
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 716
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 717
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 718
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 719
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 720
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 721
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 722
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 723
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 724
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 725
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 726
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 727
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 728
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 729
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 730
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 731
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 732
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 733
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 734
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 735
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 736
ID ABM11560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 737
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 738
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 739
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 740
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 741
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 742
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 743
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 744
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 745
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 746
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 747
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 748
ID ABM76035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 749
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 750
ID ABM25959 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 751
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 752
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 753
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 754
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 755
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 756
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 757
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 758
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 759
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 760
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 761
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 762
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 763
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 764
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 765
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 766
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 767
ID ABM04855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 768
ID ABM08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 769
ID ABO36415 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 770
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 771
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 772
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 773
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 774
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 775
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 776
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 777
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 778
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 779
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 780
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 781
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 782
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 783
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 784
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 785
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 786
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 787
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 788
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 789
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 790
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 791
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 792
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 793
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 794
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 795
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 796
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 797
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 798
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 799
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 800
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 801
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 802
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 803
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 804
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 805
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 806
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 807
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 808
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 809
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 810
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 811
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 812
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 813
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 814
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 815
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 816
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 817
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 818
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 819
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 820
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 821
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 822
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 823
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 824
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 825
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 826
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 827
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 828
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 829
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 830
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 831
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 832
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 833
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 834
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 835
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 836
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 837
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 838
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 839
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 840
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 841
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 842
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 843
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 844
ID ADA81299 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 845
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 846
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 847
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 848
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 849
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 850
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 851
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 852
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 853
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 854
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 855
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 856
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 857
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 858
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 859
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 860
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 861
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 862
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 863

ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 864
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 865
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 866
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 867
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 868
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 869
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 870
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 871
ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 872
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 873
ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 874
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 875
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 876
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 877
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 878
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 879
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 880
ID ABM06680 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 881
ID ABM09120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 882

ID ABO39160 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 883
ID ABM75425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 884
ID ABM25349 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 885
ID ABM19859 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 886
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 887
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 888
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 889
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 890
ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 891
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 892
ID ABO06820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 893
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 894
ID ABR73331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 895
ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 896
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 897
ID ABM18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 898
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 899
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 900
ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 901
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 902
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 903
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 904
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 905
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 906
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 907
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 908
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 909
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 910
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 911
ID ABM08510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 912
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 913
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 914
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 915
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 916
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 917
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 918
ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 919
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;

RESULT 920
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 921
ID ABR88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 922
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 923
ID ABM03271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 924
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 925
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 926
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 927
ID ABO05247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 928
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 929
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 930
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 931
ID ABM17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 932
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 933
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 934
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 935
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 936
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 937
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 938
ID ABM10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;

RESULT 939
ID ABM76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 940
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 941
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 942
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 943
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 944
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 945
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 946
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 947
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 948
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 949
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 950
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 951
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 952
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 953
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 954
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 955
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 956
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 957
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;

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  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 958
ID   ABM02051 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 959
ID   ABR87213 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 960
ID   ABM12780 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 961
ID   ABM30534 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 962
ID   ABM24434 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 963
ID   ABO29348 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 964
ID   ABO31178 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 965
ID   ABM14305 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 966
ID   ABM09730 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 967
ID   ABO38855 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 968
ID   ABM34620 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003104538-A1.
PD   05-JUN-2003.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 969
ID   ABO51096 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 970
ID   ADA42820 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein, #42.
PN   US2003054351-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 971
ID   ABO03922 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003036158-A1.
PD   20-FEB-2003.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 972
ID   ABO10392 standard; protein; 360 AA.
DE   Human PRO polypeptide #14.
PN   US2003036151-A1.
PD   20-FEB-2003.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 973
ID   ABR77635 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003040067-A1.
PD   27-FEB-2003.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 974
ID   ABR78845 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003054456-A1.
PD   20-MAR-2003.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 975
ID   ABO23939 standard; protein; 360 AA.
DE   Human secreted/transmembrane protein (PRO) #14.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.7%;  Score 121.5;  DB 7;  Length 360;
  Best Local Similarity   34.9%;  Pred. No. 0.0045;
RESULT 976
ID   ABR93703 standard; protein; 360 AA.
DE   Human secreted polypeptide PRO271, SEQ ID NO:28.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
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Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 977
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 978
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 979
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 980
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 981
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 982
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 983
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 984
ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 985
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 986
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 987
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 988
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 989
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 990
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 991
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 992
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 993
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 994
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 995
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 996
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 997
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 998
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 999
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1000
ID ABM22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1001
ID ABM30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1002
ID ABM21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1003
ID ABM21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1004
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1005
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1006
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1007
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1008
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1009
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1010
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1011
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1012
ID ABM31754 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1013
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1014
ID ADB77739 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1015
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1016
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1017
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1018
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1019
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1020
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1021
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1022
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1023
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1024
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1025
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1026
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1027
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1028
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1029
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1030
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1031
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1032
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1033
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1034
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1035
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1036
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1037
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1038
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1039
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1040
ID ADF95378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1041
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1042
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1043
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1044
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1045
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1046
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1047
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1048
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1049
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1050
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1051
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1052
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1053
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1054
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1055
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1056
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1057
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1058
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1059
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1060
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1061
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1062
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1063
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1064
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1065
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1066
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1067
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1068
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1069
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1070
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1071
ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1072
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1073
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1074
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1075
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1076
ID ADI65842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1077
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1078
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1079
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1080
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1081
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1082
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1083
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1084
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1085
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1086
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1087
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1088
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1089
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1090
ID ADR11100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1091
ID ADR18009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1092
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1093
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1094
ID AEA37923 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 9; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1095
ID AEA20028 standard; protein; 422 AA.
DE Novel human polypeptide SEQ ID NO 722.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 10.7%; Score 121.5; DB 9; Length 422;
Best Local Similarity 34.9%; Pred. No. 0.0056;
RESULT 1096
ID AAW59882 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 10.7%; Score 121; DB 2; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1097

ID AAB61241 standard; protein; 528 AA.
DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 121; DB 4; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1098
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 10.7%; Score 121; DB 6; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1099
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1100
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1101
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.7%; Score 121; DB 8; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0084;
RESULT 1102
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 10.6%; Score 120.5; DB 2; Length 912;
Best Local Similarity 24.6%; Pred. No. 0.02;
RESULT 1103
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match 10.5%; Score 119; DB 7; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.011;
RESULT 1104
ID ADJ55382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 119; DB 8; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.011;
RESULT 1105
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.4%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.067;
RESULT 1106
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.4%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.067;
RESULT 1107
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.088;
RESULT 1108
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.088;
RESULT 1109
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.4%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1110
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.4%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1111
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.4%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1112
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.4%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1113
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.4%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1114
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 10.4%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1115
ID ADZ09841 standard; protein; 3396 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 10.4%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1116
ID ADZ70548 standard; protein; 3396 AA.
DE Human protein from lung cancer marker gene CSPG2.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 10.4%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1117
ID AEA04473 standard; protein; 3396 AA.
DE Human protein from gene overexpressed in cancer, CSPG2.
PN WO2005044990-A2.
PD 19-MAY-2005.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 10.4%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1118
ID AEB17604 standard; protein; 3396 AA.
DE Human CSPG2 protein SeqID18.
PN JP2005110602-A.
PD 28-APR-2005.
PA (SUMU) SUMITOMO SEIYAKU KK.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 10.4%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.18;
RESULT 1119
ID ADZ09886 standard; protein; 6792 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 10.4%; Score 118.5; DB 9; Length 6792;
Best Local Similarity 25.5%; Pred. No. 0.45;
RESULT 1120
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 10.3%; Score 116.5; DB 2; Length 1257;
Best Local Similarity 23.9%; Pred. No. 0.074;
RESULT 1121
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.2%; Score 116; DB 8; Length 2397;
Best Local Similarity 28.4%; Pred. No. 0.2;
RESULT 1122
ID AAR85443 standard; protein; 908 AA.
DE Rat brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 10.1%; Score 115; DB 2; Length 908;
Best Local Similarity 22.2%; Pred. No. 0.068;
RESULT 1123
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 114; DB 7; Length 656;
Best Local Similarity 28.4%; Pred. No. 0.055;
RESULT 1124
ID ADP71273 standard; protein; 191 AA.
DE Human LP2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 9.9%; Score 112.5; DB 8; Length 191;
Best Local Similarity 26.6%; Pred. No. 0.015;
RESULT 1125
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 112.5; DB 4; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.026;
RESULT 1126
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.9%; Score 112.5; DB 5; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.026;
RESULT 1127
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 9.9%; Score 112.5; DB 8; Length 340;
Best Local Similarity 26.6%; Pred. No. 0.032;
RESULT 1128
ID ABU11635 standard; protein; 343 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.9%; Score 112.5; DB 6; Length 343;
Best Local Similarity 26.6%; Pred. No. 0.033;
RESULT 1129
ID ABJ10588 standard; protein; 897 AA.
DE Human novel protein NOV1c SEQ ID NO: 211.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 112; DB 5; Length 897;
Best Local Similarity 29.0%; Pred. No. 0.13;

RESULT 1130
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 112; DB 8; Length 897;
Best Local Similarity 29.0%; Pred. No. 0.13;
RESULT 1131
ID ADO09968 standard; protein; 897 AA.
DE Human NOV1c cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 9.9%; Score 112; DB 8; Length 897;
Best Local Similarity 29.0%; Pred. No. 0.13;
RESULT 1132
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 9.9%; Score 112; DB 5; Length 1394;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1133
ID ABG72499 standard; protein; 1416 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 9.9%; Score 112; DB 6; Length 1416;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1134
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 112; DB 8; Length 1502;
Best Local Similarity 29.0%; Pred. No. 0.26;
RESULT 1135
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 112; DB 8; Length 1510;
Best Local Similarity 29.0%; Pred. No. 0.26;
RESULT 1136
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 9.9%; Score 112; DB 6; Length 1653;
Best Local Similarity 29.0%; Pred. No. 0.3;
RESULT 1137
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 9.9%; Score 112; DB 8; Length 1895;
Best Local Similarity 29.0%; Pred. No. 0.36;
RESULT 1138
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 112; DB 8; Length 2551;
Best Local Similarity 29.0%; Pred. No. 0.53;
RESULT 1139
ID ADP71271 standard; protein; 200 AA.
DE Human aggrecan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 9.8%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.022;
RESULT 1140
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match 9.8%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.11;
RESULT 1141
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.8%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.11;
RESULT 1142
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 9.8%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1143
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 9.8%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1144
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.8%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1145
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.8%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1146
ID ADV70260 standard; protein; 2409 AA.
DE Tumor-associated antigenic target polypeptide TAT498.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 111; DB 9; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1147
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.7%; Score 110.5; DB 8; Length 1257;
Best Local Similarity 23.4%; Pred. No. 0.29;
RESULT 1148
ID ABJ10586 standard; protein; 2675 AA.
DE Human novel protein NOV1a SEQ ID NO: 2.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.7%; Score 110; DB 5; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.89;
RESULT 1149
ID ADO09971 standard; protein; 2675 AA.
DE Human NOV1a variant.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 9.7%; Score 110; DB 8; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.89;
RESULT 1150
ID ADO09836 standard; protein; 2675 AA.
DE Human NOV1a.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 9.7%; Score 110; DB 8; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.89;
RESULT 1151
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 9.6%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.075;
RESULT 1152
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.44;
RESULT 1153
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 9.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.44;
RESULT 1154
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.44;
RESULT 1155
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.6%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.44;
RESULT 1156
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.

PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.083;
RESULT 1157
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.083;
RESULT 1158
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.094;
RESULT 1159
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1160
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1161
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1162
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1163
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1164
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1165
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1166
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1167
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1168
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1169
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1170
ID ABJ56899 standard; protein; 354 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1171
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1172
ID ABJ56893 standard; protein; 354 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1173
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1174
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;

Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1175
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1176
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant 121P1F1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1177
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1178
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 108; DB 8; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.095;
RESULT 1179
ID AAR77034 standard; protein; 355 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 9.5%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.095;
RESULT 1180
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.17;
RESULT 1181
ID ABJ56890 standard; protein; 721 AA.
DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.24;
RESULT 1182
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.24;
RESULT 1183
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.24;
RESULT 1184
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 9.4%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.02;
RESULT 1185
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.1;
RESULT 1186
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.1;
RESULT 1187
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.4%; Score 107; DB 3; Length 339;
Best Local Similarity 28.6%; Pred. No. 0.11;
RESULT 1188
ID ABJ56915 standard; protein; 354 AA.
DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.4%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.12;
RESULT 1189
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.4%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.12;
RESULT 1190
ID ABJ56907 standard; protein; 355 AA.
DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.4%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.12;
RESULT 1191
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.2;
RESULT 1192
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.2;

RESULT 1193
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1194
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1195
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1196
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1197
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1198
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.21;
RESULT 1199
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.22;
RESULT 1200
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.4%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 0.34;
RESULT 1201
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.4%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 0.36;
RESULT 1202
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.4%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 0.65;
RESULT 1203
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 1.5;
RESULT 1204
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.5;
RESULT 1205
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 9.4%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.5;
RESULT 1206
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.3%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.27;
RESULT 1207
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.3%; Score 105.5; DB 3; Length 341;
Best Local Similarity 28.9%; Pred. No. 0.16;
RESULT 1208
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.

PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.2%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.19;
RESULT 1209
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.2%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.19;
RESULT 1210
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.067;
RESULT 1211
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.067;
RESULT 1212
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.2%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.067;
RESULT 1213
ID ADY16502 standard; protein; 139 AA.
DE PRO polypeptide SEQ ID NO 2308.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 9.2%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.067;
RESULT 1214
ID AEB29759 standard; protein; 139 AA.
DE Human CD44 isoform RC.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 9.2%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.067;
RESULT 1215
ID ADP71269 standard; protein; 195 AA.
DE Human LP1 protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 9.2%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.11;
RESULT 1216
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 9.2%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.11;
RESULT 1217
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.2%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.42;
RESULT 1218
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.9%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 0.45;
RESULT 1219
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 8.8%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.62;
RESULT 1220
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 8.8%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.62;
RESULT 1221
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.8%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.62;
RESULT 1222
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 8.8%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 0.64;
RESULT 1223
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 8.8%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 0.63;
RESULT 1224
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Query Match 8.8%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 0.77;
RESULT 1225
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.

Query Match 8.7%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.34;
RESULT 1226
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.7%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.34;
RESULT 1227
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.7%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 1.5;
RESULT 1228
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 4.7;
RESULT 1229
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.6%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 9.9;
RESULT 1230
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 3; Length 2870;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1231
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 8; Length 2870;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1232
ID ADW79951 standard; protein; 2870 AA.
DE Nematode location of vulva (lov-1) mutant protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 9; Length 2870;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1233
ID AAY95556 standard; protein; 3178 AA.
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 3; Length 3178;
Best Local Similarity 22.4%; Pred. No. 27;
RESULT 1234
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 8; Length 3178;
Best Local Similarity 22.4%; Pred. No. 27;
RESULT 1235
ID ADW79940 standard; protein; 3178 AA.
DE Nematode location of vulva (lov-1) protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 8.5%; Score 96; DB 9; Length 3178;
Best Local Similarity 22.4%; Pred. No. 27;
RESULT 1236
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.4%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 0.91;
RESULT 1237
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.3%; Score 94.5; DB 4; Length 183;
Best Local Similarity 34.5%; Pred. No. 0.84;
RESULT 1238
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.3%; Score 94.5; DB 4; Length 1795;
Best Local Similarity 33.0%; Pred. No. 18;
RESULT 1239
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID No 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1240
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1241
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.2%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1242
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1243
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID No 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 8.2%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1244
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1245
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.2%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1246
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.7;
RESULT 1247
ID ABP73157 standard; protein; 40 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 8.1%; Score 92.5; DB 6; Length 40;
Best Local Similarity 54.1%; Pred. No. 0.17;
RESULT 1248
ID ADP04445 standard; protein; 1381 AA.
DE Sea squirt protein with tissue specific expression in development Seq40.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 8.1%; Score 92.5; DB 8; Length 1381;
Best Local Similarity 22.6%; Pred. No. 20;
RESULT 1249
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.5;
RESULT 1250
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.5;
RESULT 1251
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.1%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.5;
RESULT 1252
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.5;
RESULT 1253
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.1%; Score 91.5; DB 4; Length 1126;
Best Local Similarity 32.3%; Pred. No. 19;
RESULT 1254
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 8.0%; Score 90.5; DB 6; Length 402;
Best Local Similarity 22.0%; Pred. No. 6;
RESULT 1255
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brsa-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match 8.0%; Score 90.5; DB 8; Length 505;
Best Local Similarity 27.0%; Pred. No. 8.1;
RESULT 1256
ID ABB69419 standard; protein; 1976 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.0%; Score 90.5; DB 4; Length 1976;
Best Local Similarity 38.5%; Pred. No. 50;
RESULT 1257
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.9%; Score 90; DB 8; Length 1103;
Best Local Similarity 23.5%; Pred. No. 26;
RESULT 1258
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 5.8;
RESULT 1259
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 7.8%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1260
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.

PD 18-NOV-1999.
PA (EPIM-) EPIMMUNE INC.
Query Match 7.8%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1261
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 7.8%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1262
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.8%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1263
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 7.8%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1264
ID ADP23231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.8%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1265
ID ADU60107 standard; protein; 416 AA.
DE Housekeeping gene protein, SEQ ID 68.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 7.8%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1266
ID ADW85920 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein-1.
PN WO2005012912-A2.
PD 10-FEB-2005.
PA (CHIR) CHIRON CORP.
Query Match 7.8%; Score 89; DB 9; Length 416;
Best Local Similarity 23.6%; Pred. No. 8.8;
RESULT 1267
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.8%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 11;
RESULT 1268
ID AAY52525 standard; protein; 536 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87.5; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 17;
RESULT 1269
ID AAU96329 standard; protein; 536 AA.
DE Der HMW-map polypeptide #16.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87.5; DB 5; Length 536;
Best Local Similarity 23.9%; Pred. No. 17;
RESULT 1270
ID AAY52523 standard; protein; 555 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87.5; DB 3; Length 555;
Best Local Similarity 23.9%; Pred. No. 18;
RESULT 1271
ID AAU96327 standard; protein; 555 AA.
DE Der HMW-map polypeptide #14.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 18;
RESULT 1272
ID AAU96328 standard; protein; 555 AA.
DE Der HMW-map polypeptide #15.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 18;
RESULT 1273
ID AAW54844 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.7%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1274
ID AAY41778 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.7%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1275
ID AAW89563 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor BoPCaR 1.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.7%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1276
ID AAY51825 standard; protein; 1085 AA.
DE Bovine calcium receptor BoPCaR1 protein.
PN US6031003-A.
PD 29-FEB-2000.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.7%; Score 87.5; DB 3; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1277
ID AAB47820 standard; protein; 1085 AA.
DE BoPCaR1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSP-) NPS PHARM INC.
Query Match 7.7%; Score 87.5; DB 5; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1278
ID ADJ93194 standard; protein; 1085 AA.

DE Bovine extracellular Ca-sensing receptor.
PN WO200296946-A1.
PD 05-DEC-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.7%; Score 87.5; DB 7; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1279
ID ADI40961 standard; protein; 1085 AA.
DE Bovine GPCR CASR.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 7.7%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1280
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 7.7%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1281
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.7%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 6.4;
RESULT 1282
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1283
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1284
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1285
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1286
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1287
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 8.5;
RESULT 1288
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 7.7%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 14;
RESULT 1289
ID AAP91941 standard; peptide; 400 AA.
DE Sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 7.6%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 15;
RESULT 1290
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 7.6%; Score 86.5; DB 2; Length 410;
Best Local Similarity 20.7%; Pred. No. 15;
RESULT 1291
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 7.6%; Score 86.5; DB 2; Length 708;
Best Local Similarity 23.4%; Pred. No. 31;
RESULT 1292
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 21;
RESULT 1293
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 21;
RESULT 1294
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 85.5; DB 5; Length 343;
Best Local Similarity 30.2%; Pred. No. 15;
RESULT 1295
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.

Query Match 7.5%; Score 85.5; DB 3; Length 346;
Best Local Similarity 22.4%; Pred. No. 15;
RESULT 1296
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 7.5%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 15;
RESULT 1297
ID ABB08065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 7.5%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 15;
RESULT 1298
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 7.5%; Score 85.5; DB 6; Length 346;
Best Local Similarity 22.4%; Pred. No. 15;
RESULT 1299
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 16;
RESULT 1300
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.5%; Score 85.5; DB 8; Length 363;
Best Local Similarity 25.6%; Pred. No. 16;
RESULT 1301
ID ADY37611 standard; protein; 363 AA.
DE Lung cancer related protein, SEQ ID 87.
PN US2005048589-A1.
PD 03-MAR-2005.
PA (JEND/) JENDOUBI M.
Query Match 7.5%; Score 85.5; DB 9; Length 363;
Best Local Similarity 25.6%; Pred. No. 16;
RESULT 1302
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 35;
RESULT 1303
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 50;
RESULT 1304
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.5%; Score 85.5; DB 8; Length 951;
Best Local Similarity 26.0%; Pred. No. 59;
RESULT 1305
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 61;
RESULT 1306
ID ABU54710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.5%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1307
ID ABU54858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.5%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1308
ID ABU54707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.5%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1309
ID AEB29721 standard; protein; 2448 AA.
DE Human Mucin 5 (subtypes A and C).
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.5%; Score 85.5; DB 9; Length 2448;
Best Local Similarity 24.8%; Pred. No. 2.1e+02;
RESULT 1310
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 7.5%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 6.6e+02;
RESULT 1311
ID ABU54721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.5%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 1.7e+03;
RESULT 1312
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.5%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 3.9e+03;
RESULT 1313
ID ABB50001 standard; protein; 569 AA.
DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 7.5%; Score 85; DB 5; Length 569;
Best Local Similarity 22.9%; Pred. No. 33;

RESULT 1314
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.5%; Score 85; DB 6; Length 569;
Best Local Similarity 22.9%; Pred. No. 33;
RESULT 1315
ID ABB55236 standard; protein; 627 AA.
DE Lactococcus lactis protein ytfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 7.5%; Score 85; DB 5; Length 627;
Best Local Similarity 21.5%; Pred. No. 38;
RESULT 1316
ID ADS29466 standard; protein; 627 AA.
DE Bacterial polypeptide #18499.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.5%; Score 85; DB 8; Length 627;
Best Local Similarity 21.5%; Pred. No. 38;
RESULT 1317
ID AAG83274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.5%; Score 85; DB 4; Length 631;
Best Local Similarity 27.7%; Pred. No. 38;
RESULT 1318
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.5%; Score 85; DB 5; Length 631;
Best Local Similarity 27.7%; Pred. No. 38;
RESULT 1319
ID ADD42755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.5%; Score 85; DB 7; Length 664;
Best Local Similarity 27.7%; Pred. No. 41;
RESULT 1320
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PN WO200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.5%; Score 85; DB 4; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1321
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PN WO200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 7.5%; Score 85; DB 5; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1322
ID ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.5%; Score 85; DB 7; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1323
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 95.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 7.5%; Score 85; DB 7; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1324
ID ADW29028 standard; protein; 1016 AA.
DE C_trachomatis polymorphic membrane protein (PmpH) Seq 22.
PN WO2005002619-A2.
PD 13-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 7.5%; Score 85; DB 9; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1325
ID AEA19092 standard; protein; 1016 AA.
DE Chlamydia trachomatis protein - SEQ ID 95.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match 7.5%; Score 85; DB 9; Length 1016;
Best Local Similarity 27.7%; Pred. No. 72;
RESULT 1326
ID ABB60387 standard; protein; 1049 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.5%; Score 85; DB 4; Length 1049;
Best Local Similarity 22.1%; Pred. No. 75;
RESULT 1327
ID ADX67527 standard; protein; 349 AA.
DE Plant full length insert polypeptide seqid 38370.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.4%; Score 84.5; DB 8; Length 349;
Best Local Similarity 25.0%; Pred. No. 19;
RESULT 1328
ID ABM88426 standard; protein; 494 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6672.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.4%; Score 84.5; DB 7; Length 494;
Best Local Similarity 24.2%; Pred. No. 31;
RESULT 1329
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 7.4%; Score 84.5; DB 8; Length 2234;
Best Local Similarity 27.2%; Pred. No. 2.3e+02;
RESULT 1330
ID ADR72871 standard; protein; 22152 AA.
DE Human ovarian cancer-related tumour marker CA125 protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 7.4%; Score 84.5; DB 8; Length 22152;
Best Local Similarity 27.2%; Pred. No. 4.9e+03;

RESULT 1331
ID AAB11729 standard; protein; 216 AA.
DE Cryptosporidium parvum Iowa isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 11;
RESULT 1332
ID AAB11734 standard; protein; 216 AA.
DE Cryptosporidium parvum NINC isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 11;
RESULT 1333
ID ABJ04047 standard; protein; 216 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 8.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 5; Length 216;
Best Local Similarity 26.7%; Pred. No. 11;
RESULT 1334
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 84; DB 3; Length 330;
Best Local Similarity 27.5%; Pred. No. 20;
RESULT 1335
ID ABB59598 standard; protein; 330 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5586.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.4%; Score 84; DB 4; Length 330;
Best Local Similarity 30.6%; Pred. No. 20;
RESULT 1336
ID ADO61979 standard; protein; 335 AA.
DE Transcription factor G2571, SEQ ID 446.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.4%; Score 84; DB 8; Length 335;
Best Local Similarity 26.4%; Pred. No. 20;
RESULT 1337
ID AEA27053 standard; protein; 335 AA.
DE Stress tolerant plant-related transcription factor protein SeqID894.
PN WO2005047516-A2.
PD 26-MAY-2005.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.4%; Score 84; DB 9; Length 335;
Best Local Similarity 26.4%; Pred. No. 20;
RESULT 1338
ID AAB96091 standard; protein; 1362 AA.
DE Putative P. abyssi amylopullulanase.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 7.4%; Score 84; DB 4; Length 1362;
Best Local Similarity 26.5%; Pred. No. 1.3e+02;
RESULT 1339
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 2; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.8e+02;
RESULT 1340
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 3; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.8e+02;
RESULT 1341
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 5; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.8e+02;
RESULT 1342
ID AAB11726 standard; protein; 1837 AA.
DE Cryptosporidium parvum Iowa isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 3; Length 1837;
Best Local Similarity 26.7%; Pred. No. 2e+02;
RESULT 1343
ID ABJ04044 standard; protein; 1837 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 5.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.4%; Score 84; DB 5; Length 1837;
Best Local Similarity 26.7%; Pred. No. 2e+02;
RESULT 1344
ID ADT07505 standard; protein; 2109 AA.
DE Human colon-specific polypeptide (CSP) #22.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 7.4%; Score 84; DB 8; Length 2109;
Best Local Similarity 31.5%; Pred. No. 2.4e+02;
RESULT 1345
ID ADT07506 standard; protein; 2254 AA.
DE Human colon-specific polypeptide (CSP) #23.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 7.4%; Score 84; DB 8; Length 2254;
Best Local Similarity 31.5%; Pred. No. 2.6e+02;
RESULT 1346
ID ADT07507 standard; protein; 2401 AA.
DE Human colon-specific polypeptide (CSP) #24.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 7.4%; Score 84; DB 8; Length 2401;
Best Local Similarity 31.5%; Pred. No. 2.8e+02;
RESULT 1347
ID AEB56507 standard; protein; 5858 AA.
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.
PN WO2005073411-A1.
PD 11-AUG-2005.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 7.4%; Score 84; DB 9; Length 5858;
Best Local Similarity 31.5%; Pred. No. 9.3e+02;
RESULT 1348
ID ABU53165 standard; protein; 143 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #25.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 143;
Best Local Similarity 30.7%; Pred. No. 7.4;
RESULT 1349

ID ABU53163 standard; protein; 247 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #23.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 247;
Best Local Similarity 30.7%; Pred. No. 15;
RESULT 1350
ID ABU53158 standard; protein; 260 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 260;
Best Local Similarity 30.7%; Pred. No. 16;
RESULT 1351
ID ADX94171 standard; protein; 357 AA.
DE Plant full length insert polypeptide seqid 56835.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.4%; Score 83.5; DB 8; Length 357;
Best Local Similarity 24.0%; Pred. No. 25;
RESULT 1352
ID ABU53157 standard; protein; 368 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #17.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 368;
Best Local Similarity 30.7%; Pred. No. 26;
RESULT 1353
ID ABU53156 standard; protein; 385 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #16.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 385;
Best Local Similarity 30.7%; Pred. No. 28;
RESULT 1354
ID ABU53159 standard; protein; 386 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #19.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 386;
Best Local Similarity 30.7%; Pred. No. 28;
RESULT 1355
ID ABU53161 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 28;
RESULT 1356
ID AAM50241 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 7.4%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 28;
RESULT 1357
ID AAU76423 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase clone wr1.pk0059.g9.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 7.4%; Score 83.5; DB 5; Length 393;
Best Local Similarity 26.5%; Pred. No. 28;
RESULT 1358
ID ABU53160 standard; protein; 395 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 395;
Best Local Similarity 30.7%; Pred. No. 29;
RESULT 1359
ID ABB10349 standard; protein; 553 AA.
DE Human cDNA SEQ ID NO: 657.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 83.5; DB 4; Length 553;
Best Local Similarity 22.9%; Pred. No. 45;
RESULT 1360
ID ABP66936 standard; protein; 553 AA.
DE Human polypeptide SEQ ID NO 657.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 7.4%; Score 83.5; DB 5; Length 553;
Best Local Similarity 22.9%; Pred. No. 45;
RESULT 1361
ID ABU53144 standard; protein; 717 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 717;
Best Local Similarity 30.7%; Pred. No. 63;
RESULT 1362
ID AAY54466 standard; protein; 788 AA.
DE Amino acid sequence of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 7.4%; Score 83.5; DB 3; Length 788;
Best Local Similarity 26.5%; Pred. No. 72;
RESULT 1363
ID AAY54467 standard; protein; 807 AA.
DE Amini acid sequence of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 7.4%; Score 83.5; DB 3; Length 807;
Best Local Similarity 26.5%; Pred. No. 74;
RESULT 1364
ID ABU62079 standard; protein; 4123 AA.
DE Human jelly belly (jeb) protein.
PN US2003054485-A1.
PD 20-MAR-2003.
PA (SCOT/) SCOTT M P.
PA (WEIS/) WEISS J B.
Query Match 7.4%; Score 83.5; DB 7; Length 4123;
Best Local Similarity 22.7%; Pred. No. 6.5e+02;
RESULT 1365
ID ADH48718 standard; protein; 4219 AA.
DE NOV1 protein sequence, SEQ ID 2.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 83.5; DB 5; Length 4219;
Best Local Similarity 22.7%; Pred. No. 6.7e+02;
RESULT 1366

ID AEA04533 standard; protein; 5178 AA.
DE Human protein from gene under-expressed in cancer, MUC2.
PN WO2005044990-A2.
PD 19-MAY-2005.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.4%; Score 83.5; DB 9; Length 5178;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1367
ID AAM24516 standard; protein; 5179 AA.
DE C899P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.4%; Score 83.5; DB 4; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1368
ID ABP55365 standard; protein; 5179 AA.
DE Human colon tumour protein for clone C899P SEQ ID NO:1068.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.4%; Score 83.5; DB 6; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1369
ID ABO07258 standard; protein; 5179 AA.
DE Human p53 modifying protein, SEQ ID 218.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 7.4%; Score 83.5; DB 6; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1370
ID ADD48091 standard; protein; 5179 AA.
DE Human Protein NP_002448, SEQ ID NO 13789.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.4%; Score 83.5; DB 7; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1371
ID ADD44998 standard; protein; 5179 AA.
DE Human Protein Q02817, SEQ ID NO 10430.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.4%; Score 83.5; DB 7; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1372
ID ADQ29695 standard; protein; 5179 AA.
DE Human colorectal cancer-associated protein #50.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.4%; Score 83.5; DB 8; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1373
ID ADQ80379 standard; protein; 5179 AA.
DE Intestinal/tracheal mucin 2 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.4%; Score 83.5; DB 8; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1374
ID AEA27639 standard; protein; 5179 AA.
DE Human intestinal mucin.
PN WO2005047321-A2.
PD 26-MAY-2005.
PA (UYCR-) UNIV CREIGHTON.
Query Match 7.4%; Score 83.5; DB 9; Length 5179;
Best Local Similarity 30.7%; Pred. No. 8.8e+02;
RESULT 1375
ID ADN95228 standard; protein; 5737 AA.
DE Human BEC/LEC-related protein sequence SeqID150.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.4%; Score 83.5; DB 7; Length 5737;
Best Local Similarity 22.7%; Pred. No. 1e+03;
RESULT 1376
ID AAR07670 standard; protein; 166 AA.
DE Intestinal mucin deduced from clone SMUC 40.
PN WO9012892-A.
PD 01-NOV-1990.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.3%; Score 83; DB 2; Length 166;
Best Local Similarity 29.9%; Pred. No. 10;
RESULT 1377
ID AAW75700 standard; peptide; 409 AA.
DE Vpr protein binding HHR23B amino acid sequence.
PN WO9835234-A1.
PD 13-AUG-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.3%; Score 83; DB 2; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1378
ID AAW68186 standard; protein; 409 AA.
DE Vpr binding protein HHR23B amino acid sequence.
PN WO9835032-A2.
PD 13-AUG-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.3%; Score 83; DB 2; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1379
ID ABU07460 standard; protein; 409 AA.
DE Protein differentially regulated in prostate cancer #63.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 7.3%; Score 83; DB 6; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1380
ID ADN03716 standard; protein; 409 AA.
DE Antipsoriatic protein sequence #55.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 83; DB 8; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1381
ID ADQ65876 standard; protein; 409 AA.
DE Novel human protein sequence #849.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 83; DB 8; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1382
ID ADW08718 standard; protein; 409 AA.
DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 55.
PN EP1493750-A2.
PD 05-JAN-2005.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 7.3%; Score 83; DB 9; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1383
ID ADY14438 standard; protein; 409 AA.
DE PRO polypeptide SEQ ID NO 244.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 83; DB 9; Length 409;
Best Local Similarity 28.6%; Pred. No. 34;
RESULT 1384
ID ABB61785 standard; protein; 471 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12147.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 83; DB 4; Length 471;
Best Local Similarity 35.0%; Pred. No. 40;
RESULT 1385
ID ADS43586 standard; protein; 605 AA.
DE Bacterial polypeptide #22016.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.3%; Score 83; DB 8; Length 605;
Best Local Similarity 31.8%; Pred. No. 56;
RESULT 1386
ID ADX97567 standard; protein; 2624 AA.
DE Pancreatic cancer associated human protein, SEQ ID 115.
PN EP1471075-A2.
PD 27-OCT-2004.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
Query Match 7.3%; Score 83; DB 8; Length 2624;
Best Local Similarity 27.8%; Pred. No. 4e+02;
RESULT 1387
ID AAG34201 standard; protein; 280 AA.
DE Zea mays protein fragment SEQ ID NO: 41576.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 82.5; DB 3; Length 280;
Best Local Similarity 28.7%; Pred. No. 23;
RESULT 1388
ID AAG40817 standard; protein; 346 AA.
DE Zea mays protein fragment SEQ ID NO: 50697.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 82.5; DB 3; Length 346;
Best Local Similarity 28.7%; Pred. No. 30;
RESULT 1389
ID ADY11098 standard; protein; 463 AA.
DE Plant full length insert polypeptide seqid 66913.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.3%; Score 82.5; DB 8; Length 463;
Best Local Similarity 22.7%; Pred. No. 44;
RESULT 1390
ID ADS44071 standard; protein; 825 AA.
DE Bacterial polypeptide #22501.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.3%; Score 82.5; DB 8; Length 825;
Best Local Similarity 24.8%; Pred. No. 96;
RESULT 1391
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 82.5; DB 4; Length 843;
Best Local Similarity 24.0%; Pred. No. 99;
RESULT 1392
ID AAW38272 standard; protein; 1085 AA.
DE Bovine parathyroid cell calcium receptor 1 (BoPCaR 1).
PN US5688938-A.
PD 18-NOV-1997.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (NPSP-) NPS PHARM INC.
Query Match 7.3%; Score 82.5; DB 2; Length 1085;
Best Local Similarity 22.4%; Pred. No. 1.4e+02;
RESULT 1393
ID ABB69011 standard; protein; 1371 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33825.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 82.5; DB 4; Length 1371;
Best Local Similarity 33.0%; Pred. No. 1.9e+02;
RESULT 1394
ID ABB60186 standard; protein; 1714 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 82.5; DB 4; Length 1714;
Best Local Similarity 26.1%; Pred. No. 2.5e+02;
RESULT 1395
ID AAM21657 standard; protein; 89 AA.
DE Peptide #8091 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1396
ID ABB44016 standard; peptide; 89 AA.
DE Peptide #11522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1397
ID AAM37960 standard; protein; 89 AA.
DE Peptide #11997 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1398
ID ABB26922 standard; protein; 89 AA.
DE Protein #8921 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1399
ID AAM77746 standard; protein; 89 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38052.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;

Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1400
ID AAM65031 standard; protein; 89 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37136.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1401
ID ABG59403 standard; peptide; 89 AA.
DE Human liver peptide, SEQ ID No 38051.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1402
ID ABG46774 standard; peptide; 89 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36439.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.2%; Score 82; DB 5; Length 89;
Best Local Similarity 28.9%; Pred. No. 5.5;
RESULT 1403
ID ABB67754 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 82; DB 4; Length 339;
Best Local Similarity 25.4%; Pred. No. 33;
RESULT 1404
ID ADQ18080 standard; protein; 477 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 897.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.2%; Score 82; DB 8; Length 477;
Best Local Similarity 32.1%; Pred. No. 52;
RESULT 1405
ID ABG70759 standard; protein; 553 AA.
DE T. maritima endoglucanse protein.
PN US2002120118-A1.
PD 29-AUG-2002.
PA (SHOR/) SHORT J M.
PA (LAMD/) LAM D E.
PA (MATH/) MATHUR E J.
Query Match 7.2%; Score 82; DB 5; Length 553;
Best Local Similarity 28.2%; Pred. No. 63;
RESULT 1406
ID AAW34999 standard; protein; 628 AA.
DE Archaebacterium AEPII1a endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOCATALYSIS INC.
Query Match 7.2%; Score 82; DB 2; Length 628;
Best Local Similarity 28.2%; Pred. No. 75;
RESULT 1407
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.2%; Score 82; DB 6; Length 637;
Best Local Similarity 24.2%; Pred. No. 76;
RESULT 1408
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PD 02-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 82; DB 3; Length 667;
Best Local Similarity 24.2%; Pred. No. 81;
RESULT 1409
ID AAW34985 standard; protein; 841 AA.
DE Archaebacterial thermostable endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOCATALYSIS INC.
Query Match 7.2%; Score 82; DB 2; Length 841;
Best Local Similarity 28.2%; Pred. No. 1.1e+02;
RESULT 1410
ID AAR22234 standard; protein; 995 AA.
DE Sequence encoded by ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBS-) WEBSTER A PTY LTD.
Query Match 7.2%; Score 82; DB 2; Length 995;
Best Local Similarity 31.7%; Pred. No. 1.4e+02;
RESULT 1411
ID ADM47185 standard; protein; 1671 AA.
DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 82; DB 7; Length 1671;
Best Local Similarity 24.2%; Pred. No. 2.7e+02;
RESULT 1412
ID ABU23564 standard; protein; 386 AA.
DE Protein encoded by Prokaryotic essential gene #9091.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 81.5; DB 6; Length 386;
Best Local Similarity 22.0%; Pred. No. 44;
RESULT 1413
ID ABM87947 standard; protein; 525 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6193.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.2%; Score 81.5; DB 7; Length 525;
Best Local Similarity 20.7%; Pred. No. 66;
RESULT 1414
ID ABO58564 standard; protein; 800 AA.
DE Human genome derived single exon protein #4798.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 7.2%; Score 81.5; DB 8; Length 800;
Best Local Similarity 35.8%; Pred. No. 1.2e+02;
RESULT 1415
ID ADX96680 standard; protein; 929 AA.
DE Plant full length insert polypeptide seqid 59344.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.2%; Score 81.5; DB 8; Length 929;
Best Local Similarity 27.9%; Pred. No. 1.4e+02;
RESULT 1416
ID AAY59288 standard; protein; 957 AA.
DE Human MUC11 polypeptide.
PN WO200004142-A1.
PD 27-JAN-2000.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.

Query Match 7.2%; Score 81.5; DB 3; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.5e+02;
RESULT 1417
ID AAM24513 standard; protein; 957 AA.
DE C900P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 81.5; DB 4; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.5e+02;
RESULT 1418
ID ABP55362 standard; protein; 957 AA.
DE Human colon tumour protein for clone C900P SEQ ID NO:1065.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 81.5; DB 6; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.5e+02;
RESULT 1419
ID AEA20406 standard; protein; 1004 AA.
DE Novel human polypeptide SEQ ID NO 1100.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.2%; Score 81.5; DB 9; Length 1004;
Best Local Similarity 29.0%; Pred. No. 1.6e+02;
RESULT 1420
ID AEA20405 standard; protein; 1032 AA.
DE Novel human polypeptide SEQ ID NO 1099.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.2%; Score 81.5; DB 9; Length 1032;
Best Local Similarity 29.0%; Pred. No. 1.6e+02;
RESULT 1421
ID ADC31682 standard; protein; 1205 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1764.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 81.5; DB 7; Length 1205;
Best Local Similarity 29.0%; Pred. No. 2e+02;
RESULT 1422
ID ABB69973 standard; protein; 1354 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 81.5; DB 4; Length 1354;
Best Local Similarity 21.9%; Pred. No. 2.3e+02;
RESULT 1423
ID AAU50934 standard; protein; 176 AA.
DE Propionibacterium acnes immunogenic protein #11830.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 81; DB 4; Length 176;
Best Local Similarity 26.9%; Pred. No. 17;
RESULT 1424
ID ABM47453 standard; protein; 176 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12129.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 81; DB 6; Length 176;
Best Local Similarity 26.9%; Pred. No. 17;
RESULT 1425
ID AAY93912 standard; protein; 289 AA.
DE A human hyaluronan-binding protein, designated OE-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.

Query Match 7.1%; Score 81; DB 3; Length 289;
Best Local Similarity 24.4%; Pred. No. 33;
RESULT 1426
ID ABB64749 standard; protein; 294 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21039.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 81; DB 4; Length 294;
Best Local Similarity 22.0%; Pred. No. 34;
RESULT 1427
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kB agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 7.1%; Score 81; DB 2; Length 862;
Best Local Similarity 21.8%; Pred. No. 1.4e+02;
RESULT 1428
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 7.1%; Score 81; DB 2; Length 894;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 1429
ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 7.1%; Score 81; DB 2; Length 894;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 1430
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1431
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1432
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1433
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;

RESULT 1434
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1435
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1436
ID ADS44054 standard; protein; 1128 AA.
DE Bacterial polypeptide #22484.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1128;
Best Local Similarity 22.8%; Pred. No. 2e+02;
RESULT 1437
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 7.1%; Score 81; DB 2; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1438
ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 7.1%; Score 81; DB 8; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1439
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1440
ID ADR18921 standard; protein; 1569 AA.
DE Human mucin glycoprotein, MUC6.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 1569;
Best Local Similarity 25.5%; Pred. No. 3.2e+02;
RESULT 1441
ID ADN18882 standard; protein; 1609 AA.
DE Bacterial polypeptide #1535.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.4%; Pred. No. 3.3e+02;
RESULT 1442
ID ADR18914 standard; protein; 2240 AA.
DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2240;
Best Local Similarity 25.5%; Pred. No. 5.1e+02;
RESULT 1443
ID ADR18913 standard; protein; 2258 AA.
DE Human mucin-like protein, SCS0004, variant SEQ ID 3.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2258;
Best Local Similarity 25.5%; Pred. No. 5.2e+02;
RESULT 1444
ID ADR18915 standard; protein; 2264 AA.
DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2264;
Best Local Similarity 25.5%; Pred. No. 5.2e+02;
RESULT 1445
ID ABB69480 standard; protein; 2977 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35232.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 81; DB 4; Length 2977;
Best Local Similarity 18.8%; Pred. No. 7.5e+02;
RESULT 1446
ID ABP07042 standard; protein; 128 AA.
DE Human ORFX protein sequence SEQ ID NO:14066.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 80.5; DB 5; Length 128;
Best Local Similarity 33.8%; Pred. No. 13;
RESULT 1447
ID ADD46369 standard; protein; 148 AA.
DE Rat Protein CAA34901, SEQ ID NO 12049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 80.5; DB 7; Length 148;
Best Local Similarity 23.5%; Pred. No. 15;
RESULT 1448
ID ABU26248 standard; protein; 323 AA.
DE Protein encoded by Prokaryotic essential gene #11775.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 80.5; DB 6; Length 323;
Best Local Similarity 27.1%; Pred. No. 43;
RESULT 1449
ID ABP28528 standard; protein; 540 AA.
DE Streptococcus polypeptide SEQ ID NO 6232.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.1%; Score 80.5; DB 5; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1450

ID ADU69670 standard; protein; 540 AA.
DE S agalactiae hyperimmune serum reactive antigen seqid 365.
PN WO2004099242-A2.
PD 18-NOV-2004.
PA (INTE-) INTERCELL AG.
Query Match 7.1%; Score 80.5; DB 8; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1451
ID ADV88602 standard; protein; 540 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 996.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.1%; Score 80.5; DB 8; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1452
ID ADV79855 standard; protein; 540 AA.
DE Streptococcus agalactiae protein, SEQ ID 996.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.1%; Score 80.5; DB 8; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1453
ID ADV82007 standard; protein; 540 AA.
DE Streptococcus agalactiae protein, SEQ ID 3148.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.1%; Score 80.5; DB 8; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1454
ID ABB57757 standard; protein; 1167 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 63.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 80.5; DB 4; Length 1167;
Best Local Similarity 28.2%; Pred. No. 2.4e+02;
RESULT 1455
ID AAR77036 standard; protein; 52 AA.
DE Human brain-enriched hyaluronan binding protein PTR1 domain.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 7.0%; Score 80; DB 2; Length 52;
Best Local Similarity 35.0%; Pred. No. 4.2;
RESULT 1456
ID ABP63646 standard; protein; 89 AA.
DE Human ORF16.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 7.0%; Score 80; DB 5; Length 89;
Best Local Similarity 32.6%; Pred. No. 8.7;
RESULT 1457
ID ABO79758 standard; protein; 95 AA.
DE Pseudomonas aeruginosa polypeptide #11933.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.0%; Score 80; DB 7; Length 95;
Best Local Similarity 28.3%; Pred. No. 9.4;
RESULT 1458
ID ADX73466 standard; protein; 169 AA.
DE Plant full length insert polypeptide seqid 42832.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.0%; Score 80; DB 8; Length 169;
Best Local Similarity 23.2%; Pred. No. 20;
RESULT 1459
ID ADR09088 standard; protein; 272 AA.
DE Human protein useful for treating neurological disease Seq 2594.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.0%; Score 80; DB 8; Length 272;
Best Local Similarity 23.4%; Pred. No. 38;
RESULT 1460
ID ADF58702 standard; protein; 351 AA.
DE Human polypeptide sequence SEQ ID NO:1110.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 80; DB 7; Length 351;
Best Local Similarity 23.4%; Pred. No. 54;
RESULT 1461
ID ADY08994 standard; protein; 365 AA.
DE Plant full length insert polypeptide seqid 64809.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.0%; Score 80; DB 8; Length 365;
Best Local Similarity 22.2%; Pred. No. 57;
RESULT 1462
ID ABB66171 standard; protein; 449 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25305.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 80; DB 4; Length 449;
Best Local Similarity 23.9%; Pred. No. 75;
RESULT 1463
ID AAY01077 standard; protein; 473 AA.
DE H. insolens Cel6A fungal cellulase protien sequence.
PN WO9901544-A1.
PD 14-JAN-1999.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.0%; Score 80; DB 2; Length 473;
Best Local Similarity 28.1%; Pred. No. 80;
RESULT 1464
ID ADY24635 standard; protein; 575 AA.
DE Plant full length insert polypeptide seqid 72419.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 7.0%; Score 80; DB 8; Length 575;
Best Local Similarity 18.8%; Pred. No. 1e+02;
RESULT 1465
ID ADN19351 standard; protein; 725 AA.
DE Bacterial polypeptide #2004.
PN US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.0%; Score 80; DB 8; Length 725;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1466
ID ABU09610 standard; protein; 729 AA.
DE Mouse retinoic acid-regulated nuclear matrix-associated protein.
PN US2003003485-A1.
PD 02-JAN-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 7.0%; Score 80; DB 6; Length 729;
Best Local Similarity 20.6%; Pred. No. 1.4e+02;
RESULT 1467
ID ABG23210 standard; protein; 791 AA.
DE Novel human diagnostic protein #23201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 80; DB 4; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.6e+02;
RESULT 1468
ID ADS12299 standard; protein; 791 AA.
DE Human therapeutic contig protein - SEQ ID 2536.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.0%; Score 80; DB 8; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.6e+02;
RESULT 1469
ID AAG70752 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL070C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 7.0%; Score 80; DB 4; Length 881;
Best Local Similarity 23.6%; Pred. No. 1.8e+02;
RESULT 1470
ID AEA08149 standard; protein; 4262 AA.
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 7.0%; Score 80; DB 9; Length 4262;
Best Local Similarity 24.2%; Pred. No. 1.5e+03;
RESULT 1471
ID AEA08148 standard; protein; 4493 AA.
DE Human mucin 17 protein - SEQ ID 3.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 7.0%; Score 80; DB 9; Length 4493;
Best Local Similarity 24.2%; Pred. No. 1.6e+03;
RESULT 1472
ID ABU54861 standard; protein; 10431 AA.
DE Human CA125 amino terminal extension.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.0%; Score 80; DB 6; Length 10431;
Best Local Similarity 22.3%; Pred. No. 5e+03;
RESULT 1473
ID ADY53881 standard; protein; 114 AA.
DE Candida albicans glycosylphosphatidylinositol-anchored protein- SEQ ID 1.
PN WO2005021789-A1.
PD 10-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 7.0%; Score 79.5; DB 9; Length 114;
Best Local Similarity 28.0%; Pred. No. 13;

RESULT 1474
ID ABU53162 standard; protein; 277 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #22.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.0%; Score 79.5; DB 4; Length 277;
Best Local Similarity 29.4%; Pred. No. 44;
RESULT 1475
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 79.5; DB 4; Length 320;
Best Local Similarity 25.7%; Pred. No. 53;
RESULT 1476
ID ABO62076 standard; protein; 324 AA.
DE Klebsiella pneumoniae polypeptide seqid 8593.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.0%; Score 79.5; DB 7; Length 324;
Best Local Similarity 21.3%; Pred. No. 54;
RESULT 1477
ID ABG07923 standard; protein; 366 AA.
DE Novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 79.5; DB 4; Length 366;
Best Local Similarity 25.7%; Pred. No. 64;
RESULT 1478
ID ABB63033 standard; protein; 583 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79.5; DB 4; Length 583;
Best Local Similarity 23.5%; Pred. No. 1.2e+02;
RESULT 1479
ID AAU38948 standard; protein; 583 AA.
DE Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79.5; DB 4; Length 583;
Best Local Similarity 23.5%; Pred. No. 1.2e+02;
RESULT 1480
ID ADC35826 standard; protein; 583 AA.
DE Drosophila G protein coupled receptor seq id 28.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 7.0%; Score 79.5; DB 7; Length 583;
Best Local Similarity 23.5%; Pred. No. 1.2e+02;
RESULT 1481
ID ABU53155 standard; protein; 692 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #15.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.0%; Score 79.5; DB 4; Length 692;
Best Local Similarity 29.4%; Pred. No. 1.5e+02;
RESULT 1482
ID ABB63128 standard; protein; 796 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16176.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79.5; DB 4; Length 796;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
RESULT 1483

ID ABB49326 standard; protein; 860 AA.
DE Listeria monocytogenes protein #2030.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 7.0%; Score 79.5; DB 5; Length 860;
Best Local Similarity 20.3%; Pred. No. 2e+02;
RESULT 1484
ID ABU32996 standard; protein; 860 AA.
DE Protein encoded by Prokaryotic essential gene #18523.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.0%; Score 79.5; DB 6; Length 860;
Best Local Similarity 20.3%; Pred. No. 2e+02;
RESULT 1485
ID ABB71072 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40008.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79.5; DB 4; Length 875;
Best Local Similarity 29.5%; Pred. No. 2e+02;
RESULT 1486
ID AAW00634 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9508622-A1.
PD 30-MAR-1995.
PA (SYTR) SYNTRO CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.4e+02;
RESULT 1487
ID AAW06786 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9629396-A1.
PD 26-SEP-1996.
PA (SYTR) SYNTRO CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.4e+02;
RESULT 1488
ID AAY41092 standard; protein; 1114 AA.
DE Peptide Seq ID No: 34 of WO9945111.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.8e+02;
RESULT 1489
ID AAB15730 standard; protein; 1114 AA.
DE Protein encoded by cDNA generated from RACE3.3 and clone 3.3 sequences.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 3; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.8e+02;
RESULT 1490
ID AAY41086 standard; protein; 1123 AA.
DE Human lectomedin-1beta polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.9e+02;
RESULT 1491
ID AAB15724 standard; protein; 1123 AA.
DE Human lectomedin-1beta.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 3; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.9e+02;
RESULT 1492
ID AAY41085 standard; protein; 1177 AA.
DE Human lectomedin-1alpha.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 1177;
Best Local Similarity 20.8%; Pred. No. 3e+02;
RESULT 1493
ID AAB15723 standard; protein; 1177 AA.
DE Human lectomedin-1alpha.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 3; Length 1177;
Best Local Similarity 20.8%; Pred. No. 3e+02;
RESULT 1494
ID ADD46682 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 12367.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.5e+02;
RESULT 1495
ID ADE55337 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 1151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.5e+02;
RESULT 1496
ID AAY41087 standard; protein; 1403 AA.
DE Human lectomedin-1gamma polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 2; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.8e+02;
RESULT 1497
ID AAB15725 standard; protein; 1403 AA.
DE Human lectomedin-1gamma cDNA.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.0%; Score 79.5; DB 3; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.8e+02;
RESULT 1498
ID ABP81675 standard; protein; 1403 AA.
DE Human latrophilin-2 protein SEQ ID NO:526.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 7.0%; Score 79.5; DB 6; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.8e+02;
RESULT 1499
ID ADD89067 standard; protein; 1403 AA.
DE TAT254.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.8e+02;
RESULT 1500
ID ADN95548 standard; protein; 1403 AA.
DE Human BEC/LEC-related protein sequence SeqID471.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.0%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.8e+02;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 37.3585 Seconds
(without alignments)
2460.550 Million cell updates/sec

Perfect score: 1136
Sequence: 1 TTRLLVQGSLRAEELSIQVS.....TEPFVENKAAFKNEAAGFGG 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
3	1136	100.0	322	3	US-09-905-291A-201	Sequence 201, App
93	1136	100.0	322	4	US-10-223-085-32	Sequence 32, Appl
94	1136	100.0	322	4	US-10-223-084-32	Sequence 32, Appl
95	1136	100.0	322	4	US-10-223-088-32	Sequence 32, Appl
96	1136	100.0	322	4	US-10-223-090-32	Sequence 32, Appl
98	1136	100.0	322	4	US-10-223-087-32	Sequence 32, Appl
101	1136	100.0	322	4	US-10-223-083-32	Sequence 32, Appl
102	1136	100.0	322	4	US-10-079-111-1	Sequence 1, Appli
103	1136	100.0	322	4	US-10-223-089-32	Sequence 32, Appl
108	1136	100.0	322	4	US-10-299-976-201	Sequence 201, App
136	1136	100.0	322	4	US-10-063-742-6	Sequence 6, Appli
211	1136	100.0	322	4	US-10-299-937-201	Sequence 201, App
214	1136	100.0	322	4	US-10-223-081-32	Sequence 32, Appl
224	1136	100.0	322	4	US-10-223-082-32	Sequence 32, Appl
230	1136	100.0	322	4	US-10-298-993-201	Sequence 201, App
231	1136	100.0	322	4	US-10-305-654-32	Sequence 32, Appl
232	1136	100.0	322	4	US-10-448-923-201	Sequence 201, App
233	1136	100.0	322	4	US-10-449-656-201	Sequence 201, App
234	1136	100.0	322	4	US-10-448-713-201	Sequence 201, App
235	1136	100.0	322	4	US-10-425-447-201	Sequence 201, App
236	1136	100.0	322	4	US-10-081-056-32	Sequence 32, Appl
238	1136	100.0	322	4	US-10-215-371-201	Sequence 201, App
239	1136	100.0	322	4	US-10-797-366-201	Sequence 201, App
240	1136	100.0	322	4	US-10-771-187-201	Sequence 201, App
241	1136	100.0	322	5	US-10-972-317-6	Sequence 6, Appli
242	1136	100.0	322	5	US-10-963-467-201	Sequence 201, App
243	1136	100.0	322	5	US-10-978-255-201	Sequence 201, App
244	1136	100.0	322	5	US-10-820-474A-64	Sequence 64, Appl
245	1136	100.0	322	5	US-10-756-149-5685	Sequence 5685, Ap
246	1136	100.0	322	5	US-10-970-823-201	Sequence 201, App
247	1136	100.0	344	4	US-10-276-774-2349	Sequence 2349, Ap
248	1130	99.5	322	4	US-10-291-634-2	Sequence 2, Appli
249	1130	99.5	322	4	US-10-264-237-2665	Sequence 2665, Ap
250	1117	98.3	322	5	US-10-723-860-3909	Sequence 3909, Ap
251	990.5	87.2	297	4	US-10-138-588-2	Sequence 2, Appli
252	680	59.9	255	3	US-09-866-050A-700	Sequence 700, App
253	213.5	18.8	339	4	US-10-291-634-3	Sequence 3, Appli
254	213.5	18.8	364	5	US-10-024-607-8	Sequence 8, Appli
255	208.5	18.4	668	4	US-10-741-601-341	Sequence 341, App
256	208.5	18.4	668	5	US-10-473-127-1285	Sequence 1285, Ap
257	208.5	18.4	668	5	US-10-741-600-1047	Sequence 1047, Ap
258	208.5	18.4	668	5	US-10-482-029-253	Sequence 253, App
259	203	17.9	742	4	US-10-648-593-176	Sequence 176, App
260	203	17.9	742	5	US-10-473-127-1282	Sequence 1282, Ap
261	203	17.9	742	5	US-10-473-127-1319	Sequence 1319, Ap
262	203	17.9	742	5	US-10-741-600-1054	Sequence 1054, Ap
263	203	17.9	742	5	US-10-287-436A-545	Sequence 545, App
264	203	17.9	742	5	US-10-287-436A-1236	Sequence 1236, Ap
265	202	17.8	675	5	US-10-473-127-1284	Sequence 1284, Ap
266	202	17.8	691	4	US-10-741-601-344	Sequence 344, App
267	202	17.8	691	5	US-10-473-127-1287	Sequence 1287, Ap
268	202	17.8	691	5	US-10-741-600-1053	Sequence 1053, Ap
269	202	17.8	742	3	US-09-983-000A-16	Sequence 16, Appl
270	202	17.8	742	4	US-10-116-275-206	Sequence 206, App
271	202	17.8	742	4	US-10-663-244-1	Sequence 1, Appli
272	202	17.8	742	4	US-10-741-601-338	Sequence 338, App
273	202	17.8	742	4	US-10-741-601-339	Sequence 339, App
274	202	17.8	742	5	US-10-473-127-1286	Sequence 1286, Ap
275	202	17.8	742	5	US-10-473-127-1311	Sequence 1311, Ap
276	202	17.8	742	5	US-10-690-880-40	Sequence 40, Appl
277	202	17.8	742	5	US-10-741-600-1046	Sequence 1046, Ap
278	202	17.8	742	5	US-10-741-600-1049	Sequence 1049, Ap
279	202	17.8	742	5	US-10-652-981-16	Sequence 16, Appl
280	200.5	17.6	607	5	US-10-486-226-2	Sequence 2, Appli
281	200.5	17.6	699	5	US-10-505-769-6	Sequence 6, Appli
282	200.5	17.6	700	5	US-10-473-127-1306	Sequence 1306, Ap
283	200.5	17.6	700	5	US-10-505-769-4	Sequence 4, Appli
284	199.5	17.6	493	3	US-09-836-544-34	Sequence 34, Appl
285	199.5	17.6	493	5	US-10-473-127-1279	Sequence 1279, Ap
286	199.5	17.6	493	5	US-10-473-127-1293	Sequence 1293, Ap
287	199.5	17.6	493	5	US-10-473-127-1297	Sequence 1297, Ap
288	199.5	17.6	493	5	US-10-473-127-1299	Sequence 1299, Ap
289	199.5	17.6	493	5	US-10-473-127-1301	Sequence 1301, Ap
290	199.5	17.6	493	5	US-10-473-127-1303	Sequence 1303, Ap
291	199.5	17.6	493	5	US-10-473-127-1305	Sequence 1305, Ap
292	199.5	17.6	493	6	US-11-037-713-34	Sequence 34, Appl
293	198.5	17.5	365	3	US-09-870-759-73	Sequence 73, Appl
294	198.5	17.5	365	3	US-09-751-708A-73	Sequence 73, Appl
295	198.5	17.5	365	4	US-10-428-817A-69	Sequence 69, Appl
296	198.5	17.5	365	5	US-10-937-758A-50	Sequence 50, Appl
297	198.5	17.5	493	4	US-10-663-244-2	Sequence 2, Appli
298	198.5	17.5	493	5	US-10-473-127-1278	Sequence 1278, Ap
299	198.5	17.5	493	5	US-10-473-127-1289	Sequence 1289, Ap
300	198	17.4	425	5	US-10-473-127-1283	Sequence 1283, Ap
301	197	17.3	361	3	US-09-836-544-32	Sequence 32, Appl
302	197	17.3	361	5	US-10-473-127-1275	Sequence 1275, Ap
303	197	17.3	361	5	US-10-473-127-1276	Sequence 1276, Ap
304	197	17.3	361	5	US-10-473-127-1292	Sequence 1292, Ap
305	197	17.3	361	5	US-10-473-127-1296	Sequence 1296, Ap
306	197	17.3	361	5	US-10-473-127-1298	Sequence 1298, Ap
307	197	17.3	361	5	US-10-473-127-1300	Sequence 1300, Ap
308	197	17.3	361	5	US-10-473-127-1302	Sequence 1302, Ap
309	197	17.3	361	5	US-10-473-127-1304	Sequence 1304, Ap
310	197	17.3	361	5	US-10-473-127-1309	Sequence 1309, Ap
311	197	17.3	361	5	US-10-473-127-1310	Sequence 1310, Ap
312	197	17.3	361	5	US-10-482-029-255	Sequence 255, App
313	197	17.3	361	5	US-10-852-335A-131	Sequence 131, App
314	197	17.3	431	5	US-10-473-127-1307	Sequence 1307, Ap
315	197	17.3	436	5	US-10-473-127-1308	Sequence 1308, Ap
316	197	17.3	719	5	US-10-473-127-1270	Sequence 1270, Ap
317	197	17.3	719	5	US-10-473-127-1316	Sequence 1316, Ap

318	196.5	17.3	535	4	US-10-741-601-336	Sequence 336, App
319	196.5	17.3	535	5	US-10-741-600-1044	Sequence 1044, Ap
320	196.5	17.3	699	5	US-10-473-127-1274	Sequence 1274, Ap
321	196.5	17.3	699	5	US-10-473-127-1280	Sequence 1280, Ap
322	196.5	17.3	699	5	US-10-473-127-1313	Sequence 1313, Ap
323	196.5	17.3	699	5	US-10-696-639-71	Sequence 71, Appl
324	196.5	17.3	700	4	US-10-012-969C-2	Sequence 2, Appli
325	196	17.3	293	5	US-10-473-127-1277	Sequence 1277, Ap
326	196	17.3	294	5	US-10-473-127-1290	Sequence 1290, Ap
327	196	17.3	294	5	US-10-473-127-1312	Sequence 1312, Ap
328	196	17.3	361	4	US-10-663-244-3	Sequence 3, Appli
329	196	17.3	361	4	US-10-741-601-340	Sequence 340, App
330	196	17.3	361	5	US-10-473-127-1288	Sequence 1288, Ap
331	196	17.3	361	5	US-10-741-600-1048	Sequence 1048, Ap
332	196	17.3	361	5	US-10-505-769-2	Sequence 2, Appli
333	196	17.3	395	4	US-10-741-601-345	Sequence 345, App
334	196	17.3	395	5	US-10-473-127-1281	Sequence 1281, Ap
335	196	17.3	395	5	US-10-741-600-1052	Sequence 1052, Ap
336	196	17.3	425	4	US-10-741-601-337	Sequence 337, App
337	196	17.3	425	5	US-10-741-600-1045	Sequence 1045, Ap
338	196	17.3	493	4	US-10-741-601-343	Sequence 343, App
339	196	17.3	493	5	US-10-741-600-1051	Sequence 1051, Ap
340	194.5	17.1	742	5	US-10-450-763-47430	Sequence 47430, A
341	194	17.1	361	5	US-10-473-127-1273	Sequence 1273, Ap
342	191.5	16.9	676	5	US-10-473-127-1268	Sequence 1268, Ap
343	191.5	16.9	676	5	US-10-473-127-1318	Sequence 1318, Ap
344	191	16.8	271	5	US-10-473-127-1272	Sequence 1272, Ap
345	191	16.8	271	5	US-10-473-127-1314	Sequence 1314, Ap
346	191	16.8	338	5	US-10-473-127-1271	Sequence 1271, Ap
347	191	16.8	338	5	US-10-473-127-1315	Sequence 1315, Ap
348	191	16.8	470	5	US-10-473-127-1269	Sequence 1269, Ap
349	191	16.8	470	5	US-10-473-127-1317	Sequence 1317, Ap
350	187	16.5	112	5	US-10-487-620-2	Sequence 2, Appli
351	186.5	16.4	113	5	US-10-487-620-6	Sequence 6, Appli
352	185	16.3	112	5	US-10-487-620-8	Sequence 8, Appli
353	183	16.1	112	5	US-10-487-620-10	Sequence 10, Appl
354	182	16.0	112	5	US-10-487-620-4	Sequence 4, Appli
355	181	15.9	112	5	US-10-487-620-12	Sequence 12, Appl
356	175.5	15.4	920	5	US-10-450-763-47426	Sequence 47426, A
357	170	15.0	34	3	US-09-864-761-47905	Sequence 47905, A
358	161	14.2	90	3	US-09-799-118-3	Sequence 3, Appli
359	153.5	13.5	90	3	US-09-927-463-8	Sequence 8, Appli
360	153.5	13.5	90	4	US-10-837-671-8	Sequence 8, Appli
361	150	13.2	510	4	US-10-104-047-2580	Sequence 2580, Ap
362	148.5	13.1	80	5	US-10-487-620-23	Sequence 23, Appl
363	145	12.8	277	3	US-09-799-118-2	Sequence 2, Appli
364	145	12.8	277	4	US-10-247-671-185	Sequence 185, App
365	145	12.8	277	4	US-10-295-027-292	Sequence 292, App
366	145	12.8	277	4	US-10-295-027-1237	Sequence 1237, Ap
367	145	12.8	277	5	US-10-723-860-4326	Sequence 4326, Ap
368	145	12.8	2626	4	US-10-634-574-4	Sequence 4, Appli
369	144	12.7	275	5	US-10-960-275-12	Sequence 12, Appl
370	143.5	12.6	95	4	US-10-424-599-248857	Sequence 248857,
371	131.5	11.6	883	4	US-10-195-970-3	Sequence 3, Appli
372	131.5	11.6	883	4	US-10-453-420-3	Sequence 3, Appli
373	130.5	11.5	883	3	US-09-759-130B-342	Sequence 342, App
374	130.5	11.5	883	4	US-10-189-123-72	Sequence 72, Appl
375	130.5	11.5	883	4	US-10-188-495-72	Sequence 72, Appl
376	130.5	11.5	883	4	US-10-741-790-342	Sequence 342, App
377	130.5	11.5	2316	5	US-10-287-436A-566	Sequence 566, App
378	129	11.4	1431	3	US-09-842-930A-2	Sequence 2, Appli
379	129	11.4	1431	4	US-10-133-172-2	Sequence 2, Appli
380	129	11.4	1431	5	US-10-990-844-2	Sequence 2, Appli
381	128.5	11.3	95	5	US-10-473-127-1291	Sequence 1291, Ap
382	127.5	11.2	649	3	US-09-759-130B-333	Sequence 333, App
383	127.5	11.2	649	4	US-10-189-123-63	Sequence 63, Appl
384	127.5	11.2	649	4	US-10-188-495-63	Sequence 63, Appl
385	127.5	11.2	649	4	US-10-741-790-333	Sequence 333, App
386	127.5	11.2	671	3	US-09-759-130B-331	Sequence 331, App
387	127.5	11.2	671	3	US-09-983-000A-14	Sequence 14, Appl
388	127.5	11.2	671	4	US-10-189-123-61	Sequence 61, Appl
389	127.5	11.2	671	4	US-10-188-495-61	Sequence 61, Appl
390	127.5	11.2	671	4	US-10-741-790-331	Sequence 331, App
391	127.5	11.2	671	5	US-10-652-981-14	Sequence 14, Appl
392	127.5	11.2	671	5	US-10-936-626-90	Sequence 90, Appl
393	127.5	11.2	671	5	US-10-938-061-90	Sequence 90, Appl
394	127.5	11.2	671	5	US-10-852-335A-97	Sequence 97, Appl
395	127.5	11.2	883	4	US-10-195-970-6	Sequence 6, Appli
396	127.5	11.2	883	4	US-10-453-420-6	Sequence 6, Appli
405	127.5	11.2	911	4	US-10-237-535-52	Sequence 52, Appl
414	127.5	11.2	911	4	US-10-239-196-52	Sequence 52, Appl
505	127.5	11.2	911	4	US-10-453-420-8	Sequence 8, Appli
506	127.5	11.2	911	4	US-10-295-027-260	Sequence 260, App
507	127.5	11.2	911	4	US-10-312-352-24	Sequence 24, Appl
508	127.5	11.2	911	5	US-10-936-626-89	Sequence 89, Appl
509	127.5	11.2	911	5	US-10-938-061-89	Sequence 89, Appl
510	127.5	11.2	911	5	US-10-983-340-21	Sequence 21, Appl
511	127	11.2	277	4	US-10-295-027-294	Sequence 294, App
512	127	11.2	277	4	US-10-755-889-118	Sequence 118, App
513	124	10.9	482	4	US-10-104-047-3794	Sequence 3794, Ap
514	124	10.9	2570	4	US-10-028-248A-42	Sequence 42, Appl
515	124	10.9	2570	4	US-10-107-782-42	Sequence 42, Appl
516	123	10.8	457	5	US-10-960-275-5	Sequence 5, Appli
517	123	10.8	1082	4	US-10-264-237-2725	Sequence 2725, Ap
518	123	10.8	2157	5	US-10-960-275-2	Sequence 2, Appli
519	123	10.8	2212	4	US-10-028-248A-43	Sequence 43, Appl
520	123	10.8	2212	4	US-10-107-782-43	Sequence 43, Appl
523	121.5	10.7	360	3	US-09-905-291A-213	Sequence 213, App
1054	121.5	10.7	360	4	US-10-174-587-28	Sequence 28, Appl
1089	121.5	10.7	360	4	US-10-299-976-213	Sequence 213, App
1091	121.5	10.7	360	4	US-10-299-937-213	Sequence 213, App
1101	121.5	10.7	360	4	US-10-298-993-213	Sequence 213, App
1106	121.5	10.7	360	4	US-10-448-923-213	Sequence 213, App
1107	121.5	10.7	360	4	US-10-449-656-213	Sequence 213, App
1108	121.5	10.7	360	4	US-10-448-713-213	Sequence 213, App
1110	121.5	10.7	360	4	US-10-425-447-213	Sequence 213, App
1118	121.5	10.7	360	4	US-10-215-371-213	Sequence 213, App
1119	121.5	10.7	360	4	US-10-797-366-213	Sequence 213, App
1120	121.5	10.7	360	4	US-10-771-187-213	Sequence 213, App
1121	121.5	10.7	360	5	US-10-963-467-213	Sequence 213, App
1122	121.5	10.7	360	5	US-10-978-255-213	Sequence 213, App
1126	121.5	10.7	360	5	US-10-970-823-213	Sequence 213, App
1127	121	10.7	528	3	US-09-759-130B-341	Sequence 341, App
1128	121	10.7	528	4	US-10-189-123-71	Sequence 71, Appl
1129	121	10.7	528	4	US-10-188-495-71	Sequence 71, Appl
1130	121	10.7	528	4	US-10-741-790-341	Sequence 341, App
1131	121	10.7	528	5	US-10-314-942-20	Sequence 20, Appl
1132	119	10.5	457	3	US-09-774-639-108	Sequence 108, App
1133	119	10.5	457	3	US-09-969-730-110	Sequence 110, App
1134	119	10.5	457	4	US-10-621-363-110	Sequence 110, App
1135	118.5	10.4	1642	5	US-10-741-600-1176	Sequence 1176, Ap
1136	118.5	10.4	1642	5	US-10-741-600-1178	Sequence 1178, Ap
1137	118.5	10.4	3396	4	US-10-788-792-170	Sequence 170, App
1138	118.5	10.4	3396	5	US-10-741-600-1172	Sequence 1172, Ap
1139	118.5	10.4	3396	5	US-10-741-600-1173	Sequence 1173, Ap
1140	118.5	10.4	3396	5	US-10-631-467-773	Sequence 773, App
1141	116	10.2	2397	5	US-10-631-467-1518	Sequence 1518, Ap
1142	113.5	10.0	97	3	US-09-799-118-5	Sequence 5, Appli
1143	112.5	9.9	287	3	US-09-764-853-576	Sequence 576, App
1144	112.5	9.9	340	4	US-10-112-944-397	Sequence 397, App
1145	112	9.9	897	4	US-10-028-248A-41	Sequence 41, Appl
1146	112	9.9	897	4	US-10-028-248A-211	Sequence 211, App
1147	112	9.9	897	4	US-10-107-782-41	Sequence 41, Appl
1148	112	9.9	897	4	US-10-107-782-211	Sequence 211, App
1149	112	9.9	1192	4	US-10-028-248A-40	Sequence 40, Appl
1150	112	9.9	1192	4	US-10-107-782-40	Sequence 40, Appl
1151	112	9.9	1394	3	US-09-842-930A-25	Sequence 25, Appl
1152	112	9.9	1394	5	US-10-990-844-25	Sequence 25, Appl
1153	112	9.9	1416	4	US-10-133-172-4	Sequence 4, Appli
1154	112	9.9	1653	4	US-10-133-172-20	Sequence 20, Appl
1155	111	9.8	104	4	US-10-028-248A-46	Sequence 46, Appl
1156	111	9.8	104	4	US-10-107-782-46	Sequence 46, Appl
1157	111	9.8	655	4	US-10-270-253-2	Sequence 2, Appli
1158	111	9.8	655	5	US-10-741-600-1174	Sequence 1174, Ap
1159	111	9.8	2409	4	US-10-177-293-90	Sequence 90, Appl
1160	111	9.8	2409	5	US-10-741-600-1175	Sequence 1175, Ap

1161	111	9.8	2409	5	US-10-741-600-1177	Sequence 1177, Ap
1162	111	9.8	2409	5	US-10-482-029-194	Sequence 194, App
1163	111	9.8	2409	5	US-10-852-335A-184	Sequence 184, App
1164	110.5	9.7	1257	4	US-10-698-190-22	Sequence 22, Appl
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1166	110	9.7	2675	4	US-10-107-782-2	Sequence 2, Appli
1167	109	9.6	353	5	US-10-960-275-11	Sequence 11, Appl
1168	109	9.6	1069	4	US-10-028-248A-39	Sequence 39, Appl
1169	109	9.6	1069	4	US-10-107-782-39	Sequence 39, Appl
1170	109	9.6	1321	4	US-10-241-220-82	Sequence 82, Appl
1171	109	9.6	1321	4	US-10-295-027-262	Sequence 262, App
1172	109	9.6	1321	4	US-10-408-765A-1421	Sequence 1421, Ap
1173	109	9.6	1321	4	US-10-698-190-18	Sequence 18, Appl
1174	109	9.6	1321	5	US-10-872-972-82	Sequence 82, Appl
1175	109	9.6	1321	5	US-10-872-991-82	Sequence 82, Appl
1176	108	9.5	322	4	US-10-120-907A-32	Sequence 32, Appl
1177	108	9.5	322	4	US-10-120-907A-33	Sequence 33, Appl
1178	108	9.5	354	4	US-10-120-907A-3	Sequence 3, Appli
1179	108	9.5	354	4	US-10-120-907A-7	Sequence 7, Appli
1180	108	9.5	354	4	US-10-120-907A-9	Sequence 9, Appli
1181	108	9.5	354	4	US-10-120-907A-11	Sequence 11, Appl
1182	108	9.5	354	4	US-10-120-907A-13	Sequence 13, Appl
1183	108	9.5	354	4	US-10-120-907A-15	Sequence 15, Appl
1184	108	9.5	354	4	US-10-120-907A-17	Sequence 17, Appl
1185	108	9.5	354	4	US-10-120-907A-19	Sequence 19, Appl
1186	108	9.5	354	4	US-10-120-907A-21	Sequence 21, Appl
1187	108	9.5	354	4	US-10-120-907A-23	Sequence 23, Appl
1188	108	9.5	354	4	US-10-120-907A-24	Sequence 24, Appl
1189	108	9.5	354	4	US-10-120-907A-28	Sequence 28, Appl
1190	108	9.5	354	4	US-10-120-907A-29	Sequence 29, Appl
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1192	108	9.5	354	4	US-10-120-907A-36	Sequence 36, Appl
1193	108	9.5	354	4	US-10-120-907A-38	Sequence 38, Appl
1194	108	9.5	354	4	US-10-120-907A-42	Sequence 42, Appl
1195	108	9.5	354	4	US-10-120-907A-64	Sequence 64, Appl
1196	108	9.5	354	4	US-10-120-907A-66	Sequence 66, Appl
1197	108	9.5	354	5	US-10-754-473-19	Sequence 19, Appl
1198	108	9.5	354	5	US-10-754-473-22	Sequence 22, Appl
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1201	108	9.5	721	4	US-10-120-907A-43	Sequence 43, Appl
1202	108	9.5	721	4	US-10-120-907A-65	Sequence 65, Appl
1203	108	9.5	721	4	US-10-120-907A-67	Sequence 67, Appl
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1205	107	9.4	315	4	US-10-667-723-4	Sequence 4, Appli
1206	107	9.4	339	5	US-10-754-473-21	Sequence 21, Appl
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1208	107	9.4	355	4	US-10-120-907A-31	Sequence 31, Appl
1209	107	9.4	355	5	US-10-754-473-20	Sequence 20, Appl
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1211	107	9.4	1268	4	US-10-698-190-24	Sequence 24, Appl
1212	107	9.4	2420	4	US-10-028-248A-4	Sequence 4, Appli
1213	107	9.4	2420	4	US-10-107-782-4	Sequence 4, Appli
1214	105.5	9.3	341	3	US-09-948-820-48	Sequence 48, Appl
1215	105.5	9.3	341	5	US-10-613-076-48	Sequence 48, Appl
1216	105	9.2	354	4	US-10-120-907A-37	Sequence 37, Appl
1217	105	9.2	354	5	US-10-754-473-18	Sequence 18, Appl
1218	104	9.2	98	3	US-09-799-118-4	Sequence 4, Appli
1219	104	9.2	139	4	US-10-741-601-342	Sequence 342, App
1220	104	9.2	139	5	US-10-473-127-2037	Sequence 2037, Ap
1221	104	9.2	139	5	US-10-473-127-2040	Sequence 2040, Ap
1222	104	9.2	139	5	US-10-741-600-1050	Sequence 1050, Ap
1223	101.5	8.9	380	4	US-10-369-493-6206	Sequence 6206, Ap
1224	100.5	8.8	402	4	US-10-343-953-2	Sequence 2, Appli
1225	100.5	8.8	402	4	US-10-257-174-47	Sequence 47, Appl
1226	99.5	8.8	402	5	US-10-481-698-17	Sequence 17, Appl
1227	99	8.7	201	4	US-10-120-907A-40	Sequence 40, Appl
1228	99	8.7	201	4	US-10-120-907A-41	Sequence 41, Appl
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1231	94.5	8.3	183	6	US-11-097-143-24753	Sequence 24753, A
1232	94.5	8.3	1795	6	US-11-097-143-36210	Sequence 36210, A
1233	93.5	8.2	258	3	US-09-764-853-840	Sequence 840, App
1234	93.5	8.2	258	4	US-10-091-438-205	Sequence 205, App
1235	93.5	8.2	261	3	US-09-764-853-669	Sequence 669, App
1236	93.5	8.2	261	4	US-10-091-438-144	Sequence 144, App
1237	92.5	8.1	40	5	US-10-487-620-26	Sequence 26, Appl
1238	91.5	8.1	166	3	US-09-764-853-777	Sequence 777, App
1239	91.5	8.1	166	4	US-10-091-438-181	Sequence 181, App
1240	91.5	8.1	1126	6	US-11-097-143-35952	Sequence 35952, A
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1244	90	7.9	1103	4	US-10-369-493-3228	Sequence 3228, Ap
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1246	89	7.8	416	4	US-10-371-525-26	Sequence 26, Appl
1247	89	7.8	416	4	US-10-371-069-26	Sequence 26, Appl
1248	89	7.8	416	4	US-10-371-645-26	Sequence 26, Appl
1249	89	7.8	416	4	US-10-371-260-26	Sequence 26, Appl
1250	89	7.8	416	5	US-10-684-422-68	Sequence 68, Appl
1251	89	7.8	416	5	US-10-287-436A-533	Sequence 533, App
1252	89	7.8	416	5	US-10-287-436A-1224	Sequence 1224, Ap
1253	89	7.8	1441	4	US-10-437-963-138354	Sequence 138354,
1254	89	7.8	2588	4	US-10-437-963-138279	Sequence 138279,
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1256	87.5	7.7	555	4	US-10-218-743-15	Sequence 15, Appl
1257	87.5	7.7	555	4	US-10-218-743-18	Sequence 18, Appl
1258	87.5	7.7	1085	4	US-10-159-339-10	Sequence 10, Appl
1259	87.5	7.7	1085	4	US-10-041-615-108	Sequence 108, App
1260	87.5	7.7	1085	4	US-10-436-715-21	Sequence 21, Appl
1261	87.5	7.7	1085	4	US-10-436-715-75	Sequence 75, Appl
1262	87	7.7	288	3	US-09-216-393-341	Sequence 341, App
1263	87	7.7	288	3	US-09-216-393-344	Sequence 344, App
1264	87	7.7	288	4	US-10-321-856-341	Sequence 341, App
1265	87	7.7	288	4	US-10-321-856-344	Sequence 344, App
1266	86.5	7.6	245	4	US-10-425-115-334180	Sequence 334180,
1267	86.5	7.6	585	5	US-10-868-381-58	Sequence 58, Appl
1268	86	7.6	390	5	US-10-732-923-20210	Sequence 20210, A
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1271	85.5	7.5	346	5	US-10-498-778-6	Sequence 6, Appli
1272	85.5	7.5	363	5	US-10-926-543-87	Sequence 87, Appl
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1279	85.5	7.5	1794	3	US-09-965-738-299	Sequence 299, App
1280	85.5	7.5	1799	3	US-09-965-738-149	Sequence 149, App
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1282	85.5	7.5	5877	4	US-10-142-515-11	Sequence 11, Appl
1283	85.5	7.5	5935	4	US-10-243-243A-8	Sequence 8, Appli
1284	85.5	7.5	6995	5	US-10-983-340-4	Sequence 4, Appli
1285	85.5	7.5	11721	3	US-09-965-738-162	Sequence 162, App
1286	85.5	7.5	22152	4	US-10-715-066-5	Sequence 5, Appli
1287	85	7.5	569	4	US-10-282-122A-60442	Sequence 60442, A
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1290	85	7.5	631	5	US-10-872-155-325	Sequence 325, App
1291	85	7.5	664	5	US-10-197-220-168	Sequence 168, App
1292	85	7.5	664	6	US-11-109-468-168	Sequence 168, App
1293	85	7.5	1016	3	US-09-841-260-95	Sequence 95, Appl
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1295	85	7.5	1016	4	US-10-467-534-41	Sequence 41, Appl
1296	85	7.5	1016	4	US-10-762-058-95	Sequence 95, Appl
1297	85	7.5	1016	5	US-10-197-220-95	Sequence 95, Appl
1298	85	7.5	1016	5	US-10-498-327-95	Sequence 95, Appl
1299	85	7.5	1016	6	US-11-109-468-95	Sequence 95, Appl
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1305	84	7.4	330	6	US-11-097-143-5586	Sequence 5586, Ap
1306	84	7.4	335	5	US-10-732-923-5372	Sequence 5372, Ap

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1310	83.5	7.4	553	3	US-09-764-853-657	Sequence 657, App
1311	83.5	7.4	591	4	US-10-437-963-161046	Sequence 161046,
1312	83.5	7.4	615	4	US-10-239-818-14	Sequence 14, Appl
1313	83.5	7.4	4123	4	US-10-213-509-5	Sequence 5, Appli
1314	83.5	7.4	4219	4	US-10-085-198-2	Sequence 2, Appli
1315	83.5	7.4	5179	3	US-09-922-217-1068	Sequence 1068, Ap
1316	83.5	7.4	5179	3	US-09-833-263-1068	Sequence 1068, Ap
1317	83.5	7.4	5179	4	US-10-025-380-1068	Sequence 1068, Ap
1318	83.5	7.4	5179	4	US-10-734-564-121	Sequence 121, App
1319	83	7.3	471	6	US-11-097-143-12147	Sequence 12147, A
1320	83	7.3	605	3	US-09-801-368-428	Sequence 428, App
1321	83	7.3	605	4	US-10-369-493-22016	Sequence 22016, A
1322	82.5	7.3	463	4	US-10-425-114-66913	Sequence 66913, A
1323	82.5	7.3	463	4	US-10-425-115-322413	Sequence 322413,
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1326	82.5	7.3	1371	6	US-11-097-143-33825	Sequence 33825, A
1327	82.5	7.3	1714	6	US-11-097-143-7350	Sequence 7350, Ap
1328	82	7.2	89	3	US-09-864-761-42220	Sequence 42220, A
1329	82	7.2	339	6	US-11-097-143-30054	Sequence 30054, A
1330	82	7.2	477	5	US-10-723-860-897	Sequence 897, App
1331	82	7.2	477	5	US-10-756-149-4935	Sequence 4935, Ap
1332	82	7.2	553	3	US-09-888-224-2	Sequence 2, Appli
1333	82	7.2	637	4	US-10-094-749-2621	Sequence 2621, Ap
1334	82	7.2	1099	5	US-10-732-923-8770	Sequence 8770, Ap
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1337	81.5	7.2	186	4	US-10-437-963-186467	Sequence 186467,
1338	81.5	7.2	352	4	US-10-424-599-195846	Sequence 195846,
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1344	81.5	7.2	957	3	US-09-833-263-1065	Sequence 1065, Ap
1345	81.5	7.2	957	4	US-10-025-380-1065	Sequence 1065, Ap
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1349	81	7.1	260	5	US-10-897-911-3	Sequence 3, Appli
1350	81	7.1	260	5	US-10-898-615-3	Sequence 3, Appli
1351	81	7.1	289	5	US-10-960-275-8	Sequence 8, Appli
1352	81	7.1	294	6	US-11-097-143-21039	Sequence 21039, A
1353	81	7.1	746	4	US-10-156-761-11411	Sequence 11411, A
1354	81	7.1	1128	4	US-10-369-493-22484	Sequence 22484, A
1355	81	7.1	1537	3	US-09-801-368-104	Sequence 104, App
1356	81	7.1	1537	4	US-10-369-493-1398	Sequence 1398, Ap
1357	81	7.1	1537	5	US-10-324-035-17	Sequence 17, Appl
1358	81	7.1	1609	4	US-10-369-493-1535	Sequence 1535, Ap
1359	81	7.1	2977	6	US-11-097-143-35232	Sequence 35232, A
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1362	80.5	7.1	901	4	US-10-425-115-323903	Sequence 323903,
1363	80.5	7.1	1167	6	US-11-097-143-63	Sequence 63, Appl
1364	80	7.0	89	3	US-09-867-550-32	Sequence 32, Appl
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119	73	6.4	708	6	US-10-636-320-2	Sequence 2, Appli
120	73	6.4	918	6	US-10-995-561-696	Sequence 696, App
121	73	6.4	1150	7	US-11-139-435-1	Sequence 1, Appli
122	73	6.4	1158	6	US-10-467-657-3112	Sequence 3112, Ap
123	72.5	6.4	498	6	US-10-510-947-9	Sequence 9, Appli
124	72.5	6.4	582	7	US-11-096-568A-24623	Sequence 24623, A
125	72.5	6.4	605	7	US-11-096-568A-24622	Sequence 24622, A
126	72.5	6.4	630	6	US-10-517-939-42	Sequence 42, Appl
127	72.5	6.4	673	7	US-11-096-568A-24621	Sequence 24621, A
128	72	6.3	458	6	US-10-540-091-24	Sequence 24, Appl
129	72	6.3	784	6	US-10-467-657-5968	Sequence 5968, Ap
130	72	6.3	825	6	US-10-453-372-644	Sequence 644, App
131	72	6.3	941	7	US-11-169-232-14	Sequence 14, Appl
132	72	6.3	1009	6	US-10-514-531-11	Sequence 11, Appl
133	72	6.3	1022	7	US-11-169-232-84	Sequence 84, Appl
134	72	6.3	1038	7	US-11-169-232-74	Sequence 74, Appl
135	72	6.3	1049	7	US-11-169-232-58	Sequence 58, Appl
136	72	6.3	1140	7	US-11-169-232-104	Sequence 104, App
137	72	6.3	1270	7	US-11-169-232-44	Sequence 44, Appl
138	72	6.3	1307	7	US-11-072-512-2438	Sequence 2438, Ap
139	72	6.3	1311	7	US-11-169-232-42	Sequence 42, Appl
140	72	6.3	1313	7	US-11-169-232-142	Sequence 142, App
141	72	6.3	1314	7	US-11-169-232-50	Sequence 50, Appl
142	72	6.3	1320	7	US-11-169-232-46	Sequence 46, Appl
143	72	6.3	1320	7	US-11-169-232-60	Sequence 60, Appl
144	72	6.3	1354	7	US-11-169-232-48	Sequence 48, Appl
145	72	6.3	1361	7	US-11-169-232-40	Sequence 40, Appl
146	72	6.3	1363	7	US-11-169-232-52	Sequence 52, Appl
147	72	6.3	1404	7	US-11-169-232-2	Sequence 2, Appli
148	72	6.3	1404	7	US-11-169-232-62	Sequence 62, Appl
149	71.5	6.3	232	6	US-10-884-730-366	Sequence 366, App
150	71.5	6.3	312	7	US-11-096-568A-12515	Sequence 12515, A
151	71.5	6.3	541	7	US-11-201-916-4	Sequence 4, Appli
152	71	6.2	626	7	US-11-010-748A-1	Sequence 1, Appli
153	71	6.2	1014	7	US-11-204-187-20	Sequence 20, Appl
154	71	6.2	1118	7	US-11-113-751-42	Sequence 42, Appl
155	71	6.2	1153	7	US-11-113-751-44	Sequence 44, Appl
156	70.5	6.2	163	7	US-11-096-568A-4288	Sequence 4288, Ap
157	70.5	6.2	231	7	US-11-096-568A-1421	Sequence 1421, Ap
158	70.5	6.2	232	6	US-10-884-730-363	Sequence 363, App
159	70.5	6.2	232	6	US-10-884-730-364	Sequence 364, App
160	70.5	6.2	232	6	US-10-884-730-365	Sequence 365, App
161	70.5	6.2	292	7	US-11-073-226-6	Sequence 6, Appli
162	70.5	6.2	308	7	US-11-096-568A-20980	Sequence 20980, A
163	70.5	6.2	348	7	US-11-096-568A-20979	Sequence 20979, A
164	70.5	6.2	364	7	US-11-087-177-31	Sequence 31, Appl
165	70.5	6.2	364	7	US-11-087-177-33	Sequence 33, Appl
166	70.5	6.2	368	7	US-11-096-568A-20978	Sequence 20978, A
167	70.5	6.2	512	6	US-10-821-234-1032	Sequence 1032, Ap
169	70.5	6.2	678	7	US-11-102-240-34	Sequence 34, Appl
170	70.5	6.2	678	7	US-11-103-195-34	Sequence 34, Appl
171	70	6.2	609	7	US-11-110-082-40	Sequence 40, Appl
172	69.5	6.1	106	7	US-11-096-568A-19298	Sequence 19298, A
173	69.5	6.1	215	6	US-10-467-657-476	Sequence 476, App
174	69.5	6.1	519	7	US-11-087-099-9352	Sequence 9352, Ap
175	69.5	6.1	554	5	US-09-978-360A-410	Sequence 410, App
176	69.5	6.1	558	7	US-11-052-554A-20	Sequence 20, Appl
177	69.5	6.1	558	7	US-11-134-563-12	Sequence 12, Appl
178	69.5	6.1	2801	6	US-10-330-773-630	Sequence 630, App
179	69	6.1	143	7	US-11-096-568A-8463	Sequence 8463, Ap
180	69	6.1	180	7	US-11-096-568A-12758	Sequence 12758, A
181	69	6.1	545	7	US-11-201-916-8	Sequence 8, Appli
182	69	6.1	705	7	US-11-087-099-10564	Sequence 10564, A
183	69	6.1	820	7	US-11-087-099-12246	Sequence 12246, A
184	69	6.1	910	7	US-11-206-587-17	Sequence 17, Appl
185	69	6.1	2343	6	US-10-330-773-904	Sequence 904, App
186	68.5	6.0	330	7	US-11-098-686-10903	Sequence 10903, A
187	68.5	6.0	436	7	US-11-124-368A-236	Sequence 236, App
188	68.5	6.0	484	7	US-11-096-568A-6203	Sequence 6203, Ap
189	68.5	6.0	488	7	US-11-096-568A-6202	Sequence 6202, Ap
190	68.5	6.0	499	7	US-11-096-568A-6201	Sequence 6201, Ap
191	68.5	6.0	709	7	US-11-072-512-2349	Sequence 2349, Ap
192	68.5	6.0	748	6	US-10-330-773-394	Sequence 394, App
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194	68.5	6.0	2244	7	US-11-131-263-41	Sequence 41, Appl
195	68	6.0	305	7	US-11-080-091-13	Sequence 13, Appl
196	68	6.0	347	7	US-11-096-568A-16579	Sequence 16579, A
197	68	6.0	406	7	US-11-096-568A-15346	Sequence 15346, A
198	68	6.0	415	7	US-11-096-568A-15345	Sequence 15345, A
199	68	6.0	802	7	US-11-087-099-4882	Sequence 4882, Ap
200	68	6.0	1323	6	US-10-517-939-312	Sequence 312, App
201	68	6.0	1340	7	US-11-098-686-11135	Sequence 11135, A
202	68	6.0	2053	7	US-11-013-759-9	Sequence 9, Appli
203	68	6.0	3712	7	US-11-019-711-48	Sequence 48, Appl
204	68	6.0	3712	7	US-11-019-711-51	Sequence 51, Appl
205	67.5	5.9	96	7	US-11-096-568A-6177	Sequence 6177, Ap
206	67.5	5.9	411	7	US-11-024-959-330	Sequence 330, App
207	67.5	5.9	413	7	US-11-096-568A-20771	Sequence 20771, A
208	67.5	5.9	423	7	US-11-098-686-10135	Sequence 10135, A
209	67.5	5.9	497	7	US-11-072-512-3773	Sequence 3773, Ap
210	67.5	5.9	630	7	US-11-236-198-5	Sequence 5, Appli
211	67.5	5.9	637	7	US-11-096-568A-27876	Sequence 27876, A
212	67.5	5.9	649	7	US-11-236-198-3	Sequence 3, Appli
213	67.5	5.9	704	7	US-11-096-568A-27875	Sequence 27875, A
214	67.5	5.9	732	7	US-11-096-568A-27874	Sequence 27874, A
215	67.5	5.9	775	6	US-10-453-372-656	Sequence 656, App
216	67.5	5.9	793	6	US-10-995-561-925	Sequence 925, App
217	67.5	5.9	804	6	US-10-453-372-650	Sequence 650, App
218	67.5	5.9	834	6	US-10-453-372-658	Sequence 658, App
219	67.5	5.9	847	6	US-10-453-372-654	Sequence 654, App
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224	67.5	5.9	961	7	US-11-113-424-35	Sequence 35, Appl
225	67.5	5.9	963	6	US-10-995-561-923	Sequence 923, App
226	67.5	5.9	963	6	US-10-453-372-660	Sequence 660, App
227	67.5	5.9	1012	6	US-10-453-372-646	Sequence 646, App
228	67.5	5.9	1267	7	US-11-096-568A-28960	Sequence 28960, A
229	67.5	5.9	1274	7	US-11-096-568A-28959	Sequence 28959, A
230	67.5	5.9	1448	6	US-10-485-517-212	Sequence 212, App
231	67.5	5.9	1480	7	US-11-096-568A-28958	Sequence 28958, A
232	67.5	5.9	4374	7	US-11-128-572-2	Sequence 2, Appli
233	67	5.9	209	7	US-11-096-568A-3341	Sequence 3341, Ap
234	67	5.9	317	7	US-11-087-099-9345	Sequence 9345, Ap
235	67	5.9	331	7	US-11-096-568A-11026	Sequence 11026, A
236	67	5.9	332	7	US-11-096-568A-11025	Sequence 11025, A
237	67	5.9	336	7	US-11-087-099-4886	Sequence 4886, Ap
238	67	5.9	341	7	US-11-096-568A-11024	Sequence 11024, A
239	67	5.9	389	7	US-11-188-743-23	Sequence 23, Appl
240	67	5.9	443	7	US-11-087-099-7683	Sequence 7683, Ap
241	67	5.9	514	7	US-11-195-739-1	Sequence 1, Appli
242	67	5.9	521	7	US-11-096-568A-31277	Sequence 31277, A
243	67	5.9	536	7	US-11-018-868-42	Sequence 42, Appl
244	67	5.9	543	7	US-11-096-568A-31276	Sequence 31276, A
245	67	5.9	581	7	US-11-096-568A-31275	Sequence 31275, A
246	67	5.9	619	6	US-10-517-939-352	Sequence 352, App
247	67	5.9	681	7	US-11-067-121-9	Sequence 9, Appli
248	67	5.9	823	7	US-11-087-099-1971	Sequence 1971, Ap

249	67	5.9	4384	6	US-10-821-234-1120	Sequence 1120, Ap
250	66.5	5.9	160	7	US-11-087-099-4973	Sequence 4973, Ap
251	66.5	5.9	319	7	US-11-096-568A-24347	Sequence 24347, A
252	66.5	5.9	374	7	US-11-072-175-148	Sequence 148, App
253	66.5	5.9	380	7	US-11-087-099-1300	Sequence 1300, Ap
254	66.5	5.9	502	7	US-11-098-686-10593	Sequence 10593, A
255	66.5	5.9	648	6	US-10-917-905-6	Sequence 6, Appli
256	66.5	5.9	897	7	US-11-087-099-11042	Sequence 11042, A
257	66.5	5.9	1256	6	US-10-517-696-111	Sequence 111, App
258	66	5.8	149	7	US-11-087-099-7791	Sequence 7791, Ap
259	66	5.8	292	7	US-11-129-143-96	Sequence 96, Appl
260	66	5.8	300	7	US-11-096-568A-27037	Sequence 27037, A
261	66	5.8	305	7	US-11-087-177-11	Sequence 11, Appl
262	66	5.8	305	7	US-11-087-177-13	Sequence 13, Appl
263	66	5.8	337	7	US-11-087-099-3435	Sequence 3435, Ap
264	66	5.8	343	7	US-11-016-564-17	Sequence 17, Appl
265	66	5.8	380	7	US-11-087-099-6673	Sequence 6673, Ap
266	66	5.8	567	7	US-11-016-503-2	Sequence 2, Appli
267	66	5.8	581	7	US-11-087-099-9181	Sequence 9181, Ap
268	66	5.8	581	7	US-11-087-099-11208	Sequence 11208, A
269	66	5.8	581	7	US-11-087-099-12146	Sequence 12146, A
271	66	5.8	607	6	US-10-973-115B-344	Sequence 344, App
272	66	5.8	607	7	US-11-176-863-2	Sequence 2, Appli
273	66	5.8	758	7	US-11-043-693-1	Sequence 1, Appli
274	66	5.8	780	7	US-11-087-099-251	Sequence 251, App
275	66	5.8	823	7	US-11-087-099-11109	Sequence 11109, A
276	66	5.8	1052	7	US-11-124-367A-323	Sequence 323, App
277	66	5.8	1061	7	US-11-000-463-347	Sequence 347, App
278	66	5.8	1061	7	US-11-124-367A-325	Sequence 325, App
279	66	5.8	1091	7	US-11-000-463-348	Sequence 348, App
280	66	5.8	1122	7	US-11-191-374-3	Sequence 3, Appli
281	66	5.8	1122	7	US-11-191-375-3	Sequence 3, Appli
282	66	5.8	1122	7	US-11-191-588-3	Sequence 3, Appli
283	66	5.8	1338	6	US-10-821-234-1622	Sequence 1622, Ap
284	66	5.8	1338	7	US-11-109-156-23	Sequence 23, Appl
285	66	5.8	1338	7	US-11-075-047A-2	Sequence 2, Appli
286	66	5.8	1419	7	US-11-124-367A-324	Sequence 324, App
287	66	5.8	1428	7	US-11-124-367A-320	Sequence 320, App
288	66	5.8	2011	7	US-11-080-991-56	Sequence 56, Appl
289	65.5	5.8	145	6	US-10-793-626-1504	Sequence 1504, Ap
290	65.5	5.8	175	7	US-11-087-099-6466	Sequence 6466, Ap
292	65.5	5.8	208	6	US-10-973-115B-510	Sequence 510, App
293	65.5	5.8	257	7	US-11-096-568A-25250	Sequence 25250, A
294	65.5	5.8	362	7	US-11-256-548-3	Sequence 3, Appli
295	65.5	5.8	436	7	US-11-024-959-394	Sequence 394, App
296	65.5	5.8	445	6	US-10-467-657-5092	Sequence 5092, Ap
297	65.5	5.8	472	7	US-11-165-211-7	Sequence 7, Appli
298	65.5	5.8	472	7	US-11-165-226-7	Sequence 7, Appli
299	65.5	5.8	485	7	US-11-096-568A-26552	Sequence 26552, A
300	65.5	5.8	541	7	US-11-201-916-17	Sequence 17, Appl
301	65.5	5.8	567	6	US-10-485-517-216	Sequence 216, App
302	65.5	5.8	618	7	US-11-087-099-6625	Sequence 6625, Ap
303	65.5	5.8	644	7	US-11-087-099-11826	Sequence 11826, A
304	65.5	5.8	707	7	US-11-072-512-3162	Sequence 3162, Ap
305	65.5	5.8	713	7	US-11-256-548-2	Sequence 2, Appli
306	65.5	5.8	877	6	US-10-485-517-200	Sequence 200, App
307	65.5	5.8	3069	7	US-11-235-732-2	Sequence 2, Appli
308	65.5	5.8	3095	7	US-11-235-732-4	Sequence 4, Appli
309	65.5	5.8	3100	7	US-11-235-732-7	Sequence 7, Appli
310	65.5	5.8	3567	6	US-10-453-372-1112	Sequence 1112, Ap
311	65	5.7	181	6	US-10-746-959C-10	Sequence 10, Appl
312	65	5.7	234	7	US-11-096-568A-21717	Sequence 21717, A
313	65	5.7	235	7	US-11-159-597-2	Sequence 2, Appli
314	65	5.7	235	7	US-11-219-359-5	Sequence 5, Appli
315	65	5.7	244	7	US-11-052-554A-60	Sequence 60, Appl
316	65	5.7	248	7	US-11-096-568A-13135	Sequence 13135, A
317	65	5.7	253	7	US-11-096-568A-21716	Sequence 21716, A
318	65	5.7	379	7	US-11-087-099-10889	Sequence 10889, A
319	65	5.7	380	7	US-11-087-099-4525	Sequence 4525, Ap
320	65	5.7	380	7	US-11-087-099-4810	Sequence 4810, Ap
322	65	5.7	449	6	US-10-973-115B-224	Sequence 224, App
323	65	5.7	509	7	US-11-008-727-16	Sequence 16, Appl
324	65	5.7	512	7	US-11-108-172-1093	Sequence 1093, Ap
325	65	5.7	557	7	US-11-016-503-4	Sequence 4, Appli
326	65	5.7	567	7	US-11-016-503-10	Sequence 10, Appl
327	65	5.7	578	7	US-11-087-099-542	Sequence 542, App
328	65	5.7	579	7	US-11-087-099-6979	Sequence 6979, Ap
329	65	5.7	579	7	US-11-087-099-7852	Sequence 7852, Ap
330	65	5.7	581	7	US-11-087-099-2154	Sequence 2154, Ap
331	65	5.7	581	7	US-11-087-099-2375	Sequence 2375, Ap
332	65	5.7	581	7	US-11-087-099-3070	Sequence 3070, Ap
333	65	5.7	581	7	US-11-087-099-3227	Sequence 3227, Ap
334	65	5.7	581	7	US-11-087-099-3736	Sequence 3736, Ap
335	65	5.7	581	7	US-11-087-099-5261	Sequence 5261, Ap
336	65	5.7	581	7	US-11-087-099-7613	Sequence 7613, Ap
337	65	5.7	581	7	US-11-087-099-8783	Sequence 8783, Ap
338	65	5.7	581	7	US-11-087-099-10957	Sequence 10957, A
339	65	5.7	581	7	US-11-087-099-11354	Sequence 11354, A
340	65	5.7	582	7	US-11-087-099-4567	Sequence 4567, Ap
341	65	5.7	619	7	US-11-136-244-3	Sequence 3, Appli
342	65	5.7	628	7	US-11-037-243-86	Sequence 86, Appl
343	65	5.7	640	7	US-11-136-244-4	Sequence 4, Appli
344	65	5.7	648	7	US-11-096-568A-27576	Sequence 27576, A
345	65	5.7	654	6	US-10-528-031-1	Sequence 1, Appli
346	65	5.7	673	6	US-10-330-773-674	Sequence 674, App
347	65	5.7	1131	7	US-11-072-512-2866	Sequence 2866, Ap
348	65	5.7	1992	7	US-11-013-759-3	Sequence 3, Appli
349	65	5.7	1992	7	US-11-013-759-13	Sequence 13, Appl
350	65	5.7	2047	7	US-11-013-759-4	Sequence 4, Appli
351	65	5.7	2047	7	US-11-013-759-7	Sequence 7, Appli
352	64.5	5.7	160	6	US-10-533-811-13	Sequence 13, Appl
353	64.5	5.7	223	7	US-11-087-099-7197	Sequence 7197, Ap
354	64.5	5.7	250	7	US-11-096-568A-3195	Sequence 3195, Ap
355	64.5	5.7	367	7	US-11-072-512-2763	Sequence 2763, Ap
356	64.5	5.7	370	7	US-11-096-568A-3216	Sequence 3216, Ap
357	64.5	5.7	370	7	US-11-096-568A-3217	Sequence 3217, Ap
358	64.5	5.7	371	6	US-10-467-657-1926	Sequence 1926, Ap
359	64.5	5.7	378	7	US-11-087-099-8872	Sequence 8872, Ap
360	64.5	5.7	378	7	US-11-087-099-11183	Sequence 11183, A
361	64.5	5.7	393	7	US-11-096-568A-3215	Sequence 3215, Ap
362	64.5	5.7	453	7	US-11-052-554A-224	Sequence 224, App
363	64.5	5.7	482	6	US-10-821-234-972	Sequence 972, App
364	64.5	5.7	519	7	US-11-087-099-5406	Sequence 5406, Ap
365	64.5	5.7	2910	7	US-11-087-100-2	Sequence 2, Appli
366	64.5	5.7	2910	7	US-11-087-084-2	Sequence 2, Appli
367	64.5	5.7	2910	7	US-11-087-085-2	Sequence 2, Appli
368	64	5.6	131	7	US-11-096-568A-12238	Sequence 12238, A
369	64	5.6	145	7	US-11-152-601-43	Sequence 43, Appl
370	64	5.6	187	7	US-11-096-568A-11277	Sequence 11277, A
371	64	5.6	198	7	US-11-087-099-11173	Sequence 11173, A
372	64	5.6	262	7	US-11-096-568A-11276	Sequence 11276, A
373	64	5.6	263	7	US-11-096-568A-9712	Sequence 9712, Ap
374	64	5.6	266	7	US-11-096-568A-11275	Sequence 11275, A
375	64	5.6	276	7	US-11-096-568A-30981	Sequence 30981, A
376	64	5.6	303	7	US-11-096-568A-27931	Sequence 27931, A
377	64	5.6	336	6	US-10-453-372-640	Sequence 640, App
378	64	5.6	338	7	US-11-096-568A-30980	Sequence 30980, A
379	64	5.6	346	7	US-11-096-568A-30979	Sequence 30979, A
380	64	5.6	379	7	US-11-087-099-8341	Sequence 8341, Ap
381	64	5.6	381	7	US-11-096-568A-17861	Sequence 17861, A
382	64	5.6	382	7	US-11-096-568A-17860	Sequence 17860, A
383	64	5.6	386	7	US-11-096-568A-13774	Sequence 13774, A
384	64	5.6	387	6	US-10-895-064-611	Sequence 611, App
385	64	5.6	387	7	US-11-129-741-611	Sequence 611, App
386	64	5.6	387	7	US-11-096-568A-13773	Sequence 13773, A
387	64	5.6	388	7	US-11-096-568A-17859	Sequence 17859, A
388	64	5.6	388	7	US-11-096-568A-27930	Sequence 27930, A
389	64	5.6	389	7	US-11-096-568A-27929	Sequence 27929, A
390	64	5.6	446	7	US-11-087-099-8235	Sequence 8235, Ap
391	64	5.6	537	7	US-11-087-099-4695	Sequence 4695, Ap
392	64	5.6	619	6	US-10-999-886-3	Sequence 3, Appli
393	64	5.6	640	6	US-10-999-886-4	Sequence 4, Appli
394	64	5.6	648	7	US-11-098-686-10873	Sequence 10873, A
395	64	5.6	756	6	US-10-055-877-188	Sequence 188, App
396	64	5.6	825	7	US-11-087-099-1341	Sequence 1341, Ap
397	64	5.6	997	7	US-11-080-991-50	Sequence 50, Appl

398	64	5.6	999	7	US-11-113-424-36	Sequence 36, Appl
399	64	5.6	1078	7	US-11-096-568A-30451	Sequence 30451, A
400	64	5.6	1116	7	US-11-096-568A-30450	Sequence 30450, A
401	64	5.6	1123	7	US-11-096-568A-30449	Sequence 30449, A
402	64	5.6	1198	6	US-10-451-375-4	Sequence 4, Appli
403	64	5.6	1445	7	US-11-169-041-181	Sequence 181, App
404	64	5.6	1574	7	US-11-212-443-179	Sequence 179, App
405	64	5.6	1978	7	US-11-212-443-60	Sequence 60, Appl
406	63.5	5.6	224	7	US-11-096-568A-7141	Sequence 7141, Ap
407	63.5	5.6	256	7	US-11-096-568A-7140	Sequence 7140, Ap
408	63.5	5.6	273	7	US-11-096-568A-22109	Sequence 22109, A
409	63.5	5.6	304	7	US-11-080-091-10	Sequence 10, Appl
410	63.5	5.6	335	7	US-11-087-099-4668	Sequence 4668, Ap
411	63.5	5.6	343	7	US-11-080-091-4	Sequence 4, Appli
412	63.5	5.6	345	7	US-11-087-177-19	Sequence 19, Appl
413	63.5	5.6	358	7	US-11-096-568A-21943	Sequence 21943, A
414	63.5	5.6	375	7	US-11-096-568A-21942	Sequence 21942, A
415	63.5	5.6	397	7	US-11-230-180-6	Sequence 6, Appli
416	63.5	5.6	446	7	US-11-102-621-138	Sequence 138, App
417	63.5	5.6	458	7	US-11-096-568A-21941	Sequence 21941, A
418	63.5	5.6	492	7	US-11-098-686-11360	Sequence 11360, A
419	63.5	5.6	541	7	US-11-201-916-14	Sequence 14, Appl
420	63.5	5.6	654	6	US-10-510-947-6	Sequence 6, Appli
421	63.5	5.6	693	6	US-10-995-561-632	Sequence 632, App
422	63.5	5.6	1009	6	US-10-912-971-16	Sequence 16, Appl
423	63.5	5.6	1053	6	US-10-517-939-52	Sequence 52, Appl
424	63.5	5.6	1315	6	US-10-995-561-630	Sequence 630, App
425	63.5	5.6	1992	7	US-11-069-834-58	Sequence 58, Appl
426	63.5	5.6	2000	7	US-11-069-834-56	Sequence 56, Appl
427	63.5	5.6	2145	7	US-11-087-099-10331	Sequence 10331, A
428	63.5	5.6	2176	7	US-11-193-561-25	Sequence 25, Appl
429	63.5	5.6	2176	7	US-11-193-771-25	Sequence 25, Appl
430	63.5	5.6	2176	7	US-11-193-789-25	Sequence 25, Appl
431	63.5	5.6	2176	7	US-11-193-806-25	Sequence 25, Appl
432	63.5	5.6	2176	7	US-11-193-857-25	Sequence 25, Appl
433	63.5	5.6	2296	6	US-10-995-561-633	Sequence 633, App
434	63.5	5.6	2296	7	US-11-193-561-23	Sequence 23, Appl
435	63.5	5.6	2296	7	US-11-193-771-23	Sequence 23, Appl
436	63.5	5.6	2296	7	US-11-193-789-23	Sequence 23, Appl
437	63.5	5.6	2296	7	US-11-193-806-23	Sequence 23, Appl
438	63.5	5.6	2296	7	US-11-193-857-23	Sequence 23, Appl
439	63.5	5.6	3487	7	US-11-087-099-10423	Sequence 10423, A
440	63	5.5	163	7	US-11-096-568A-9622	Sequence 9622, Ap
441	63	5.5	173	7	US-11-096-568A-9621	Sequence 9621, Ap
442	63	5.5	176	7	US-11-096-568A-9620	Sequence 9620, Ap
443	63	5.5	192	7	US-11-072-512-3585	Sequence 3585, Ap
444	63	5.5	309	7	US-11-037-243-118	Sequence 118, App
445	63	5.5	336	7	US-11-087-099-11933	Sequence 11933, A
446	63	5.5	359	7	US-11-087-099-7177	Sequence 7177, Ap
447	63	5.5	362	7	US-11-087-099-7379	Sequence 7379, Ap
448	63	5.5	363	7	US-11-087-099-9842	Sequence 9842, Ap
449	63	5.5	471	7	US-11-087-099-8817	Sequence 8817, Ap
450	63	5.5	578	7	US-11-096-568A-33961	Sequence 33961, A
451	63	5.5	581	7	US-11-236-198-7	Sequence 7, Appli
452	63	5.5	590	7	US-11-096-568A-33960	Sequence 33960, A
453	63	5.5	610	7	US-11-096-568A-33959	Sequence 33959, A
454	63	5.5	694	7	US-11-096-568A-29818	Sequence 29818, A
455	63	5.5	706	7	US-11-087-099-4237	Sequence 4237, Ap
456	63	5.5	717	7	US-11-096-568A-28799	Sequence 28799, A
457	63	5.5	738	6	US-10-880-881-23	Sequence 23, Appl
458	63	5.5	902	7	US-11-182-016-36	Sequence 36, Appl
459	63	5.5	1083	7	US-11-113-751-40	Sequence 40, Appl
460	63	5.5	1928	6	US-10-480-330-30	Sequence 30, Appl
461	63	5.5	1965	6	US-10-480-330-4	Sequence 4, Appli
462	63	5.5	1966	6	US-10-480-330-2	Sequence 2, Appli
463	63	5.5	1966	6	US-10-480-330-6	Sequence 6, Appli
464	63	5.5	1966	6	US-10-480-330-8	Sequence 8, Appli
465	63	5.5	1966	6	US-10-480-330-10	Sequence 10, Appl
466	63	5.5	1966	6	US-10-480-330-12	Sequence 12, Appl
467	63	5.5	1966	6	US-10-480-330-14	Sequence 14, Appl
468	63	5.5	1966	6	US-10-480-330-16	Sequence 16, Appl
469	63	5.5	1966	6	US-10-480-330-18	Sequence 18, Appl
470	63	5.5	1966	6	US-10-480-330-20	Sequence 20, Appl
471	63	5.5	1966	6	US-10-480-330-22	Sequence 22, Appl
472	63	5.5	1966	6	US-10-480-330-24	Sequence 24, Appl
473	63	5.5	1966	6	US-10-480-330-26	Sequence 26, Appl
474	63	5.5	1966	6	US-10-480-330-28	Sequence 28, Appl
475	63	5.5	2105	7	US-11-052-554A-173	Sequence 173, App
476	62.5	5.5	146	6	US-10-467-657-5594	Sequence 5594, Ap
477	62.5	5.5	158	7	US-11-096-568A-7142	Sequence 7142, Ap
478	62.5	5.5	298	7	US-11-080-091-9	Sequence 9, Appli
479	62.5	5.5	342	6	US-10-980-388-118	Sequence 118, App
480	62.5	5.5	342	7	US-11-174-816-18	Sequence 18, Appl
481	62.5	5.5	342	7	US-11-174-819-71	Sequence 71, Appl
482	62.5	5.5	345	7	US-11-087-177-21	Sequence 21, Appl
483	62.5	5.5	362	7	US-11-080-091-12	Sequence 12, Appl
484	62.5	5.5	404	7	US-11-096-568A-28877	Sequence 28877, A
485	62.5	5.5	432	7	US-11-124-367A-326	Sequence 326, App
486	62.5	5.5	442	7	US-11-102-621-126	Sequence 126, App
487	62.5	5.5	446	7	US-11-096-568A-28876	Sequence 28876, A
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489	62.5	5.5	513	6	US-10-641-678-66	Sequence 66, Appl
490	62.5	5.5	514	6	US-10-641-678-67	Sequence 67, Appl
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494	62.5	5.5	573	7	US-11-090-617-2	Sequence 2, Appli
495	62.5	5.5	577	7	US-11-124-368A-232	Sequence 232, App
496	62.5	5.5	585	7	US-11-108-172-1067	Sequence 1067, Ap
497	62.5	5.5	915	7	US-11-156-084-119	Sequence 119, App
498	62.5	5.5	965	7	US-11-113-424-2	Sequence 2, Appli
499	62.5	5.5	1162	6	US-10-451-375-3	Sequence 3, Appli
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501	62.5	5.5	2304	6	US-10-330-773-310	Sequence 310, App
502	62.5	5.5	2367	7	US-11-051-453-42	Sequence 42, Appl
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504	62.5	5.5	2602	6	US-10-453-372-716	Sequence 716, App
505	62.5	5.5	2617	6	US-10-453-372-666	Sequence 666, App
506	62.5	5.5	2617	6	US-10-453-372-732	Sequence 732, App
507	62.5	5.5	2617	6	US-10-453-372-734	Sequence 734, App
508	62.5	5.5	2617	6	US-10-453-372-736	Sequence 736, App
509	62.5	5.5	2617	6	US-10-453-372-738	Sequence 738, App
510	62.5	5.5	2617	6	US-10-453-372-740	Sequence 740, App
511	62.5	5.5	2617	6	US-10-453-372-742	Sequence 742, App
512	62.5	5.5	2617	6	US-10-453-372-744	Sequence 744, App
513	62.5	5.5	2617	6	US-10-453-372-746	Sequence 746, App
514	62.5	5.5	2617	6	US-10-453-372-748	Sequence 748, App
515	62.5	5.5	2617	6	US-10-453-372-750	Sequence 750, App
516	62.5	5.5	2871	7	US-11-169-041-131	Sequence 131, App
517	62.5	5.5	3002	6	US-10-821-234-916	Sequence 916, App
518	62.5	5.5	3011	6	US-10-985-205-3	Sequence 3, Appli
519	62.5	5.5	3487	7	US-11-087-099-9068	Sequence 9068, Ap
520	62	5.5	165	6	US-10-821-234-1539	Sequence 1539, Ap
521	62	5.5	233	7	US-11-096-568A-18993	Sequence 18993, A
522	62	5.5	291	7	US-11-096-568A-6790	Sequence 6790, Ap
523	62	5.5	325	7	US-11-096-568A-23538	Sequence 23538, A
524	62	5.5	341	7	US-11-240-769-72	Sequence 72, Appl
525	62	5.5	341	7	US-11-096-568A-23537	Sequence 23537, A
526	62	5.5	341	7	US-11-151-868-2	Sequence 2, Appli
527	62	5.5	362	7	US-11-096-568A-25696	Sequence 25696, A
528	62	5.5	370	7	US-11-096-568A-6789	Sequence 6789, Ap
529	62	5.5	379	7	US-11-087-099-8218	Sequence 8218, Ap
530	62	5.5	379	7	US-11-096-568A-25695	Sequence 25695, A
531	62	5.5	395	7	US-11-124-367A-322	Sequence 322, App
532	62	5.5	447	6	US-10-641-678-58	Sequence 58, Appl
533	62	5.5	489	7	US-11-264-728-4	Sequence 4, Appli
534	62	5.5	532	7	US-11-087-099-8860	Sequence 8860, Ap
535	62	5.5	615	7	US-11-087-099-11910	Sequence 11910, A
536	62	5.5	661	6	US-10-453-372-642	Sequence 642, App
537	62	5.5	725	7	US-11-098-686-10189	Sequence 10189, A
538	62	5.5	764	7	US-11-072-512-2379	Sequence 2379, Ap
539	62	5.5	871	7	US-11-087-099-6053	Sequence 6053, Ap
540	62	5.5	895	7	US-11-098-686-10311	Sequence 10311, A
541	62	5.5	926	7	US-11-024-959-518	Sequence 518, App
542	62	5.5	1001	6	US-10-330-773-510	Sequence 510, App
543	61.5	5.4	235	7	US-11-126-126-16	Sequence 16, Appl

544	61.5	5.4	239	7	US-11-096-568A-14888	Sequence 14888, A
545	61.5	5.4	240	7	US-11-096-568A-4927	Sequence 4927, Ap
546	61.5	5.4	246	7	US-11-096-568A-4926	Sequence 4926, Ap
547	61.5	5.4	251	7	US-11-096-568A-14887	Sequence 14887, A
548	61.5	5.4	296	7	US-11-196-475-22	Sequence 22, Appl
549	61.5	5.4	340	6	US-10-501-035-354	Sequence 354, App
550	61.5	5.4	342	7	US-11-008-570-45	Sequence 45, Appl
551	61.5	5.4	370	7	US-11-096-568A-6444	Sequence 6444, Ap
552	61.5	5.4	380	7	US-11-116-939-2	Sequence 2, Appli
553	61.5	5.4	380	7	US-11-196-475-118	Sequence 118, App
554	61.5	5.4	381	6	US-10-821-234-1342	Sequence 1342, Ap
555	61.5	5.4	393	7	US-11-196-475-114	Sequence 114, App
556	61.5	5.4	431	7	US-11-096-568A-6443	Sequence 6443, Ap
557	61.5	5.4	441	7	US-11-196-475-120	Sequence 120, App
558	61.5	5.4	454	7	US-11-196-475-116	Sequence 116, App
559	61.5	5.4	455	7	US-11-096-568A-29406	Sequence 29406, A
560	61.5	5.4	455	7	US-11-096-568A-29757	Sequence 29757, A
561	61.5	5.4	459	7	US-11-096-568A-29405	Sequence 29405, A
562	61.5	5.4	461	7	US-11-132-285-6	Sequence 6, Appli
563	61.5	5.4	461	7	US-11-182-946-4	Sequence 4, Appli
564	61.5	5.4	468	7	US-11-096-568A-6442	Sequence 6442, Ap
565	61.5	5.4	510	6	US-10-641-678-43	Sequence 43, Appl
566	61.5	5.4	511	6	US-10-641-678-42	Sequence 42, Appl
567	61.5	5.4	540	6	US-10-641-678-44	Sequence 44, Appl
568	61.5	5.4	549	7	US-11-096-568A-33577	Sequence 33577, A
569	61.5	5.4	588	7	US-11-196-475-122	Sequence 122, App
570	61.5	5.4	731	7	US-11-098-686-10415	Sequence 10415, A
571	61.5	5.4	2015	7	US-11-052-554A-374	Sequence 374, App
572	61	5.4	149	7	US-11-096-568A-7117	Sequence 7117, Ap
573	61	5.4	154	7	US-11-096-568A-11923	Sequence 11923, A
574	61	5.4	202	7	US-11-096-568A-7116	Sequence 7116, Ap
575	61	5.4	244	7	US-11-096-568A-9713	Sequence 9713, Ap
576	61	5.4	246	7	US-11-052-554A-50	Sequence 50, Appl
577	61	5.4	265	7	US-11-087-099-5324	Sequence 5324, Ap
578	61	5.4	273	7	US-11-087-099-2253	Sequence 2253, Ap
579	61	5.4	288	7	US-11-052-554A-353	Sequence 353, App
580	61	5.4	293	7	US-11-096-568A-15588	Sequence 15588, A
581	61	5.4	295	7	US-11-096-568A-30519	Sequence 30519, A
582	61	5.4	297	7	US-11-096-568A-15587	Sequence 15587, A
583	61	5.4	315	7	US-11-096-568A-21620	Sequence 21620, A
584	61	5.4	317	6	US-10-674-767-2	Sequence 2, Appli
585	61	5.4	329	7	US-11-096-568A-30518	Sequence 30518, A
586	61	5.4	330	7	US-11-096-568A-21618	Sequence 21618, A
587	61	5.4	336	7	US-11-096-568A-15586	Sequence 15586, A
588	61	5.4	339	7	US-11-124-367A-265	Sequence 265, App
589	61	5.4	352	7	US-11-124-367A-267	Sequence 267, App
590	61	5.4	379	7	US-11-087-099-1412	Sequence 1412, Ap
591	61	5.4	379	7	US-11-087-099-5014	Sequence 5014, Ap
592	61	5.4	380	7	US-11-087-099-5011	Sequence 5011, Ap
593	61	5.4	380	7	US-11-087-099-8656	Sequence 8656, Ap
594	61	5.4	424	7	US-11-024-959-499	Sequence 499, App
595	61	5.4	472	7	US-11-165-211-6	Sequence 6, Appli
596	61	5.4	472	7	US-11-165-226-6	Sequence 6, Appli
597	61	5.4	473	7	US-11-096-568A-21002	Sequence 21002, A
598	61	5.4	474	7	US-11-096-568A-21001	Sequence 21001, A
599	61	5.4	523	7	US-11-087-099-6081	Sequence 6081, Ap
600	61	5.4	557	7	US-11-096-568A-21000	Sequence 21000, A
601	61	5.4	560	7	US-11-018-868-40	Sequence 40, Appl
602	61	5.4	569	7	US-11-096-568A-30517	Sequence 30517, A
603	61	5.4	600	7	US-11-072-512-3397	Sequence 3397, Ap
604	61	5.4	645	7	US-11-072-512-3418	Sequence 3418, Ap
605	61	5.4	665	7	US-11-124-368A-289	Sequence 289, App
606	61	5.4	685	7	US-11-072-512-2916	Sequence 2916, Ap
607	61	5.4	713	6	US-10-330-773-668	Sequence 668, App
608	61	5.4	843	7	US-11-129-104-89	Sequence 89, Appl
609	61	5.4	897	7	US-11-137-465-35	Sequence 35, Appl
610	61	5.4	899	7	US-11-124-368A-290	Sequence 290, App
611	61	5.4	980	6	US-10-330-773-507	Sequence 507, App
612	61	5.4	1071	6	US-10-467-657-1654	Sequence 1654, Ap
613	61	5.4	1439	7	US-11-124-368A-291	Sequence 291, App
614	61	5.4	1493	7	US-11-183-136-26	Sequence 26, Appl
615	61	5.4	1613	7	US-11-108-528-84	Sequence 84, Appl
616	61	5.4	1751	7	US-11-103-957-45	Sequence 45, Appl
617	61	5.4	1751	7	US-11-018-868-16	Sequence 16, Appl
618	61	5.4	2214	7	US-11-080-991-94	Sequence 94, Appl
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620	60.5	5.3	101	7	US-11-096-568A-26972	Sequence 26972, A
621	60.5	5.3	132	7	US-11-087-099-3992	Sequence 3992, Ap
622	60.5	5.3	154	6	US-10-475-075-802	Sequence 802, App
623	60.5	5.3	245	7	US-11-186-284-167	Sequence 167, App
624	60.5	5.3	261	7	US-11-096-568A-17990	Sequence 17990, A
625	60.5	5.3	273	7	US-11-096-568A-18389	Sequence 18389, A
626	60.5	5.3	276	7	US-11-020-602-224	Sequence 224, App
627	60.5	5.3	279	7	US-11-096-568A-8112	Sequence 8112, Ap
628	60.5	5.3	283	7	US-11-096-568A-8111	Sequence 8111, Ap
629	60.5	5.3	290	7	US-11-096-568A-18388	Sequence 18388, A
630	60.5	5.3	298	7	US-11-096-568A-8110	Sequence 8110, Ap
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632	60.5	5.3	343	6	US-10-793-626-1626	Sequence 1626, Ap
633	60.5	5.3	343	6	US-10-793-626-1964	Sequence 1964, Ap
634	60.5	5.3	444	7	US-11-004-590-232	Sequence 232, App
635	60.5	5.3	473	7	US-11-096-568A-148	Sequence 148, App
636	60.5	5.3	476	7	US-11-024-959-385	Sequence 385, App
637	60.5	5.3	477	7	US-11-024-959-261	Sequence 261, App
638	60.5	5.3	510	7	US-11-096-568A-147	Sequence 147, App
639	60.5	5.3	511	7	US-11-096-568A-146	Sequence 146, App
640	60.5	5.3	524	7	US-11-087-099-12268	Sequence 12268, A
641	60.5	5.3	545	7	US-11-201-916-34	Sequence 34, Appl
642	60.5	5.3	773	6	US-10-995-561-852	Sequence 852, App
643	60.5	5.3	858	6	US-10-995-561-854	Sequence 854, App
644	60.5	5.3	862	7	US-11-051-720-1443	Sequence 1443, Ap
645	60.5	5.3	964	7	US-11-137-465-58	Sequence 58, Appl
646	60.5	5.3	965	7	US-11-147-047-51	Sequence 51, Appl
647	60.5	5.3	1007	7	US-11-051-720-1445	Sequence 1445, Ap
648	60.5	5.3	1120	7	US-11-051-720-1733	Sequence 1733, Ap
649	60.5	5.3	1137	7	US-11-012-762-70	Sequence 70, Appl
650	60.5	5.3	1178	6	US-10-995-561-851	Sequence 851, App
651	60.5	5.3	1263	6	US-10-485-517-127	Sequence 127, App
652	60.5	5.3	1305	7	US-11-051-720-1370	Sequence 1370, Ap
653	60.5	5.3	1337	7	US-11-112-304A-33	Sequence 33, Appl
654	60.5	5.3	1637	6	US-10-821-234-1204	Sequence 1204, Ap
655	60.5	5.3	1995	7	US-11-069-834-60	Sequence 60, Appl
656	60.5	5.3	2244	7	US-11-131-263-9	Sequence 9, Appli
657	60.5	5.3	2244	7	US-11-131-263-18	Sequence 18, Appl
658	60.5	5.3	2244	7	US-11-131-263-30	Sequence 30, Appl
659	60.5	5.3	2314	7	US-11-013-759-11	Sequence 11, Appl
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661	60	5.3	109	6	US-10-517-696-115	Sequence 115, App
662	60	5.3	112	7	US-11-096-568A-7599	Sequence 7599, Ap
663	60	5.3	142	7	US-11-186-284-105	Sequence 105, App
664	60	5.3	150	6	US-10-467-657-2040	Sequence 2040, Ap
665	60	5.3	195	7	US-11-096-568A-21216	Sequence 21216, A
666	60	5.3	246	7	US-11-073-226-1	Sequence 1, Appli
667	60	5.3	264	7	US-11-087-099-772	Sequence 772, App
668	60	5.3	289	7	US-11-087-099-8567	Sequence 8567, Ap
669	60	5.3	305	7	US-11-087-099-2861	Sequence 2861, Ap
670	60	5.3	316	6	US-10-517-696-126	Sequence 126, App
671	60	5.3	324	7	US-11-087-099-4966	Sequence 4966, Ap
672	60	5.3	324	7	US-11-087-099-8018	Sequence 8018, Ap
673	60	5.3	324	7	US-11-087-099-9180	Sequence 9180, Ap
674	60	5.3	324	7	US-11-087-099-11267	Sequence 11267, A
675	60	5.3	325	6	US-10-517-696-148	Sequence 148, App
676	60	5.3	330	7	US-11-087-099-10594	Sequence 10594, A
677	60	5.3	336	6	US-10-517-696-153	Sequence 153, App
678	60	5.3	339	7	US-11-087-099-6189	Sequence 6189, Ap
679	60	5.3	342	7	US-11-087-099-10231	Sequence 10231, A
680	60	5.3	348	7	US-11-087-099-7041	Sequence 7041, Ap
681	60	5.3	350	6	US-10-517-696-125	Sequence 125, App
682	60	5.3	361	7	US-11-087-099-2191	Sequence 2191, Ap
683	60	5.3	372	6	US-10-517-696-129	Sequence 129, App
684	60	5.3	379	6	US-10-517-696-150	Sequence 150, App
685	60	5.3	379	7	US-11-087-099-8485	Sequence 8485, Ap
686	60	5.3	379	7	US-11-087-099-11680	Sequence 11680, A
687	60	5.3	380	7	US-11-087-099-6231	Sequence 6231, Ap
688	60	5.3	380	7	US-11-087-099-8371	Sequence 8371, Ap
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690	60	5.3	390	7	US-11-098-686-10913	Sequence 10913, A
691	60	5.3	396	6	US-10-517-696-147	Sequence 147, App
692	60	5.3	398	6	US-10-517-696-136	Sequence 136, App
693	60	5.3	409	6	US-10-517-696-149	Sequence 149, App
694	60	5.3	412	7	US-11-096-568A-21231	Sequence 21231, A
695	60	5.3	420	6	US-10-517-696-141	Sequence 141, App
696	60	5.3	431	6	US-10-821-234-1285	Sequence 1285, Ap
697	60	5.3	450	7	US-11-072-512-3499	Sequence 3499, Ap
698	60	5.3	462	7	US-11-177-648-27	Sequence 27, Appl
699	60	5.3	462	7	US-11-177-648-92	Sequence 92, Appl
700	60	5.3	462	7	US-11-177-648-93	Sequence 93, Appl
701	60	5.3	462	7	US-11-177-648-94	Sequence 94, Appl
702	60	5.3	462	7	US-11-177-648-95	Sequence 95, Appl
703	60	5.3	463	6	US-10-517-696-121	Sequence 121, App
704	60	5.3	475	6	US-10-501-035-309	Sequence 309, App
705	60	5.3	475	6	US-10-517-696-117	Sequence 117, App
706	60	5.3	483	6	US-10-517-696-132	Sequence 132, App
707	60	5.3	484	6	US-10-517-696-120	Sequence 120, App
708	60	5.3	485	6	US-10-517-696-142	Sequence 142, App
709	60	5.3	491	7	US-11-072-512-3243	Sequence 3243, Ap
710	60	5.3	492	6	US-10-517-696-131	Sequence 131, App
711	60	5.3	517	6	US-10-517-696-144	Sequence 144, App
712	60	5.3	524	6	US-10-517-696-122	Sequence 122, App
713	60	5.3	533	7	US-11-147-047-33	Sequence 33, Appl
714	60	5.3	548	7	US-11-052-554A-324	Sequence 324, App
715	60	5.3	611	6	US-10-517-939-156	Sequence 156, App
716	60	5.3	614	6	US-10-517-696-128	Sequence 128, App
717	60	5.3	728	6	US-10-530-340-14	Sequence 14, Appl
718	60	5.3	755	7	US-11-037-243-82	Sequence 82, Appl
719	60	5.3	756	6	US-10-055-877-34	Sequence 34, Appl
720	60	5.3	756	6	US-10-055-877-187	Sequence 187, App
721	60	5.3	756	6	US-10-055-877-189	Sequence 189, App
722	60	5.3	761	6	US-10-485-517-252	Sequence 252, App
723	60	5.3	771	7	US-11-147-047-34	Sequence 34, Appl
724	60	5.3	813	7	US-11-096-568A-31851	Sequence 31851, A
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732	60	5.3	1613	7	US-11-108-528-86	Sequence 86, Appl
733	60	5.3	1637	6	US-10-055-877-144	Sequence 144, App
734	60	5.3	1694	7	US-11-052-554A-83	Sequence 83, Appl
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736	59.5	5.2	152	7	US-11-096-568A-7426	Sequence 7426, Ap
737	59.5	5.2	162	7	US-11-096-568A-7425	Sequence 7425, Ap
738	59.5	5.2	180	7	US-11-096-568A-7424	Sequence 7424, Ap
739	59.5	5.2	181	7	US-11-087-099-9675	Sequence 9675, Ap
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741	59.5	5.2	188	7	US-11-087-099-9413	Sequence 9413, Ap
742	59.5	5.2	236	7	US-11-096-568A-22845	Sequence 22845, A
743	59.5	5.2	276	7	US-11-096-568A-12522	Sequence 12522, A
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745	59.5	5.2	298	7	US-11-096-568A-25290	Sequence 25290, A
746	59.5	5.2	299	7	US-11-096-568A-25289	Sequence 25289, A
747	59.5	5.2	304	7	US-11-087-177-4	Sequence 4, Appli
748	59.5	5.2	312	6	US-10-986-501-124	Sequence 124, App
749	59.5	5.2	313	6	US-10-485-517-123	Sequence 123, App
750	59.5	5.2	313	6	US-10-485-517-293	Sequence 293, App
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756	59.5	5.2	347	6	US-10-821-234-1379	Sequence 1379, Ap
757	59.5	5.2	375	7	US-11-087-099-7023	Sequence 7023, Ap
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761	59.5	5.2	476	7	US-11-055-822-542	Sequence 542, App
762	59.5	5.2	476	7	US-11-055-822-1122	Sequence 1122, Ap
763	59.5	5.2	476	7	US-11-055-822-1124	Sequence 1124, Ap
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766	59.5	5.2	519	7	US-11-096-568A-22132	Sequence 22132, A
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768	59.5	5.2	553	7	US-11-055-822-266	Sequence 266, App
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773	59.5	5.2	706	7	US-11-024-959-269	Sequence 269, App
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775	59.5	5.2	726	7	US-11-096-568A-2446	Sequence 2446, Ap
776	59.5	5.2	727	7	US-11-096-568A-2445	Sequence 2445, Ap
777	59.5	5.2	816	7	US-11-143-980-67	Sequence 67, Appl
778	59.5	5.2	836	7	US-11-096-568A-2444	Sequence 2444, Ap
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782	59.5	5.2	1230	7	US-11-087-099-8922	Sequence 8922, Ap
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784	59.5	5.2	1678	7	US-11-124-367A-340	Sequence 340, App
785	59.5	5.2	1678	7	US-11-124-367A-341	Sequence 341, App
786	59.5	5.2	1970	6	US-10-821-234-1641	Sequence 1641, Ap
787	59.5	5.2	2801	7	US-11-124-368A-305	Sequence 305, App
788	59.5	5.2	2801	7	US-11-124-367A-433	Sequence 433, App
789	59.5	5.2	2896	7	US-11-124-368A-306	Sequence 306, App
790	59.5	5.2	2896	7	US-11-124-367A-434	Sequence 434, App
791	59.5	5.2	3256	7	US-11-124-368A-304	Sequence 304, App
792	59.5	5.2	3256	7	US-11-124-367A-432	Sequence 432, App
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795	59	5.2	130	7	US-11-096-568A-20919	Sequence 20919, A
796	59	5.2	132	7	US-11-072-512-2471	Sequence 2471, Ap
797	59	5.2	135	7	US-11-096-568A-1418	Sequence 1418, Ap
798	59	5.2	195	7	US-11-096-568A-1417	Sequence 1417, Ap
799	59	5.2	208	7	US-11-128-440-6	Sequence 6, Appli
800	59	5.2	214	7	US-11-096-568A-1416	Sequence 1416, Ap
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802	59	5.2	220	7	US-11-096-568A-21946	Sequence 21946, A
803	59	5.2	264	7	US-11-096-568A-8571	Sequence 8571, Ap
804	59	5.2	265	7	US-11-096-568A-8570	Sequence 8570, Ap
805	59	5.2	270	7	US-11-008-727-24	Sequence 24, Appl
806	59	5.2	281	7	US-11-087-177-3	Sequence 3, Appli
807	59	5.2	284	7	US-11-096-568A-20740	Sequence 20740, A
808	59	5.2	290	7	US-11-087-099-4115	Sequence 4115, Ap
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813	59	5.2	323	7	US-11-087-099-6769	Sequence 6769, Ap
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815	59	5.2	332	6	US-10-467-657-7154	Sequence 7154, Ap
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822	59	5.2	366	7	US-11-087-099-4705	Sequence 4705, Ap
823	59	5.2	379	7	US-11-087-099-1251	Sequence 1251, Ap
824	59	5.2	379	7	US-11-087-099-7723	Sequence 7723, Ap
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827	59	5.2	384	7	US-11-096-568A-33509	Sequence 33509, A
828	59	5.2	388	7	US-11-096-568A-33508	Sequence 33508, A
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832	59	5.2	440	7	US-11-196-475-178	Sequence 178, App
833	59	5.2	452	6	US-10-641-678-50	Sequence 50, Appl
834	59	5.2	461	7	US-11-183-205-32	Sequence 32, Appl
835	59	5.2	462	7	US-11-177-648-96	Sequence 96, Appl

836	59	5.2	492	6	US-10-501-035-359	Sequence 359, App
837	59	5.2	494	6	US-10-793-626-36	Sequence 36, Appl
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839	59	5.2	515	6	US-10-517-696-114	Sequence 114, App
840	59	5.2	524	6	US-10-517-696-113	Sequence 113, App
841	59	5.2	525	7	US-11-098-686-10993	Sequence 10993, A
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843	59	5.2	533	7	US-11-072-512-3224	Sequence 3224, Ap
844	59	5.2	552	7	US-11-151-601-25	Sequence 25, Appl
845	59	5.2	564	7	US-11-186-284-199	Sequence 199, App
846	59	5.2	576	6	US-10-530-340-12	Sequence 12, Appl
847	59	5.2	579	7	US-11-072-512-2360	Sequence 2360, Ap
848	59	5.2	586	7	US-11-054-281-93	Sequence 93, Appl
849	59	5.2	592	7	US-11-087-099-912	Sequence 912, App
850	59	5.2	626	7	US-11-072-512-2827	Sequence 2827, Ap
851	59	5.2	663	7	US-11-087-099-3211	Sequence 3211, Ap
852	59	5.2	681	7	US-11-096-568A-2501	Sequence 2501, Ap
853	59	5.2	696	7	US-11-256-548-23	Sequence 23, Appl
854	59	5.2	703	7	US-11-065-695-4	Sequence 4, Appli
855	59	5.2	720	7	US-11-256-548-6	Sequence 6, Appli
856	59	5.2	728	7	US-11-087-099-9526	Sequence 9526, Ap
857	59	5.2	735	7	US-11-087-099-8719	Sequence 8719, Ap
858	59	5.2	856	6	US-10-510-947-8	Sequence 8, Appli
859	59	5.2	856	7	US-11-042-988-13	Sequence 13, Appl
860	59	5.2	856	7	US-11-135-235-1	Sequence 1, Appli
861	59	5.2	932	7	US-11-188-743-17	Sequence 17, Appl
862	59	5.2	932	7	US-11-188-743-18	Sequence 18, Appl
863	59	5.2	932	7	US-11-183-294-18	Sequence 18, Appl
864	59	5.2	1121	7	US-11-087-099-10482	Sequence 10482, A
865	59	5.2	1203	7	US-11-096-568A-33183	Sequence 33183, A
866	59	5.2	1344	7	US-11-072-512-2452	Sequence 2452, Ap
867	59	5.2	1372	7	US-11-096-568A-33182	Sequence 33182, A
868	59	5.2	1395	7	US-11-096-568A-33181	Sequence 33181, A
869	59	5.2	1690	6	US-10-330-773-389	Sequence 389, App
870	59	5.2	2426	7	US-11-203-806A-11	Sequence 11, Appl
871	59	5.2	2432	6	US-10-821-234-899	Sequence 899, App
872	58.5	5.1	146	6	US-10-821-234-1225	Sequence 1225, Ap
873	58.5	5.1	190	7	US-11-096-568A-631	Sequence 631, App
874	58.5	5.1	196	6	US-10-967-527A-27	Sequence 27, Appl
875	58.5	5.1	207	7	US-11-096-568A-6266	Sequence 6266, Ap
876	58.5	5.1	209	7	US-11-096-568A-630	Sequence 630, App
877	58.5	5.1	237	7	US-11-096-568A-6265	Sequence 6265, Ap
878	58.5	5.1	253	7	US-11-096-568A-15019	Sequence 15019, A
879	58.5	5.1	258	7	US-11-096-568A-149	Sequence 149, App
880	58.5	5.1	262	7	US-11-096-568A-6264	Sequence 6264, Ap
881	58.5	5.1	277	7	US-11-096-568A-10326	Sequence 10326, A
882	58.5	5.1	284	7	US-11-096-568A-6263	Sequence 6263, Ap
883	58.5	5.1	293	7	US-11-096-568A-12293	Sequence 12293, A
884	58.5	5.1	299	7	US-11-072-512-2792	Sequence 2792, Ap
885	58.5	5.1	300	7	US-11-096-568A-10325	Sequence 10325, A
886	58.5	5.1	308	7	US-11-072-512-3898	Sequence 3898, Ap
887	58.5	5.1	316	7	US-11-096-568A-28013	Sequence 28013, A
888	58.5	5.1	325	7	US-11-096-568A-24112	Sequence 24112, A
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890	58.5	5.1	369	7	US-11-096-568A-24111	Sequence 24111, A
891	58.5	5.1	373	7	US-11-096-568A-24110	Sequence 24110, A
892	58.5	5.1	409	7	US-11-096-568A-7532	Sequence 7532, Ap
893	58.5	5.1	461	7	US-11-096-568A-22134	Sequence 22134, A
894	58.5	5.1	486	7	US-11-057-012-11	Sequence 11, Appl
895	58.5	5.1	496	7	US-11-182-016-33	Sequence 33, Appl
896	58.5	5.1	500	7	US-11-087-100-8	Sequence 8, Appli
897	58.5	5.1	500	7	US-11-087-084-8	Sequence 8, Appli
898	58.5	5.1	500	7	US-11-087-085-8	Sequence 8, Appli
899	58.5	5.1	530	7	US-11-124-367A-314	Sequence 314, App
900	58.5	5.1	540	7	US-11-212-443-167	Sequence 167, App
901	58.5	5.1	621	7	US-11-087-099-2170	Sequence 2170, Ap
902	58.5	5.1	654	7	US-11-096-568A-30428	Sequence 30428, A
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904	58.5	5.1	740	7	US-11-124-367A-293	Sequence 293, App
905	58.5	5.1	760	7	US-11-124-367A-292	Sequence 292, App
906	58.5	5.1	761	7	US-11-212-443-22	Sequence 22, Appl
907	58.5	5.1	801	7	US-11-052-554A-166	Sequence 166, App
908	58.5	5.1	807	7	US-11-096-568A-30427	Sequence 30427, A
909	58.5	5.1	810	6	US-10-453-372-1116	Sequence 1116, Ap
910	58.5	5.1	820	6	US-10-491-468-14	Sequence 14, Appl
911	58.5	5.1	820	7	US-11-165-819-1	Sequence 1, Appli
912	58.5	5.1	821	7	US-11-096-568A-30426	Sequence 30426, A
913	58.5	5.1	895	7	US-11-096-568A-29626	Sequence 29626, A
914	58.5	5.1	941	7	US-11-124-367A-313	Sequence 313, App
915	58.5	5.1	941	7	US-11-124-367A-315	Sequence 315, App
916	58.5	5.1	1236	6	US-10-873-528-109	Sequence 109, App
917	58.5	5.1	1498	6	US-10-501-035-226	Sequence 226, App
918	58.5	5.1	1532	7	US-11-212-443-62	Sequence 62, Appl
919	58.5	5.1	2059	7	US-11-087-100-4	Sequence 4, Appli
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921	58.5	5.1	2059	7	US-11-087-085-4	Sequence 4, Appli
922	58.5	5.1	3623	6	US-10-995-561-593	Sequence 593, App
923	58	5.1	121	7	US-11-096-568A-20921	Sequence 20921, A
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925	58	5.1	187	7	US-11-096-568A-32157	Sequence 32157, A
926	58	5.1	246	6	US-10-467-657-2424	Sequence 2424, Ap
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928	58	5.1	261	7	US-11-087-099-8985	Sequence 8985, Ap
929	58	5.1	292	6	US-10-858-730-18	Sequence 18, Appl
930	58	5.1	327	6	US-10-055-877-183	Sequence 183, App
931	58	5.1	339	6	US-10-498-026-35	Sequence 35, Appl
932	58	5.1	339	6	US-10-498-026-36	Sequence 36, Appl
933	58	5.1	345	7	US-11-072-512-3496	Sequence 3496, Ap
934	58	5.1	352	7	US-11-087-099-5875	Sequence 5875, Ap
935	58	5.1	361	7	US-11-087-099-4996	Sequence 4996, Ap
936	58	5.1	364	6	US-10-481-935A-201	Sequence 201, App
937	58	5.1	375	7	US-11-096-568A-23618	Sequence 23618, A
938	58	5.1	379	7	US-11-087-099-3007	Sequence 3007, Ap
939	58	5.1	379	7	US-11-087-099-3480	Sequence 3480, Ap
940	58	5.1	379	7	US-11-087-099-4624	Sequence 4624, Ap
941	58	5.1	379	7	US-11-087-099-8557	Sequence 8557, Ap
942	58	5.1	389	7	US-11-087-099-1556	Sequence 1556, Ap
943	58	5.1	406	6	US-10-821-234-1521	Sequence 1521, Ap
944	58	5.1	422	7	US-11-087-099-11257	Sequence 11257, A
945	58	5.1	441	7	US-11-024-959-280	Sequence 280, App
946	58	5.1	441	7	US-11-024-959-281	Sequence 281, App
947	58	5.1	462	7	US-11-177-648-97	Sequence 97, Appl
948	58	5.1	497	7	US-11-072-512-3603	Sequence 3603, Ap
949	58	5.1	557	6	US-10-821-234-895	Sequence 895, App
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955	58	5.1	714	7	US-11-121-419-17	Sequence 17, Appl
956	58	5.1	717	7	US-11-050-857-954	Sequence 954, App
957	58	5.1	717	7	US-11-051-720-1695	Sequence 1695, Ap
958	58	5.1	754	6	US-10-467-962B-63	Sequence 63, Appl
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963	58	5.1	1165	7	US-11-202-330-4	Sequence 4, Appli
964	58	5.1	1263	7	US-11-076-163-3	Sequence 3, Appli
965	58	5.1	1362	7	US-11-043-693-33	Sequence 33, Appl
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974	57.5	5.1	234	6	US-10-401-386B-8	Sequence 8, Appli
975	57.5	5.1	238	7	US-11-096-568A-3196	Sequence 3196, Ap
976	57.5	5.1	238	7	US-11-096-568A-3198	Sequence 3198, Ap
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980	57.5	5.1	261	7	US-11-138-242A-10	Sequence 10, Appl
981	57.5	5.1	261	7	US-11-150-066-8	Sequence 8, Appli
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984	57.5	5.1	261	7	US-11-155-288-10	Sequence 10, Appl
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994	57.5	5.1	306	6	US-10-793-626-2490	Sequence 2490, Ap
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1012	57.5	5.1	446	7	US-11-102-621-139	Sequence 139, App
1013	57.5	5.1	446	7	US-11-102-621-140	Sequence 140, App
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1067	57	5.0	241	7	US-11-149-462-4	Sequence 4, Appli
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1159	57	5.0	1129	6	US-10-995-561-706	Sequence 706, App
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1172	57	5.0	1972	6	US-10-995-561-664	Sequence 664, App
1173	57	5.0	1972	6	US-10-995-561-666	Sequence 666, App
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1180	56.5	5.0	164	7	US-11-096-568A-3342	Sequence 3342, Ap
1181	56.5	5.0	175	7	US-11-096-568A-16109	Sequence 16109, A
1182	56.5	5.0	196	7	US-11-096-568A-16108	Sequence 16108, A
1183	56.5	5.0	210	7	US-11-087-099-12364	Sequence 12364, A
1184	56.5	5.0	220	7	US-11-096-568A-21253	Sequence 21253, A
1185	56.5	5.0	221	7	US-11-112-481C-2	Sequence 2, Appli
1186	56.5	5.0	221	7	US-11-112-481C-3	Sequence 3, Appli
1187	56.5	5.0	229	7	US-11-096-568A-19426	Sequence 19426, A
1188	56.5	5.0	233	7	US-11-096-568A-29421	Sequence 29421, A
1189	56.5	5.0	248	7	US-11-096-568A-19425	Sequence 19425, A
1190	56.5	5.0	251	7	US-11-054-515-976	Sequence 976, App
1191	56.5	5.0	251	7	US-11-054-515-979	Sequence 979, App
1192	56.5	5.0	254	7	US-11-087-099-8347	Sequence 8347, Ap
1193	56.5	5.0	261	7	US-11-138-242A-3	Sequence 3, Appli
1194	56.5	5.0	261	7	US-11-150-066-3	Sequence 3, Appli
1195	56.5	5.0	262	7	US-11-096-568A-33133	Sequence 33133, A
1196	56.5	5.0	265	7	US-11-087-099-5951	Sequence 5951, Ap
1197	56.5	5.0	266	7	US-11-096-568A-22358	Sequence 22358, A
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1202	56.5	5.0	353	6	US-10-493-909-16	Sequence 16, Appl
1203	56.5	5.0	353	7	US-11-022-289-9	Sequence 9, Appli
1204	56.5	5.0	354	6	US-10-999-866-31	Sequence 31, Appl
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1206	56.5	5.0	354	7	US-11-061-821-31	Sequence 31, Appl
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1215	56.5	5.0	423	7	US-11-096-568A-29312	Sequence 29312, A
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1222	56.5	5.0	442	7	US-11-102-621-125	Sequence 125, App
1223	56.5	5.0	442	7	US-11-102-621-127	Sequence 127, App
1224	56.5	5.0	442	7	US-11-102-621-128	Sequence 128, App
1225	56.5	5.0	457	6	US-10-467-657-5134	Sequence 5134, Ap
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1231	56.5	5.0	508	7	US-11-072-512-3233	Sequence 3233, Ap
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1235	56.5	5.0	569	7	US-11-096-568A-6975	Sequence 6975, Ap
1236	56.5	5.0	596	7	US-11-087-099-2777	Sequence 2777, Ap
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1238	56.5	5.0	598	7	US-11-096-568A-6974	Sequence 6974, Ap
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1240	56.5	5.0	603	7	US-11-126-022-33	Sequence 33, Appl
1241	56.5	5.0	603	7	US-11-126-022-36	Sequence 36, Appl
1242	56.5	5.0	603	7	US-11-126-022-37	Sequence 37, Appl
1243	56.5	5.0	737	6	US-10-055-877-156	Sequence 156, App
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1246	56.5	5.0	755	6	US-10-467-657-6342	Sequence 6342, Ap
1247	56.5	5.0	755	6	US-10-517-939-330	Sequence 330, App
1248	56.5	5.0	756	7	US-11-188-743-20	Sequence 20, Appl
1249	56.5	5.0	756	7	US-11-183-294-22	Sequence 22, Appl
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1252	56.5	5.0	882	6	US-10-453-372-60	Sequence 60, Appl
1253	56.5	5.0	884	6	US-10-453-372-58	Sequence 58, Appl
1254	56.5	5.0	1048	6	US-10-912-580-6	Sequence 6, Appli
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1257	56.5	5.0	1208	6	US-10-330-773-244	Sequence 244, App
1258	56.5	5.0	1438	6	US-10-453-372-796	Sequence 796, App
1259	56.5	5.0	3104	6	US-10-453-372-34	Sequence 34, Appl
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1262	56.5	5.0	3130	6	US-10-453-372-42	Sequence 42, Appl
1263	56.5	5.0	3483	6	US-10-453-372-40	Sequence 40, Appl
1264	56.5	5.0	3546	6	US-10-453-372-32	Sequence 32, Appl
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1267	56	4.9	145	7	US-11-152-601-42	Sequence 42, Appl
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1277	56	4.9	262	7	US-11-096-568A-21488	Sequence 21488, A
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1288	56	4.9	340	7	US-11-096-568A-237	Sequence 237, App
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1303	56	4.9	396	7	US-11-087-099-7884	Sequence 7884, Ap
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1314	56	4.9	442	6	US-10-877-346-23	Sequence 23, Appl
1315	56	4.9	442	6	US-10-877-346-55	Sequence 55, Appl
1316	56	4.9	442	6	US-10-877-346-56	Sequence 56, Appl
1317	56	4.9	442	7	US-11-096-568A-20632	Sequence 20632, A
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1324	56	4.9	470	6	US-10-453-372-622	Sequence 622, App
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1327	56	4.9	512	7	US-11-072-512-3513	Sequence 3513, Ap
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1329	56	4.9	546	7	US-11-096-568A-2412	Sequence 2412, Ap
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1337	56	4.9	750	7	US-11-087-099-5543	Sequence 5543, Ap
1338	56	4.9	865	7	US-11-087-099-1496	Sequence 1496, Ap
1339	56	4.9	943	7	US-11-024-959-487	Sequence 487, App
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1342	56	4.9	1074	6	US-10-501-035-311	Sequence 311, App
1343	56	4.9	1081	7	US-11-113-751-38	Sequence 38, Appl
1344	56	4.9	1116	7	US-11-113-751-34	Sequence 34, Appl
1345	56	4.9	1140	7	US-11-087-099-11073	Sequence 11073, A
1346	56	4.9	1142	7	US-11-044-051-73	Sequence 73, Appl
1347	56	4.9	1151	7	US-11-113-751-36	Sequence 36, Appl
1348	56	4.9	1217	7	US-11-074-176-252	Sequence 252, App
1349	56	4.9	1342	7	US-11-149-003-24	Sequence 24, Appl
1350	56	4.9	1382	7	US-11-098-686-10797	Sequence 10797, A
1351	56	4.9	1477	7	US-11-149-003-8	Sequence 8, Appli
1352	56	4.9	1512	7	US-11-149-003-10	Sequence 10, Appl
1353	56	4.9	1570	6	US-10-330-773-936	Sequence 936, App
1354	56	4.9	1593	7	US-11-149-003-4	Sequence 4, Appli
1355	56	4.9	1628	7	US-11-149-003-2	Sequence 2, Appli
1356	56	4.9	1839	7	US-11-087-099-9631	Sequence 9631, Ap
1357	56	4.9	2362	7	US-11-096-568A-31778	Sequence 31778, A
1358	56	4.9	2410	7	US-11-175-689-8	Sequence 8, Appli
1359	56	4.9	2433	7	US-11-096-568A-31777	Sequence 31777, A
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1363	55.5	4.9	136	7	US-11-049-536-36	Sequence 36, Appl
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1366	55.5	4.9	149	6	US-10-714-887-160	Sequence 160, App
1367	55.5	4.9	171	7	US-11-096-568A-13784	Sequence 13784, A
1368	55.5	4.9	192	7	US-11-096-568A-19480	Sequence 19480, A
1369	55.5	4.9	200	7	US-11-096-568A-16604	Sequence 16604, A
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1373	55.5	4.9	224	7	US-11-096-568A-15262	Sequence 15262, A
1374	55.5	4.9	232	7	US-11-096-568A-244	Sequence 244, App
1375	55.5	4.9	232	7	US-11-096-568A-246	Sequence 246, App
1376	55.5	4.9	238	7	US-11-096-568A-27672	Sequence 27672, A
1377	55.5	4.9	239	7	US-11-096-568A-16153	Sequence 16153, A
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1379	55.5	4.9	244	7	US-11-090-878-68	Sequence 68, Appl
1380	55.5	4.9	244	7	US-11-090-878-69	Sequence 69, Appl
1381	55.5	4.9	245	6	US-10-948-429A-10	Sequence 10, Appl
1382	55.5	4.9	250	7	US-11-096-568A-15261	Sequence 15261, A
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1385	55.5	4.9	277	7	US-11-096-568A-1871	Sequence 1871, Ap
1386	55.5	4.9	277	7	US-11-096-568A-27199	Sequence 27199, A
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1388	55.5	4.9	291	7	US-11-096-568A-26427	Sequence 26427, A
1389	55.5	4.9	291	7	US-11-096-568A-32907	Sequence 32907, A
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1391	55.5	4.9	294	7	US-11-096-568A-19479	Sequence 19479, A
1392	55.5	4.9	311	7	US-11-087-099-5603	Sequence 5603, Ap
1393	55.5	4.9	311	7	US-11-096-568A-15260	Sequence 15260, A
1394	55.5	4.9	322	6	US-10-793-626-270	Sequence 270, App
1395	55.5	4.9	323	6	US-10-467-657-1540	Sequence 1540, Ap
1396	55.5	4.9	339	7	US-11-087-099-7254	Sequence 7254, Ap
1397	55.5	4.9	344	7	US-11-096-568A-19478	Sequence 19478, A
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1407	55.5	4.9	417	6	US-10-858-730-60	Sequence 60, Appl
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1409	55.5	4.9	419	7	US-11-087-099-4639	Sequence 4639, Ap
1410	55.5	4.9	429	7	US-11-087-099-5527	Sequence 5527, Ap
1411	55.5	4.9	431	6	US-10-467-657-2532	Sequence 2532, Ap
1412	55.5	4.9	447	7	US-11-072-512-2688	Sequence 2688, Ap
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1416	55.5	4.9	473	7	US-11-139-195-5	Sequence 5, Appli
1417	55.5	4.9	491	6	US-10-793-626-2808	Sequence 2808, Ap
1418	55.5	4.9	503	7	US-11-139-195-2	Sequence 2, Appli
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1421	55.5	4.9	539	7	US-11-201-916-18	Sequence 18, Appl
1422	55.5	4.9	548	7	US-11-087-099-5580	Sequence 5580, Ap
1423	55.5	4.9	548	7	US-11-087-099-11395	Sequence 11395, A
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1425	55.5	4.9	577	7	US-11-201-916-31	Sequence 31, Appl

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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182	79	7.0	455	2	US-09-949-016-10761	Sequence 10761, A
183	79	7.0	629	2	US-09-241-581B-6	Sequence 6, Appli
184	79	7.0	629	2	US-08-265-428-6	Sequence 6, Appli
185	79	7.0	629	4	PCT-US95-07721-6	Sequence 6, Appli
186	78.5	6.9	130	2	US-08-700-651-9	Sequence 9, Appli
187	78.5	6.9	130	2	US-08-928-361B-14	Sequence 14, Appl
188	78.5	6.9	130	2	US-09-588-995A-14	Sequence 14, Appl
189	78.5	6.9	322	2	US-09-248-796A-23680	Sequence 23680, A
190	78.5	6.9	507	2	US-09-949-016-8889	Sequence 8889, Ap
191	78.5	6.9	507	2	US-09-949-016-8897	Sequence 8897, Ap
192	78.5	6.9	590	2	US-09-520-781-12	Sequence 12, Appl
193	78.5	6.9	590	2	US-09-957-187-12	Sequence 12, Appl
194	78.5	6.9	590	2	US-09-991-053-12	Sequence 12, Appl
195	78.5	6.9	653	2	US-09-520-781-10	Sequence 10, Appl
196	78.5	6.9	653	2	US-09-957-187-10	Sequence 10, Appl
197	78.5	6.9	653	2	US-09-991-053-10	Sequence 10, Appl
198	78.5	6.9	685	2	US-09-248-796A-20197	Sequence 20197, A
199	78	6.9	261	2	US-09-248-796A-14279	Sequence 14279, A
200	78	6.9	400	2	US-10-300-819B-2	Sequence 2, Appli
201	78	6.9	609	2	US-09-198-452A-579	Sequence 579, App
202	78	6.9	1744	2	US-09-438-185A-542	Sequence 542, App
203	77.5	6.8	346	1	US-08-687-702-36	Sequence 36, Appl
204	77.5	6.8	497	2	US-09-377-557-10	Sequence 10, Appl
205	77.5	6.8	514	2	US-08-738-168B-15	Sequence 15, Appl
206	77.5	6.8	562	1	US-08-687-702-1	Sequence 1, Appli
207	77.5	6.8	673	2	US-09-949-016-7388	Sequence 7388, Ap
208	77	6.8	249	2	US-08-700-651-15	Sequence 15, Appl
209	77	6.8	249	2	US-08-928-361B-20	Sequence 20, Appl
210	77	6.8	249	2	US-09-588-995A-20	Sequence 20, Appl
211	77	6.8	714	2	US-09-949-016-7038	Sequence 7038, Ap
212	77	6.8	750	2	US-09-165-239A-4	Sequence 4, Appli
213	77	6.8	2123	2	US-08-968-685A-10	Sequence 10, Appl
214	76.5	6.7	134	2	US-09-248-796A-27317	Sequence 27317, A
215	76.5	6.7	217	2	US-09-949-016-11174	Sequence 11174, A
216	76.5	6.7	303	2	US-09-248-796A-14269	Sequence 14269, A
217	76.5	6.7	348	2	US-09-216-295-16	Sequence 16, Appl
218	76.5	6.7	348	2	US-09-632-570-16	Sequence 16, Appl
219	76.5	6.7	348	2	US-09-632-575-46	Sequence 46, Appl
220	76.5	6.7	452	2	US-09-248-796A-16219	Sequence 16219, A
221	76.5	6.7	653	2	US-09-991-181-229	Sequence 229, App
222	76.5	6.7	653	2	US-09-990-444-229	Sequence 229, App
223	76.5	6.7	653	2	US-09-997-333-229	Sequence 229, App
224	76.5	6.7	653	2	US-09-992-598-229	Sequence 229, App
225	76	6.7	321	2	US-09-248-796A-20146	Sequence 20146, A
226	76	6.7	334	2	US-09-197-970B-7	Sequence 7, Appli
227	76	6.7	380	2	US-09-134-001C-4558	Sequence 4558, Ap
228	76	6.7	509	2	US-09-907-794A-315	Sequence 315, App
229	76	6.7	509	2	US-09-905-125A-315	Sequence 315, App
230	76	6.7	509	2	US-09-902-775A-315	Sequence 315, App
231	76	6.7	509	2	US-09-906-700-315	Sequence 315, App
232	76	6.7	509	2	US-09-903-603A-315	Sequence 315, App
233	76	6.7	509	2	US-09-904-920A-315	Sequence 315, App
234	76	6.7	509	2	US-09-909-064-315	Sequence 315, App
235	76	6.7	509	2	US-09-905-381A-315	Sequence 315, App
236	76	6.7	509	2	US-09-906-618-315	Sequence 315, App
237	76	6.7	509	2	US-09-906-646-315	Sequence 315, App
238	76	6.7	509	2	US-09-904-462-315	Sequence 315, App
239	76	6.7	509	2	US-09-902-736A-315	Sequence 315, App
240	76	6.7	509	2	US-09-906-722A-315	Sequence 315, App
241	76	6.7	1426	2	US-09-136-574A-43	Sequence 43, Appl
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243	75.5	6.6	348	1	US-08-504-511A-2	Sequence 2, Appli
244	75.5	6.6	430	1	US-08-035-392-4	Sequence 4, Appli
245	75.5	6.6	430	1	US-08-504-511A-4	Sequence 4, Appli
246	75.5	6.6	453	2	US-09-230-225B-4	Sequence 4, Appli

247	75.5	6.6	468	1	US-08-959-011-3	Sequence 3, Appli
248	75.5	6.6	478	2	US-09-345-473E-51	Sequence 51, Appl
249	75.5	6.6	478	2	US-09-862-027-51	Sequence 51, Appl
250	75.5	6.6	511	1	US-08-220-151-17	Sequence 17, Appl
251	75.5	6.6	511	1	US-08-413-118-17	Sequence 17, Appl
252	75.5	6.6	511	2	US-08-473-446-17	Sequence 17, Appl
253	75.5	6.6	736	2	US-09-457-040B-26	Sequence 26, Appl
254	75	6.6	554	1	US-08-524-051-2	Sequence 2, Appli
255	75	6.6	554	2	US-09-052-778-16	Sequence 16, Appl
256	74.5	6.6	109	2	US-09-107-532A-4999	Sequence 4999, Ap
257	74.5	6.6	145	2	US-08-808-599A-41	Sequence 41, Appl
258	74.5	6.6	186	2	US-09-252-991A-20433	Sequence 20433, A
259	74.5	6.6	299	2	US-09-270-767-44350	Sequence 44350, A
260	74.5	6.6	333	2	US-09-107-532A-6475	Sequence 6475, Ap
261	74.5	6.6	494	2	US-09-248-796A-16546	Sequence 16546, A
262	74.5	6.6	794	2	US-09-252-991A-28569	Sequence 28569, A
263	74.5	6.6	998	1	US-08-449-645A-20	Sequence 20, Appl
264	74.5	6.6	998	1	US-08-702-367A-20	Sequence 20, Appl
265	74.5	6.6	998	4	PCT-US95-04681-20	Sequence 20, Appl
266	74.5	6.6	1075	2	US-09-487-558B-110	Sequence 110, App
267	74	6.5	205	2	US-09-248-796A-21984	Sequence 21984, A
268	74	6.5	323	2	US-09-270-767-44688	Sequence 44688, A
269	74	6.5	370	2	US-09-270-767-37418	Sequence 37418, A
270	74	6.5	370	2	US-09-270-767-52635	Sequence 52635, A
271	74	6.5	432	2	US-09-248-796A-18913	Sequence 18913, A
272	74	6.5	542	2	US-09-538-092-289	Sequence 289, App
273	74	6.5	2414	1	US-08-227-536-2	Sequence 2, Appli
274	74	6.5	2414	2	US-09-538-092-1289	Sequence 1289, Ap
275	74	6.5	2414	4	PCT-US95-04682-2	Sequence 2, Appli
276	73.5	6.5	124	2	US-08-700-651-11	Sequence 11, Appl
277	73.5	6.5	124	2	US-08-928-361B-16	Sequence 16, Appl
278	73.5	6.5	124	2	US-09-588-995A-16	Sequence 16, Appl
279	73.5	6.5	128	2	US-08-700-651-7	Sequence 7, Appli
280	73.5	6.5	128	2	US-08-928-361B-12	Sequence 12, Appl
281	73.5	6.5	128	2	US-09-588-995A-12	Sequence 12, Appl
282	73.5	6.5	130	2	US-08-700-651-8	Sequence 8, Appli
283	73.5	6.5	130	2	US-08-928-361B-13	Sequence 13, Appl
284	73.5	6.5	130	2	US-09-588-995A-13	Sequence 13, Appl
285	73.5	6.5	138	2	US-08-700-651-10	Sequence 10, Appl
286	73.5	6.5	138	2	US-08-928-361B-15	Sequence 15, Appl
287	73.5	6.5	138	2	US-09-588-995A-15	Sequence 15, Appl
288	73.5	6.5	251	2	US-09-248-796A-23216	Sequence 23216, A
289	73.5	6.5	427	1	US-08-282-197C-53	Sequence 53, Appl
290	73.5	6.5	451	1	US-08-287-001A-2	Sequence 2, Appli
291	73.5	6.5	451	4	PCT-US95-09941-2	Sequence 2, Appli
292	73.5	6.5	570	2	US-09-565-501A-104	Sequence 104, App
293	73.5	6.5	570	2	US-09-639-206A-104	Sequence 104, App
294	73.5	6.5	570	2	US-09-874-923-104	Sequence 104, App
295	73.5	6.5	595	1	US-08-232-087A-2	Sequence 2, Appli
296	73.5	6.5	595	2	US-09-006-353A-9	Sequence 9, Appli
297	73.5	6.5	595	2	US-09-573-986-9	Sequence 9, Appli
298	73.5	6.5	595	2	US-09-949-016-6048	Sequence 6048, Ap
299	73.5	6.5	642	2	US-09-949-016-8043	Sequence 8043, Ap
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303	73.5	6.5	795	2	US-10-055-412B-11	Sequence 11, Appl
304	73.5	6.5	821	2	US-09-193-562D-12	Sequence 12, Appl
305	73.5	6.5	821	2	US-10-055-412B-12	Sequence 12, Appl
306	73.5	6.5	905	2	US-09-193-562D-2	Sequence 2, Appli
307	73.5	6.5	905	2	US-10-055-412B-2	Sequence 2, Appli
308	73.5	6.5	1101	2	US-09-561-709B-5	Sequence 5, Appli
309	73.5	6.5	1761	2	US-09-561-709B-1	Sequence 1, Appli
310	73	6.4	155	2	US-09-252-991A-22634	Sequence 22634, A
311	73	6.4	162	2	US-08-700-651-13	Sequence 13, Appl
312	73	6.4	332	2	US-09-313-942-10	Sequence 10, Appl
313	73	6.4	332	2	US-10-282-162-10	Sequence 10, Appl
314	73	6.4	488	1	US-08-599-455B-5	Sequence 5, Appli
315	73	6.4	488	2	US-09-069-781B-5	Sequence 5, Appli
316	73	6.4	488	2	US-09-137-132-5	Sequence 5, Appli
317	73	6.4	488	2	US-08-864-564A-5	Sequence 5, Appli
318	73	6.4	488	2	US-09-094-410-5	Sequence 5, Appli
319	73	6.4	488	2	US-08-708-123D-5	Sequence 5, Appli
320	73	6.4	488	2	US-08-583-153A-5	Sequence 5, Appli
321	73	6.4	488	2	US-08-638-524B-5	Sequence 5, Appli
322	73	6.4	579	2	US-09-198-452A-918	Sequence 918, App
323	73	6.4	606	2	US-09-438-185A-853	Sequence 853, App
324	73	6.4	624	2	US-09-877-730-24	Sequence 24, Appl
325	73	6.4	639	2	US-09-949-016-6812	Sequence 6812, Ap
326	73	6.4	652	2	US-09-949-016-7323	Sequence 7323, Ap
327	73	6.4	658	1	US-08-825-558-4	Sequence 4, Appli
328	73	6.4	658	2	US-09-312-611-4	Sequence 4, Appli
329	73	6.4	708	1	US-07-797-556-2	Sequence 2, Appli
330	73	6.4	708	1	US-08-308-881-2	Sequence 2, Appli
331	73	6.4	708	1	US-09-058-263-2	Sequence 2, Appli
332	73	6.4	708	1	US-09-059-099-2	Sequence 2, Appli
333	73	6.4	708	2	US-09-058-264-2	Sequence 2, Appli
334	73	6.4	708	2	US-09-455-962-2	Sequence 2, Appli
335	73	6.4	708	4	PCT-US95-06530-2	Sequence 2, Appli
336	73	6.4	712	2	US-09-877-730-22	Sequence 22, Appl
337	73	6.4	793	2	US-09-877-730-28	Sequence 28, Appl
338	73	6.4	852	2	US-09-206-551-19	Sequence 19, Appl
339	73	6.4	859	2	US-09-313-942-7	Sequence 7, Appli
340	73	6.4	859	2	US-10-282-162-7	Sequence 7, Appli
341	73	6.4	918	1	US-08-825-558-6	Sequence 6, Appli
342	73	6.4	918	2	US-09-312-611-6	Sequence 6, Appli
343	73	6.4	918	2	US-09-853-180B-3	Sequence 3, Appli
344	73	6.4	918	2	US-09-949-002-333	Sequence 333, App
345	73	6.4	937	2	US-09-949-002-536	Sequence 536, App
346	73	6.4	951	2	US-09-313-942-9	Sequence 9, Appli
347	73	6.4	951	2	US-10-282-162-9	Sequence 9, Appli
348	73	6.4	991	2	US-09-877-730-12	Sequence 12, Appl
349	73	6.4	1069	2	US-09-877-730-2	Sequence 2, Appli
350	73	6.4	1072	2	US-09-877-730-18	Sequence 18, Appl
351	73	6.4	1150	2	US-09-877-730-8	Sequence 8, Appli
352	73	6.4	1158	2	US-09-313-942-26	Sequence 26, Appl
353	73	6.4	1158	2	US-10-282-162-26	Sequence 26, Appl
354	73	6.4	1168	2	US-09-313-942-24	Sequence 24, Appl
355	73	6.4	1168	2	US-10-282-162-24	Sequence 24, Appl
356	73	6.4	1312	2	US-09-345-882-29	Sequence 29, Appl
357	73	6.4	1312	2	US-10-071-179-29	Sequence 29, Appl
358	73	6.4	2736	2	US-09-252-991A-30227	Sequence 30227, A
359	72.5	6.4	150	2	US-08-928-361B-18	Sequence 18, Appl
360	72.5	6.4	150	2	US-09-588-995A-18	Sequence 18, Appl
361	72.5	6.4	185	2	US-09-248-796A-18311	Sequence 18311, A
362	72.5	6.4	293	2	US-09-496-320-5	Sequence 5, Appli
363	72.5	6.4	328	2	US-09-489-039A-12803	Sequence 12803, A
364	72.5	6.4	463	1	US-08-162-402B-9	Sequence 9, Appli
365	72.5	6.4	806	1	US-08-270-076A-11	Sequence 11, Appl
366	72.5	6.4	841	2	US-09-949-016-9669	Sequence 9669, Ap
367	72.5	6.4	878	2	US-09-556-706B-2	Sequence 2, Appli
368	72.5	6.4	878	2	US-09-724-418A-2	Sequence 2, Appli
369	72.5	6.4	907	2	US-08-783-774-2	Sequence 2, Appli
370	72.5	6.4	907	2	US-09-328-599A-1	Sequence 1, Appli
371	72.5	6.4	907	4	PCT-US95-04611A-19	Sequence 19, Appl
372	72	6.3	279	2	US-09-248-796A-16859	Sequence 16859, A
373	72	6.3	300	2	US-09-254-465A-10	Sequence 10, Appl
374	72	6.3	300	2	US-09-397-243D-12	Sequence 12, Appl
375	72	6.3	300	2	US-09-953-499-10	Sequence 10, Appl
376	72	6.3	489	2	US-09-545-814-29	Sequence 29, Appl
377	72	6.3	557	2	US-09-248-796A-26892	Sequence 26892, A
378	72	6.3	559	2	US-09-545-814-14	Sequence 14, Appl
379	72	6.3	583	2	US-09-545-814-2	Sequence 2, Appli
380	72	6.3	583	2	US-09-545-814-5	Sequence 5, Appli
381	72	6.3	635	2	US-09-545-814-32	Sequence 32, Appl
382	72	6.3	785	2	US-08-374-077C-3	Sequence 3, Appli
383	72	6.3	785	2	US-08-895-590-3	Sequence 3, Appli
384	72	6.3	785	2	US-09-539-879A-3	Sequence 3, Appli
385	72	6.3	941	2	US-07-757-022B-14	Sequence 14, Appl
386	72	6.3	1022	2	US-07-757-022B-84	Sequence 84, Appl
387	72	6.3	1038	2	US-07-757-022B-74	Sequence 74, Appl
388	72	6.3	1049	2	US-07-757-022B-58	Sequence 58, Appl
389	72	6.3	1129	2	US-09-023-905A-2	Sequence 2, Appli
390	72	6.3	1140	2	US-07-757-022B-104	Sequence 104, App
391	72	6.3	1203	2	US-09-351-200-2	Sequence 2, Appli
392	72	6.3	1270	2	US-07-757-022B-44	Sequence 44, Appl

393	72	6.3	1307	2	US-10-104-047-2438	Sequence 2438, Ap
394	72	6.3	1311	2	US-07-757-022B-42	Sequence 42, Appl
395	72	6.3	1313	2	US-07-757-022B-142	Sequence 142, App
396	72	6.3	1314	2	US-07-757-022B-50	Sequence 50, Appl
397	72	6.3	1320	2	US-07-757-022B-46	Sequence 46, Appl
398	72	6.3	1320	2	US-07-757-022B-60	Sequence 60, Appl
399	72	6.3	1320	2	US-10-164-595-58	Sequence 58, Appl
400	72	6.3	1322	2	US-09-487-558B-114	Sequence 114, App
401	72	6.3	1354	2	US-07-757-022B-48	Sequence 48, Appl
402	72	6.3	1361	2	US-07-757-022B-40	Sequence 40, Appl
403	72	6.3	1363	2	US-07-757-022B-52	Sequence 52, Appl
404	72	6.3	1404	2	US-07-757-022B-2	Sequence 2, Appli
405	72	6.3	1404	2	US-07-757-022B-62	Sequence 62, Appl
406	72	6.3	1404	2	US-10-164-595-78	Sequence 78, Appl
407	72	6.3	1404	2	US-09-298-970A-1	Sequence 1, Appli
408	72	6.3	1404	2	US-09-897-188-1	Sequence 1, Appli
409	72	6.3	1411	2	US-09-949-016-10827	Sequence 10827, A
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411	72	6.3	1693	2	US-08-809-523-1	Sequence 1, Appli
412	72	6.3	1693	2	US-08-471-971-1	Sequence 1, Appli
413	72	6.3	1693	2	US-09-402-776-1	Sequence 1, Appli
414	72	6.3	1693	2	US-08-470-246-1	Sequence 1, Appli
415	72	6.3	1693	2	US-08-316-765-1	Sequence 1, Appli
416	72	6.3	1693	2	US-09-724-475-1	Sequence 1, Appli
417	72	6.3	1693	4	PCT-US93-08849A-1	Sequence 1, Appli
418	72	6.3	1693	4	PCT-US93-08849-1	Sequence 1, Appli
419	72	6.3	1876	2	US-09-418-710-71	Sequence 71, Appl
420	72	6.3	1876	2	US-09-839-479-70	Sequence 70, Appl
421	72	6.3	1878	2	US-09-418-710-13	Sequence 13, Appl
422	72	6.3	1878	2	US-09-839-479-13	Sequence 13, Appl
423	71.5	6.3	135	2	US-09-252-991A-17514	Sequence 17514, A
424	71.5	6.3	232	2	US-09-333-809-217	Sequence 217, App
425	71.5	6.3	232	2	US-09-746-311B-366	Sequence 366, App
426	71.5	6.3	240	2	US-09-107-532A-4430	Sequence 4430, Ap
427	71.5	6.3	321	2	US-09-107-433-4282	Sequence 4282, Ap
428	71.5	6.3	342	2	US-09-605-703B-250	Sequence 250, App
429	71.5	6.3	386	2	US-09-248-796A-18312	Sequence 18312, A
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431	71.5	6.3	442	2	US-09-401-415-6	Sequence 6, Appli
432	71.5	6.3	482	2	US-09-991-181-513	Sequence 513, App
433	71.5	6.3	482	2	US-09-990-444-513	Sequence 513, App
434	71.5	6.3	482	2	US-09-997-333-513	Sequence 513, App
435	71.5	6.3	482	2	US-09-992-598-513	Sequence 513, App
436	71.5	6.3	529	2	US-09-248-796A-20186	Sequence 20186, A
437	71.5	6.3	540	2	US-09-583-110-3685	Sequence 3685, Ap
438	71.5	6.3	595	1	US-08-225-989-2	Sequence 2, Appli
439	71.5	6.3	595	1	US-08-570-923-2	Sequence 2, Appli
440	71.5	6.3	595	1	US-08-580-014-2	Sequence 2, Appli
441	71.5	6.3	595	2	US-09-079-785-2	Sequence 2, Appli
442	71.5	6.3	595	2	US-09-921-667-6	Sequence 6, Appli
443	71.5	6.3	595	2	US-09-628-126-2	Sequence 2, Appli
444	71.5	6.3	641	2	US-09-613-303-51	Sequence 51, Appl
445	71.5	6.3	641	2	US-10-267-311-51	Sequence 51, Appl
446	71.5	6.3	903	2	US-09-193-562D-46	Sequence 46, Appl
447	71.5	6.3	903	2	US-09-623-624-18	Sequence 18, Appl
448	71.5	6.3	903	2	US-10-055-412B-46	Sequence 46, Appl
449	71.5	6.3	903	2	US-10-270-595-18	Sequence 18, Appl
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451	71.5	6.3	1724	2	US-09-607-510-2	Sequence 2, Appli
452	71.5	6.3	1751	2	US-09-136-574A-44	Sequence 44, Appl
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455	71	6.2	189	2	US-09-270-767-54674	Sequence 54674, A
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463	71	6.2	610	1	US-08-234-265A-11	Sequence 11, Appl
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465	71	6.2	1014	2	US-09-596-248D-25	Sequence 25, Appl
466	71	6.2	1014	2	US-09-296-662-35	Sequence 35, Appl
467	71	6.2	1063	2	US-09-596-248D-47	Sequence 47, Appl
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471	70.5	6.2	213	2	US-09-538-092-1255	Sequence 1255, Ap
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473	70.5	6.2	232	2	US-09-333-809-215	Sequence 215, App
474	70.5	6.2	232	2	US-09-333-809-216	Sequence 216, App
475	70.5	6.2	232	2	US-09-746-311B-363	Sequence 363, App
476	70.5	6.2	232	2	US-09-746-311B-364	Sequence 364, App
477	70.5	6.2	232	2	US-09-746-311B-365	Sequence 365, App
478	70.5	6.2	292	1	US-08-286-888B-6	Sequence 6, Appli
479	70.5	6.2	292	2	US-08-852-020-6	Sequence 6, Appli
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488	70.5	6.2	678	2	US-09-990-444-179	Sequence 179, App
489	70.5	6.2	678	2	US-09-997-333-179	Sequence 179, App
490	70.5	6.2	678	2	US-09-992-598-179	Sequence 179, App
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519	69	6.1	397	2	US-09-143-470-4	Sequence 4, Appli
520	69	6.1	397	2	US-08-649-006A-4	Sequence 4, Appli
521	69	6.1	397	2	US-09-771-023-4	Sequence 4, Appli
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525	69	6.1	509	2	US-09-292-225-38	Sequence 38, Appl
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528	69	6.1	845	2	US-08-804-439A-94	Sequence 94, Appl
529	69	6.1	845	2	US-08-720-229-94	Sequence 94, Appl
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534	69	6.1	2035	1	US-08-393-703-5	Sequence 5, Appli
535	69	6.1	2035	4	PCT-US93-11721-5	Sequence 5, Appli
536	69	6.1	2045	2	US-09-949-016-10491	Sequence 10491, A
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561	68	6.0	873	1	US-08-909-984A-6	Sequence 6, Appli
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568	68	6.0	2441	2	US-09-686-316-2	Sequence 2, Appli
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572	68	6.0	3712	2	US-10-037-417-51	Sequence 51, Appl
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578	67.5	5.9	291	2	US-09-248-796A-14273	Sequence 14273, A
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582	67.5	5.9	365	1	US-08-437-027-20	Sequence 20, Appl
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586	67.5	5.9	427	2	US-09-328-352-5205	Sequence 5205, Ap
587	67.5	5.9	428	2	US-09-489-039A-10901	Sequence 10901, A
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593	67.5	5.9	630	1	US-08-956-268-3	Sequence 3, Appli
594	67.5	5.9	630	2	US-09-499-522-16	Sequence 16, Appl
595	67.5	5.9	630	2	US-09-269-939A-10	Sequence 10, Appl
596	67.5	5.9	649	2	US-09-499-522-14	Sequence 14, Appl
597	67.5	5.9	649	2	US-09-269-939A-8	Sequence 8, Appli
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599	67.5	5.9	656	2	US-09-214-564A-4	Sequence 4, Appli
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602	67.5	5.9	744	2	US-09-202-178A-3	Sequence 3, Appli
603	67	5.9	185	2	US-09-902-540-13687	Sequence 13687, A
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625	67	5.9	416	2	US-09-601-478-4	Sequence 4, Appli
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640	67	5.9	915	2	US-09-138-735-2	Sequence 2, Appli
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642	67	5.9	1401	2	US-09-618-166-206	Sequence 206, App
643	67	5.9	1900	2	US-09-538-092-564	Sequence 564, App
644	67	5.9	1900	2	US-09-487-558B-390	Sequence 390, App
645	67	5.9	2476	1	US-08-276-967-2	Sequence 2, Appli
646	67	5.9	4377	2	US-09-949-016-6978	Sequence 6978, Ap
647	66.5	5.9	91	2	US-08-700-651-14	Sequence 14, Appl
648	66.5	5.9	91	2	US-08-928-361B-19	Sequence 19, Appl
649	66.5	5.9	91	2	US-09-588-995A-19	Sequence 19, Appl
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652	66.5	5.9	239	2	US-09-248-796A-21096	Sequence 21096, A
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654	66.5	5.9	284	2	US-09-248-796A-20639	Sequence 20639, A
655	66.5	5.9	320	2	US-09-248-796A-20167	Sequence 20167, A
656	66.5	5.9	374	2	US-09-489-847-166	Sequence 166, App
657	66.5	5.9	382	2	US-09-907-794A-137	Sequence 137, App
658	66.5	5.9	382	2	US-09-905-125A-137	Sequence 137, App
659	66.5	5.9	382	2	US-09-902-775A-137	Sequence 137, App
660	66.5	5.9	382	2	US-09-906-700-137	Sequence 137, App
661	66.5	5.9	382	2	US-09-903-603A-137	Sequence 137, App
662	66.5	5.9	382	2	US-09-904-920A-137	Sequence 137, App
663	66.5	5.9	382	2	US-09-909-064-137	Sequence 137, App
664	66.5	5.9	382	2	US-09-905-381A-137	Sequence 137, App
665	66.5	5.9	382	2	US-09-906-618-137	Sequence 137, App
666	66.5	5.9	382	2	US-09-906-646-137	Sequence 137, App
667	66.5	5.9	382	2	US-09-904-462-137	Sequence 137, App
668	66.5	5.9	382	2	US-09-902-736A-137	Sequence 137, App
669	66.5	5.9	382	2	US-09-906-722A-137	Sequence 137, App
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671	66.5	5.9	406	2	US-09-248-796A-20860	Sequence 20860, A
672	66.5	5.9	496	2	US-09-540-236-2266	Sequence 2266, Ap
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676	66.5	5.9	516	2	US-09-320-774-8	Sequence 8, Appli
677	66.5	5.9	527	1	US-08-762-106-9	Sequence 9, Appli
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679	66.5	5.9	552	2	US-08-745-404-3	Sequence 3, Appli
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681	66.5	5.9	562	6	5258502-2	Patent No. 5258502
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683	66.5	5.9	681	2	US-08-760-615-4	Sequence 4, Appli
684	66.5	5.9	681	2	US-09-336-910A-2	Sequence 2, Appli

685	66.5	5.9	815	2	US-09-914-259-18	Sequence 18, Appl
686	66.5	5.9	872	2	US-08-337-797A-2	Sequence 2, Appli
687	66.5	5.9	872	2	US-09-258-523-2	Sequence 2, Appli
688	66.5	5.9	970	1	US-08-673-789-7	Sequence 7, Appli
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690	66.5	5.9	993	1	US-08-571-785-1	Sequence 1, Appli
691	66.5	5.9	993	2	US-09-192-435-1	Sequence 1, Appli
692	66.5	5.9	993	2	US-09-558-340-1	Sequence 1, Appli
693	66.5	5.9	1059	2	US-09-800-729-217	Sequence 217, App
694	66.5	5.9	1638	2	US-09-071-035-258	Sequence 258, App
695	66.5	5.9	1638	2	US-09-071-035-262	Sequence 262, App
696	66.5	5.9	1638	2	US-09-071-035-266	Sequence 266, App
697	66.5	5.9	1638	2	US-10-206-576-258	Sequence 258, App
698	66.5	5.9	1638	2	US-10-206-576-262	Sequence 262, App
699	66.5	5.9	1638	2	US-10-206-576-266	Sequence 266, App
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707	66	5.8	342	2	US-09-252-991A-19903	Sequence 19903, A
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709	66	5.8	380	2	US-09-270-767-43987	Sequence 43987, A
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711	66	5.8	437	2	US-09-248-796A-19098	Sequence 19098, A
712	66	5.8	440	2	US-09-270-767-37864	Sequence 37864, A
713	66	5.8	440	2	US-09-270-767-53081	Sequence 53081, A
714	66	5.8	485	2	US-10-172-502-18	Sequence 18, Appl
715	66	5.8	495	2	US-09-248-796A-14275	Sequence 14275, A
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717	66	5.8	540	2	US-08-336-251-3	Sequence 3, Appli
718	66	5.8	540	2	US-09-468-041-3	Sequence 3, Appli
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720	66	5.8	567	2	US-09-773-877B-12	Sequence 12, Appl
721	66	5.8	580	2	US-09-248-796A-26639	Sequence 26639, A
722	66	5.8	584	2	US-09-693-746-22	Sequence 22, Appl
723	66	5.8	607	2	US-09-907-794A-190	Sequence 190, App
724	66	5.8	607	2	US-09-905-125A-190	Sequence 190, App
725	66	5.8	607	2	US-09-902-775A-190	Sequence 190, App
726	66	5.8	607	2	US-09-906-700-190	Sequence 190, App
727	66	5.8	607	2	US-09-903-603A-190	Sequence 190, App
728	66	5.8	607	2	US-09-904-920A-190	Sequence 190, App
729	66	5.8	607	2	US-09-909-064-190	Sequence 190, App
730	66	5.8	607	2	US-09-905-381A-190	Sequence 190, App
731	66	5.8	607	2	US-09-906-618-190	Sequence 190, App
732	66	5.8	607	2	US-09-906-646-190	Sequence 190, App
733	66	5.8	607	2	US-09-904-462-190	Sequence 190, App
734	66	5.8	607	2	US-09-902-736A-190	Sequence 190, App
735	66	5.8	607	2	US-09-906-722A-190	Sequence 190, App
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739	66	5.8	654	2	US-09-315-127-12	Sequence 12, Appl
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742	66	5.8	687	2	US-09-427-353-2	Sequence 2, Appli
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746	66	5.8	758	2	US-09-348-886-1	Sequence 1, Appli
747	66	5.8	758	2	US-10-105-901A-1	Sequence 1, Appli
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749	66	5.8	780	1	US-08-786-164-14	Sequence 14, Appl
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752	66	5.8	1187	2	US-09-949-016-6513	Sequence 6513, Ap
753	66	5.8	1338	2	US-08-750-141A-3	Sequence 3, Appli
754	66	5.8	1338	2	US-09-119-014D-6	Sequence 6, Appli
755	66	5.8	1564	2	US-10-144-198-2	Sequence 2, Appli
756	66	5.8	1564	2	US-10-144-198-4	Sequence 4, Appli
757	66	5.8	1619	2	US-09-328-352-7347	Sequence 7347, Ap
758	66	5.8	2169	2	US-09-949-016-6930	Sequence 6930, Ap
759	66	5.8	2283	2	US-10-172-502-4	Sequence 4, Appli
760	66	5.8	3913	2	US-09-949-016-10933	Sequence 10933, A
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763	65.5	5.8	128	2	US-09-270-767-38128	Sequence 38128, A
764	65.5	5.8	128	2	US-09-270-767-53345	Sequence 53345, A
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766	65.5	5.8	144	2	US-09-252-991A-23388	Sequence 23388, A
767	65.5	5.8	145	2	US-09-252-991A-31617	Sequence 31617, A
768	65.5	5.8	145	2	US-09-710-279-1504	Sequence 1504, Ap
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773	65.5	5.8	208	2	US-09-991-181-416	Sequence 416, App
774	65.5	5.8	208	2	US-09-990-444-416	Sequence 416, App
775	65.5	5.8	208	2	US-09-832-129-36	Sequence 36, Appl
776	65.5	5.8	208	2	US-09-997-333-416	Sequence 416, App
777	65.5	5.8	208	2	US-09-992-598-416	Sequence 416, App
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779	65.5	5.8	214	2	US-08-932-411A-2	Sequence 2, Appli
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786	65.5	5.8	362	2	US-09-126-121-3	Sequence 3, Appli
787	65.5	5.8	416	2	US-08-978-289-12	Sequence 12, Appl
788	65.5	5.8	448	2	US-09-520-781-32	Sequence 32, Appl
789	65.5	5.8	448	2	US-09-957-187-32	Sequence 32, Appl
790	65.5	5.8	448	2	US-09-991-053-32	Sequence 32, Appl
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792	65.5	5.8	487	2	US-09-579-845-14	Sequence 14, Appl
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794	65.5	5.8	521	2	US-09-149-476-392	Sequence 392, App
795	65.5	5.8	540	1	US-08-368-834-20	Sequence 20, Appl
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797	65.5	5.8	541	1	US-08-447-154-19	Sequence 19, Appl
798	65.5	5.8	541	2	US-08-432-697-34	Sequence 34, Appl
799	65.5	5.8	541	2	US-08-466-248-34	Sequence 34, Appl
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803	65.5	5.8	676	2	US-09-003-570-34	Sequence 34, Appl
804	65.5	5.8	676	2	US-09-864-541A-34	Sequence 34, Appl
805	65.5	5.8	707	2	US-10-104-047-3162	Sequence 3162, Ap
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807	65.5	5.8	713	2	US-09-126-121-2	Sequence 2, Appli
808	65.5	5.8	746	2	US-09-589-892B-2	Sequence 2, Appli
809	65.5	5.8	821	1	US-07-935-311A-4	Sequence 4, Appli
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816	65.5	5.8	872	2	US-09-196-466-3	Sequence 3, Appli
817	65.5	5.8	872	2	US-09-669-459A-3	Sequence 3, Appli
818	65.5	5.8	872	4	PCT-US96-10823-3	Sequence 3, Appli
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826	65	5.7	154	2	US-09-270-767-35473	Sequence 35473, A
827	65	5.7	154	2	US-09-270-767-50690	Sequence 50690, A
828	65	5.7	156	2	US-09-621-976-4385	Sequence 4385, Ap
829	65	5.7	166	2	US-09-252-991A-25442	Sequence 25442, A
830	65	5.7	218	2	US-09-605-703B-2490	Sequence 2490, Ap

831	65	5.7	235	2	US-09-949-016-6661	Sequence 6661, Ap
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833	65	5.7	251	2	US-09-270-767-33191	Sequence 33191, A
834	65	5.7	251	2	US-09-270-767-48408	Sequence 48408, A
835	65	5.7	288	2	US-09-252-991A-17419	Sequence 17419, A
836	65	5.7	298	2	US-09-248-796A-26762	Sequence 26762, A
837	65	5.7	352	2	US-09-248-796A-26579	Sequence 26579, A
838	65	5.7	410	2	US-09-543-681A-5962	Sequence 5962, Ap
839	65	5.7	434	2	US-09-487-558B-146	Sequence 146, App
840	65	5.7	503	2	US-09-487-558B-424	Sequence 424, App
841	65	5.7	522	2	US-09-198-452A-480	Sequence 480, App
842	65	5.7	557	2	US-09-773-877B-14	Sequence 14, Appl
843	65	5.7	567	2	US-09-773-877B-20	Sequence 20, Appl
844	65	5.7	630	2	US-09-485-529-8	Sequence 8, Appli
845	65	5.7	692	2	US-09-003-574-31	Sequence 31, Appl
846	65	5.7	692	2	US-09-003-570-31	Sequence 31, Appl
847	65	5.7	692	2	US-09-864-541A-31	Sequence 31, Appl
848	65	5.7	724	2	US-09-949-016-9953	Sequence 9953, Ap
849	65	5.7	813	2	US-09-964-899-25	Sequence 25, Appl
850	65	5.7	883	2	US-09-489-039A-12755	Sequence 12755, A
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852	65	5.7	921	1	US-08-646-715-2	Sequence 2, Appli
853	65	5.7	973	2	US-09-430-723-2	Sequence 2, Appli
854	65	5.7	999	2	US-09-438-185A-455	Sequence 455, App
855	65	5.7	1047	2	US-09-957-187-85	Sequence 85, Appl
856	65	5.7	1131	2	US-10-104-047-2866	Sequence 2866, Ap
857	65	5.7	1833	2	US-08-621-944A-4	Sequence 4, Appli
858	65	5.7	1833	2	US-08-945-567D-4	Sequence 4, Appli
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860	65	5.7	1992	2	US-08-945-567D-3	Sequence 3, Appli
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862	64.5	5.7	127	2	US-09-252-991A-26303	Sequence 26303, A
863	64.5	5.7	133	2	US-09-252-991A-24089	Sequence 24089, A
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866	64.5	5.7	279	2	US-08-397-411-13	Sequence 13, Appl
867	64.5	5.7	367	2	US-10-104-047-2763	Sequence 2763, Ap
868	64.5	5.7	391	2	US-09-200-090-4	Sequence 4, Appli
869	64.5	5.7	394	2	US-09-252-991A-28045	Sequence 28045, A
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871	64.5	5.7	420	2	US-09-538-092-703	Sequence 703, App
872	64.5	5.7	425	2	US-09-748-537-14	Sequence 14, Appl
873	64.5	5.7	426	2	US-09-605-703B-2042	Sequence 2042, Ap
874	64.5	5.7	491	2	US-09-107-532A-6115	Sequence 6115, Ap
875	64.5	5.7	522	2	US-10-172-502-17	Sequence 17, Appl
876	64.5	5.7	553	2	US-09-949-016-10648	Sequence 10648, A
877	64.5	5.7	566	2	US-09-513-783A-142	Sequence 142, App
878	64.5	5.7	566	2	US-09-430-656-142	Sequence 142, App
879	64.5	5.7	566	2	US-10-100-957A-142	Sequence 142, App
880	64.5	5.7	571	2	US-09-252-991A-30957	Sequence 30957, A
881	64.5	5.7	626	2	US-09-957-187-83	Sequence 83, Appl
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883	64.5	5.7	630	2	US-09-520-781-30	Sequence 30, Appl
884	64.5	5.7	630	2	US-09-957-187-30	Sequence 30, Appl
885	64.5	5.7	630	2	US-09-991-053-30	Sequence 30, Appl
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887	64.5	5.7	638	1	US-08-463-989-11	Sequence 11, Appl
888	64.5	5.7	638	2	US-09-003-574-11	Sequence 11, Appl
889	64.5	5.7	638	2	US-09-003-570-11	Sequence 11, Appl
890	64.5	5.7	638	2	US-09-864-541A-11	Sequence 11, Appl
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892	64.5	5.7	659	2	US-09-562-737-14	Sequence 14, Appl
893	64.5	5.7	669	2	US-09-107-532A-6532	Sequence 6532, Ap
894	64.5	5.7	712	2	US-09-949-016-10600	Sequence 10600, A
895	64.5	5.7	763	2	US-09-949-016-10382	Sequence 10382, A
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898	64.5	5.7	812	2	US-09-513-783A-6	Sequence 6, Appli
899	64.5	5.7	812	2	US-09-430-656-4	Sequence 4, Appli
900	64.5	5.7	812	2	US-09-430-656-6	Sequence 6, Appli
901	64.5	5.7	812	2	US-10-100-957A-4	Sequence 4, Appli
902	64.5	5.7	812	2	US-10-100-957A-6	Sequence 6, Appli
903	64.5	5.7	919	2	US-09-949-016-6954	Sequence 6954, Ap
904	64.5	5.7	939	2	US-09-520-781-4	Sequence 4, Appli
905	64.5	5.7	939	2	US-09-957-187-4	Sequence 4, Appli
906	64.5	5.7	939	2	US-09-991-053-4	Sequence 4, Appli
907	64.5	5.7	994	2	US-09-248-796A-15273	Sequence 15273, A
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909	64.5	5.7	1030	2	US-09-856-681A-7	Sequence 7, Appli
910	64.5	5.7	1039	2	US-09-902-540-13739	Sequence 13739, A
911	64.5	5.7	1056	2	US-09-513-783A-32	Sequence 32, Appl
912	64.5	5.7	1056	2	US-09-430-656-32	Sequence 32, Appl
913	64.5	5.7	1056	2	US-10-100-957A-32	Sequence 32, Appl
914	64.5	5.7	1125	2	US-09-513-783A-152	Sequence 152, App
915	64.5	5.7	1125	2	US-09-430-656-152	Sequence 152, App
916	64.5	5.7	1125	2	US-10-100-957A-152	Sequence 152, App
917	64.5	5.7	1140	2	US-09-538-092-647	Sequence 647, App
918	64.5	5.7	1310	2	US-09-170-496D-290	Sequence 290, App
919	64.5	5.7	1310	2	US-09-364-425B-55	Sequence 55, Appl
920	64.5	5.7	1481	2	US-09-231-899-70	Sequence 70, Appl
921	64.5	5.7	1610	2	US-09-513-783A-22	Sequence 22, Appl
922	64.5	5.7	1610	2	US-09-430-656-22	Sequence 22, Appl
923	64.5	5.7	1610	2	US-10-100-957A-22	Sequence 22, Appl
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926	64.5	5.7	3011	1	US-08-710-637-2	Sequence 2, Appli
927	64.5	5.7	3011	4	PCT-US93-00907-2	Sequence 2, Appli
928	64	5.6	134	2	US-09-270-767-40850	Sequence 40850, A
929	64	5.6	134	2	US-09-270-767-56066	Sequence 56066, A
930	64	5.6	152	2	US-09-252-991A-19284	Sequence 19284, A
931	64	5.6	176	2	US-09-252-991A-21933	Sequence 21933, A
932	64	5.6	198	2	US-09-252-991A-18773	Sequence 18773, A
933	64	5.6	198	2	US-09-248-796A-19318	Sequence 19318, A
934	64	5.6	219	1	US-08-463-115-91	Sequence 91, Appl
935	64	5.6	219	1	US-08-465-388-91	Sequence 91, Appl
936	64	5.6	306	2	US-09-902-540-9859	Sequence 9859, Ap
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941	64	5.6	416	2	US-08-858-876A-4	Sequence 4, Appli
942	64	5.6	416	2	US-09-472-880-4	Sequence 4, Appli
943	64	5.6	423	2	US-09-991-181-241	Sequence 241, App
944	64	5.6	423	2	US-09-990-444-241	Sequence 241, App
945	64	5.6	423	2	US-09-997-333-241	Sequence 241, App
946	64	5.6	423	2	US-09-992-598-241	Sequence 241, App
947	64	5.6	501	2	US-09-248-796A-14118	Sequence 14118, A
948	64	5.6	511	2	US-09-248-796A-14125	Sequence 14125, A
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951	64	5.6	547	2	US-09-489-039A-13843	Sequence 13843, A
952	64	5.6	562	2	US-09-538-092-779	Sequence 779, App
953	64	5.6	574	2	US-09-248-796A-16162	Sequence 16162, A
954	64	5.6	588	2	US-09-248-796A-20295	Sequence 20295, A
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956	64	5.6	614	4	PCT-US95-10579-7	Sequence 7, Appli
957	64	5.6	623	2	US-09-485-529-7	Sequence 7, Appli
958	64	5.6	636	2	US-09-949-016-11656	Sequence 11656, A
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962	64	5.6	693	2	US-09-248-796A-26890	Sequence 26890, A
963	64	5.6	728	2	US-09-949-016-8296	Sequence 8296, Ap
964	64	5.6	737	1	US-08-188-582-16	Sequence 16, Appl
965	64	5.6	737	1	US-08-646-715-16	Sequence 16, Appl
966	64	5.6	740	2	US-09-949-016-10931	Sequence 10931, A
967	64	5.6	750	2	US-09-185-160-14	Sequence 14, Appl
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972	64	5.6	923	2	US-09-825-147-2	Sequence 2, Appli
973	64	5.6	932	2	US-09-813-148-2	Sequence 2, Appli
974	64	5.6	999	2	US-09-747-371-2	Sequence 2, Appli
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1219	62.5	5.5	635	1	US-08-909-984A-10	Sequence 10, Appl
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1223	62.5	5.5	847	2	US-09-476-242-2	Sequence 2, Appli
1224	62.5	5.5	857	2	US-09-902-540-12028	Sequence 12028, A
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1226	62.5	5.5	875	1	US-08-909-984A-8	Sequence 8, Appli
1227	62.5	5.5	875	1	US-08-909-983-8	Sequence 8, Appli
1228	62.5	5.5	877	1	US-08-916-917-2	Sequence 2, Appli
1229	62.5	5.5	877	1	US-08-972-631-2	Sequence 2, Appli
1230	62.5	5.5	877	1	US-08-972-629-2	Sequence 2, Appli
1231	62.5	5.5	877	1	US-08-972-630-2	Sequence 2, Appli
1232	62.5	5.5	877	1	US-08-672-211-2	Sequence 2, Appli
1233	62.5	5.5	877	2	US-09-225-170-2	Sequence 2, Appli
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1238	62.5	5.5	1416	2	US-09-071-035-404	Sequence 404, App
1239	62.5	5.5	1416	2	US-10-206-576-404	Sequence 404, App
1240	62.5	5.5	1448	2	US-09-071-035-402	Sequence 402, App
1241	62.5	5.5	1448	2	US-10-206-576-402	Sequence 402, App
1242	62.5	5.5	1577	1	US-08-793-824-2	Sequence 2, Appli
1243	62.5	5.5	1769	2	US-09-949-016-8280	Sequence 8280, Ap
1244	62.5	5.5	1769	2	US-09-949-016-8281	Sequence 8281, Ap
1245	62.5	5.5	1769	2	US-09-949-016-8282	Sequence 8282, Ap
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1247	62.5	5.5	1784	2	US-08-652-426A-2	Sequence 2, Appli
1248	62.5	5.5	1813	2	US-09-949-016-8283	Sequence 8283, Ap
1249	62.5	5.5	1813	2	US-09-949-016-8284	Sequence 8284, Ap
1250	62.5	5.5	1813	2	US-09-949-016-8285	Sequence 8285, Ap
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1266	62.5	5.5	2032	2	US-10-010-720-42	Sequence 42, Appl
1267	62.5	5.5	2048	2	US-09-854-856-62	Sequence 62, Appl
1268	62.5	5.5	2048	2	US-10-010-720-62	Sequence 62, Appl

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1270	62.5	5.5	2064	2	US-10-010-720-26	Sequence 26, Appl
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1272	62.5	5.5	2076	2	US-10-010-720-46	Sequence 46, Appl
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1282	62.5	5.5	2141	2	US-10-010-720-56	Sequence 56, Appl
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1286	62.5	5.5	2169	2	US-10-010-720-40	Sequence 40, Appl
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1314	62.5	5.5	2475	2	US-09-413-814-48	Sequence 48, Appl
1315	62.5	5.5	2772	2	US-08-444-818-89	Sequence 89, Appl
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1323	62.5	5.5	2995	2	US-08-444-818-138	Sequence 138, App
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1340	62.5	5.5	3012	2	US-09-034-756-2	Sequence 2, Appli
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1343	62	5.5	115	2	US-09-605-703B-312	Sequence 312, App
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1351	62	5.5	154	2	US-09-003-570-9	Sequence 9, Appli
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1355	62	5.5	165	2	US-09-676-739-2	Sequence 2, Appli
1356	62	5.5	165	2	US-09-675-362-2	Sequence 2, Appli
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1358	62	5.5	165	2	US-09-677-152-2	Sequence 2, Appli
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1361	62	5.5	167	1	US-08-997-362-112	Sequence 112, App
1362	62	5.5	167	2	US-09-095-855-112	Sequence 112, App
1363	62	5.5	167	2	US-09-324-542-112	Sequence 112, App
1364	62	5.5	167	2	US-09-205-426-112	Sequence 112, App
1365	62	5.5	180	2	US-09-133-341-12	Sequence 12, Appl
1366	62	5.5	180	2	US-09-739-852-12	Sequence 12, Appl
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1370	62	5.5	209	2	US-09-059-625-86	Sequence 86, Appl
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1383	62	5.5	265	2	US-09-282-357-39	Sequence 39, Appl
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1387	62	5.5	285	2	US-09-205-426-197	Sequence 197, App
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1393	62	5.5	341	2	US-09-991-181-297	Sequence 297, App
1394	62	5.5	341	2	US-09-990-444-297	Sequence 297, App
1395	62	5.5	341	2	US-09-997-333-297	Sequence 297, App
1396	62	5.5	341	2	US-09-992-598-297	Sequence 297, App
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1412	62	5.5	556	2	US-09-487-558B-426	Sequence 426, App
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1418	62	5.5	654	1	US-08-478-373-12	Sequence 12, Appl
1419	62	5.5	654	2	US-08-474-671-12	Sequence 12, Appl
1420	62	5.5	654	2	US-08-483-577A-12	Sequence 12, Appl
1421	62	5.5	654	2	US-08-897-438-12	Sequence 12, Appl
1422	62	5.5	654	2	US-08-637-654-12	Sequence 12, Appl
1423	62	5.5	654	2	US-08-649-518-12	Sequence 12, Appl
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1429	62	5.5	748	2	US-09-095-855-154	Sequence 154, App
1430	62	5.5	748	2	US-09-324-542-154	Sequence 154, App
1431	62	5.5	748	2	US-09-205-426-154	Sequence 154, App
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1442	62	5.5	1248	2	US-09-566-047-6	Sequence 6, Appli
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1445	62	5.5	1311	2	US-08-901-710-5	Sequence 5, Appli
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1459	61.5	5.4	183	2	US-09-489-847-136	Sequence 136, App
1460	61.5	5.4	183	6	5168049-3	Patent No. 5168049
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1463	61.5	5.4	204	2	US-09-252-991A-16784	Sequence 16784, A
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1468	61.5	5.4	263	2	US-08-483-857-5	Sequence 5, Appli
1469	61.5	5.4	263	2	US-08-988-197-2	Sequence 2, Appli
1470	61.5	5.4	263	2	US-10-385-072-2	Sequence 2, Appli
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1477	61.5	5.4	296	2	US-08-479-017-3	Sequence 3, Appli
1478	61.5	5.4	296	2	US-08-455-829-11	Sequence 11, Appl
1479	61.5	5.4	296	2	US-08-235-836C-22	Sequence 22, Appl
1480	61.5	5.4	296	2	US-08-455-973-11	Sequence 11, Appl
1481	61.5	5.4	303	2	US-09-270-767-57613	Sequence 57613, A
1482	61.5	5.4	322	2	US-09-252-991A-31608	Sequence 31608, A
1483	61.5	5.4	323	1	US-08-435-149-2	Sequence 2, Appli
1484	61.5	5.4	323	2	US-08-311-731A-115	Sequence 115, App
1485	61.5	5.4	324	1	US-08-310-416A-14	Sequence 14, Appl
1486	61.5	5.4	324	1	US-08-888-171-14	Sequence 14, Appl
1487	61.5	5.4	327	2	US-09-270-767-42324	Sequence 42324, A
1488	61.5	5.4	338	2	US-09-328-352-4529	Sequence 4529, Ap
1489	61.5	5.4	338	2	US-09-807-933B-1	Sequence 1, Appli
1490	61.5	5.4	340	1	US-08-446-875-16	Sequence 16, Appl
1491	61.5	5.4	347	2	US-09-540-236-3596	Sequence 3596, Ap
1492	61.5	5.4	347	2	US-08-126-505A-17	Sequence 17, Appl
1493	61.5	5.4	357	1	US-08-078-683A-8	Sequence 8, Appli
1494	61.5	5.4	357	2	US-08-471-970A-8	Sequence 8, Appli
1495	61.5	5.4	357	2	US-09-723-677B-8	Sequence 8, Appli
1496	61.5	5.4	376	2	US-09-844-311-2	Sequence 2, Appli
1497	61.5	5.4	380	2	US-08-235-836C-118	Sequence 118, App
1498	61.5	5.4	380	2	US-09-273-164-33	Sequence 33, Appl
1499	61.5	5.4	381	2	US-09-014-240-2	Sequence 2, Appli
1500	61.5	5.4	381	2	US-09-844-311-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-232-160-21
; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
;  APPLICANT: Steve Daniel
;  APPLICANT: James Gilmore
;  APPLICANT: Susan G. Stuart
;  APPLICANT: Laura Stuve
;  TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
;  TITLE OF INVENTION: PROLIFERATION
;  FILE REFERENCE: PA-0003 US
;  CURRENT APPLICATION NUMBER: US/09/232,160
;  CURRENT FILING DATE: 1999-01-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PERL Program
; SEQ ID NO 21
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 3044710
US-09-232-160-21

  Query Match            100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
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Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 2
US-09-907-794A-201
; Sequence 201, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
```

```
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 3
US-09-905-125A-201
; Sequence 201, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
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;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
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;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-905-125A-201

  Query Match           100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
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Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 4
US-09-902-775A-201
; Sequence 201, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-775A-201

  Query Match           100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 5
US-09-906-700-201
; Sequence 201, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
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;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,700
;  CURRENT FILING DATE:  2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
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;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
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;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
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;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-700-201
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  Query Match           100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              ||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235
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RESULT 6
US-09-903-603A-201
; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: GNE.1618P2C12
;  CURRENT APPLICATION NUMBER: US/09/903,603A
;  CURRENT FILING DATE:  2001-07-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
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;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-903-603A-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 7
US-09-904-920A-201
; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann .
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,920A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-904-920A-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235
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RESULT 8
US-09-909-064-201
; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,064
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-909-064-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 9
US-09-905-381A-201
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,381A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-905-381A-201

Query Match 100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235
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RESULT 10
US-09-906-618-201
; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-906-618-201

Query Match 100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195
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Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 11
US-09-906-646-201
; Sequence 201, Application US/09906646
; Patent No. 6852848
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,646
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-646-201

  Query Match           100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
              ||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 12
US-09-904-462-201
; Sequence 201, Application US/09904462
; Patent No. 6878807
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,462
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
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;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-462-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
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Db        196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 235


RESULT 13
US-09-902-736A-201
; Sequence 201, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,736A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-736A-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135
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Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 220
              |||||||||||||||||||||||||||||||||||||||||
Db        196 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 235


RESULT 14
US-09-906-722A-201
; Sequence 201, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: GNE.1618P2C61
;  CURRENT APPLICATION NUMBER: US/09/906,722A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-722A-201

  Query Match             100.0%;  Score 1136;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 75

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 135

Qy        121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180
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Db        136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 195

Qy        181 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 220
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Db        196 RKKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGG 235


RESULT 15
US-09-949-016-7765
; Sequence 7765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7765
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7765

  Query Match             100.0%;  Score 1136;  DB 2;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 3e-115;
  Matches  220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 60
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Db         38 TTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVE 97

Qy         61 TALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTW 120
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Db        158 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 217

Qy        181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGG 220
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:29 ; Search time 13.7123 Seconds
(without alignments)
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Title: US-10-063-510-6_COPY_17_322
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
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2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	229	14.5	363	2	A37009	CD44 homolog membr
2	222.5	14.1	362	2	A30901	lymphocyte adhesio
3	222	14.1	365	2	A34424	CD44 membrane glyc
4	217.5	13.8	362	2	A35616	T-cell surface gly
5	217	13.8	503	2	B38745	cell adhesion mole
6	208.5	13.2	366	2	A53286	cell-surface glyco
7	205	13.0	361	2	JH0417	cell adhesion mole
8	202	12.8	351	2	S45305	CD44 antigen precu
9	202	12.8	742	2	A47195	lymphocyte homing
10	199.5	12.7	426	2	JH0518	lymphocyte homing
11	199.5	12.7	493	2	S13530	CD44E protein, epi
12	198	12.6	395	2	I77371	CD44R5 - human
13	196.5	12.5	699	2	I37369	epican - human
14	186	11.8	359	2	S24240	lymphocyte surface
15	148.5	9.4	2109	1	I50421	aggrecan precursor
16	145.5	9.2	3562	2	A47171	chondroitin sulfat
17	145	9.2	277	2	A41735	hyaluronate-bindin
18	145	9.2	1069	2	T42681	hypothetical prote
19	144	9.1	275	2	JC6506	tumor necrosis fac
20	143	9.1	2327	2	T42630	aggrecan - bovine
21	137	8.7	276	2	A47290	TSG-6 homolog PS4
22	131.5	8.3	2124	2	A28452	proteoglycan core
23	131	8.3	2132	1	A55182	aggrecan precursor
24	130.5	8.3	883	2	S57653	brevican precursor
25	130.5	8.3	883	2	S49126	brevican precursor
26	130.5	8.3	2415	1	A39086	aggrecan precursor
27	128.5	8.2	912	2	A54423	brevican precursor
28	121	7.7	1340	2	A39808	proteoglycan core
29	116	7.4	2397	1	A55535	versican precursor
30	115	7.3	370	2	S29139	aggrecan - pig (fr
31	115	7.3	1643	2	T14274	versican precursor
32	115	7.3	3381	2	T42389	versican precursor
33	114.5	7.3	1257	2	S28764	neurocan precursor
34	112.5	7.1	340	2	JC7505	brain link protein
35	112	7.1	390	1	QQBE77	glycoprotein I pre
36	111.5	7.1	402	2	S73773	dihydrolipoamide a
37	111.5	7.1	909	1	QRXLL2	LDL receptor 2 pre
38	111	7.0	2409	1	A60979	versican precursor
39	108	6.9	354	1	LKHU	proteoglycan link
40	108	6.9	645	2	T29818	hypothetical prote
41	107.5	6.8	739	2	T21769	hypothetical prote
42	107	6.8	355	1	LKCH	proteoglycan link
43	107	6.8	371	2	A53908	brevican precursor
44	107	6.8	408	1	LKRT2	proteoglycan link
45	107	6.8	1268	2	S52781	neurocan - mouse
46	105.5	6.7	113	2	A55885	chondroitin sulfat
47	104.5	6.6	862	2	S43922	versican - pig-tai
48	104	6.6	354	1	S04243	proteoglycan link
49	104	6.6	354	1	S42938	proteoglycan link
50	103.5	6.6	1229	2	T25697	hypothetical prote
51	101.5	6.4	380	2	T28081	hypothetical prote
52	101	6.4	708	2	T19474	hypothetical prote
53	100	6.3	378	2	I46268	brevican precursor
54	99.5	6.3	1092	1	JN0635	neural cell adhesi
55	99	6.3	896	2	T22061	hypothetical prote
56	99	6.3	5376	2	T42215	zonadhesin - mouse
57	97.5	6.2	909	1	QRXLL1	LDL receptor 1 pre
58	96.5	6.1	465	2	S46759	hypothetical prote
59	96.5	6.1	660	2	JW0067	chitinase (EC 3.2.
60	96	6.1	449	2	T33257	hypothetical prote
61	96	6.1	796	2	T21460	hypothetical prote
62	96	6.1	1088	1	IJXLNL	neural cell adhesi
63	95.5	6.1	1471	2	B48218	neurexin III-alpha
64	95	6.0	1251	2	T21389	hypothetical prote
65	94.5	6.0	1272	2	S26180	neurofascin - chic
66	94.5	6.0	1390	2	T18883	hypothetical prote
67	94	6.0	1241	2	S01827	period clock prote
68	92.5	5.9	477	2	S53362	mucin 5AC (clone J
69	92.5	5.9	569	2	AI1347	hypothetical prote
70	92.5	5.9	851	2	T22696	hypothetical prote
71	92.5	5.9	927	2	T24031	hypothetical prote
72	92.5	5.9	1367	2	S74285	BUD3 protein - yea
73	92	5.8	846	2	T21700	hypothetical prote
74	92	5.8	966	2	S25365	CYC8 protein - yea
75	91.5	5.8	639	2	S20887	actA protein precu
76	91.5	5.8	639	2	AE1100	actin-assembly ind
77	91.5	5.8	672	2	T32557	hypothetical prote
78	91.5	5.8	930	2	B72537	hypothetical prote
79	91	5.8	246	2	T33965	hypothetical prote
80	91	5.8	747	2	T34329	hypothetical prote
81	91	5.8	2172	2	T20145	hypothetical prote
82	90.5	5.7	575	2	S29315	chaperonin 60 - cu
83	90	5.7	388	2	S36500	E2 protein - human
84	90	5.7	1007	2	T24643	hypothetical prote
85	90	5.7	1367	1	S48478	glucan 1,4-alpha-g
86	89.5	5.7	411	2	A33664	96K lysosomal memb
87	89.5	5.7	518	2	T49778	hypothetical prote
88	89.5	5.7	1369	2	S70713	protein-tyrosine k
89	89	5.7	307	1	GSFF3	salivary glue prot
90	89	5.7	416	1	A31959	lysosome-associate
91	89	5.7	429	1	JC5861	endo-1,4-beta-xyla
92	89	5.7	517	2	T20658	probable zinc meta
93	89	5.7	5170	2	T15348	hypothetical prote
94	88.5	5.6	193	2	A71415	hypothetical prote
95	88.5	5.6	376	2	S52137	MID2 protein - yea
96	88.5	5.6	721	2	B90487	hypothetical prote
97	88.5	5.6	770	2	T22808	hypothetical prote
98	88.5	5.6	1101	2	S15271	endoglucanase C (E
99	88	5.6	456	2	T31483	hypothetical prote
100	88	5.6	564	2	T25945	hypothetical prote
101	88	5.6	602	2	AD2067	hypothetical prote
102	88	5.6	1631	1	SAZQK1	major merozoite su

103	88	5.6	3507	2	T34513	hypothetical prote
104	88	5.6	3570	2	T45025	mucin MUC5B, trach
105	87.5	5.6	825	2	T48431	hypothetical prote
106	87.5	5.6	1085	2	S40476	Ca(2+)-sensing rec
107	87.5	5.6	1091	1	IJCHNL	neural cell adhesi
108	87.5	5.6	1802	2	S69703	HKR1 protein precu
109	87	5.5	235	2	PC2022	mucin like protein
110	87	5.5	752	2	E72616	hypothetical prote
111	87	5.5	1016	2	H71460	probable outer mem
112	87	5.5	1506	2	T30886	integumentary muci
113	87	5.5	1537	2	S53465	flocculation prote
114	86.5	5.5	400	1	A28172	spasmolysin precur
115	86.5	5.5	461	2	T22946	hypothetical prote
116	86.5	5.5	503	2	S63257	probable membrane
117	86.5	5.5	550	2	T29919	hypothetical prote
118	86.5	5.5	681	2	S33316	structural protein
119	86.5	5.5	740	1	FOLJHD	gag polyprotein -
120	86.5	5.5	768	2	T00073	hypothetical prote
121	86.5	5.5	1777	2	T34369	hypothetical prote
122	86.5	5.5	2616	2	A57096	nudel protein prec
123	86	5.5	1785	2	A45546	major merozoite su
124	85.5	5.4	575	2	S29316	chaperonin 60 - cu
125	85.5	5.4	649	2	T04606	protein kinase hom
126	85.5	5.4	786	2	T16509	hypothetical prote
127	85.5	5.4	895	2	T02597	Mutator-like trans
128	85	5.4	265	2	T33695	hypothetical prote
129	85	5.4	576	2	S59829	hypothetical prote
130	85	5.4	627	2	G86860	serine/threonine p
131	85	5.4	761	2	T00940	hypothetical prote
132	85	5.4	989	2	T47503	hypothetical prote
133	85	5.4	990	2	I51618	nucleolar phosphop
134	85	5.4	1162	2	T21557	hypothetical prote
135	85	5.4	1779	2	T31085	xylanase - Caldice
136	84.5	5.4	463	2	B82001	probable amino-aci
137	84.5	5.4	493	2	JC5486	membrane glycoprot
138	84.5	5.4	562	2	A57088	nucleoporin-like p
139	84.5	5.4	658	2	T39500	serine/threonine-s
140	84.5	5.4	658	2	S60170	protein kinase Pak
141	84.5	5.4	709	2	T28712	hypothetical prote
142	84.5	5.4	1102	2	S65235	probable membrane
143	84.5	5.4	1161	2	S57180	probable membrane
144	84.5	5.4	2481	2	D90011	FmtB protein [impo
145	84	5.3	262	2	S76772	hypothetical prote
146	84	5.3	335	2	H96667	AP2-containing DNA
147	84	5.3	420	2	AB2426	hypothetical prote
148	84	5.3	426	2	B53580	neurexin III beta
149	84	5.3	543	2	S35047	mucin JUL7 - human
150	84	5.3	636	1	VCVWFS	env polyprotein -
151	84	5.3	662	2	A45155	mucin FIM-C.1 - Af
152	84	5.3	793	2	AH1094	probable peptidogl
153	84	5.3	996	2	JE0237	apolipoprotein E r
154	84	5.3	1075	2	S48992	flocculation prote
155	84	5.3	1331	2	A48954	mannan endo-1,4-be
156	84	5.3	1362	2	A75207	amylopullulanase P
157	84	5.3	1832	2	T31113	mucin-like glycopr
158	84	5.3	3020	2	A43932	mucin 2 precursor,
159	83.5	5.3	216	2	I51920	mucin - rhesus mac
160	83.5	5.3	279	2	S53363	mucin 5AC (clone J
161	83.5	5.3	446	2	T45525	WSC4 homolog [impo
162	83.5	5.3	1043	2	F97302	hypothetical prote
163	83.5	5.3	1286	2	A88396	protein M01E10.2 [
164	83	5.3	221	2	S53649	ribosomal protein
165	83	5.3	409	2	S44346	RAD23 protein homo
166	83	5.3	463	2	T38444	hypothetical prote
167	83	5.3	605	2	S48940	hypothetical prote
168	83	5.3	737	1	S64767	probable serine/th
169	83	5.3	797	1	VGBEX1	glycoprotein X pre
170	83	5.3	866	2	T45462	membrane glycoprot
171	83	5.3	867	2	T45463	membrane glycoprot
172	83	5.3	977	2	T16232	hypothetical prote
173	82.5	5.2	383	1	S15624	E2 protein - human
174	82.5	5.2	416	2	B84030	stage VI sporulati
175	82.5	5.2	456	1	H64099	probable amino aci
176	82.5	5.2	569	2	B84470	Mutator-like trans
177	82.5	5.2	726	2	S67044	NFI1 protein - yea
178	82.5	5.2	825	2	S62042	probable membrane
179	82.5	5.2	871	2	T43427	pob1 protein - fis
180	82.5	5.2	1206	2	S24407	formin isoform IV
181	82.5	5.2	1407	2	T18381	latrophilin-2 (spl
182	82.5	5.2	1420	2	T18385	latrophilin-2 (spl
183	82.5	5.2	1422	2	T18383	latrophilin-2, spl
184	82.5	5.2	1435	2	T18387	latrophilin-2 (spl
185	82.5	5.2	1450	2	T18382	latrophilin-2 (spl
186	82.5	5.2	1460	2	D81675	polymorphic membra
187	82.5	5.2	1463	2	T18386	latrophilin-2 (spl
188	82.5	5.2	1465	2	T18384	latrophilin-2 (spl
189	82.5	5.2	1468	2	S11515	formin - mouse
190	82.5	5.2	1478	2	T18388	latrophilin-2 (spl
191	82.5	5.2	2311	1	TVCHSR	kinase-related pro
192	82	5.2	389	2	T33340	hypothetical prote
193	82	5.2	476	2	A46118	myosin-binding pro
194	82	5.2	544	2	T15175	hypothetical prote
195	82	5.2	577	2	G89430	protein K02E2.3 [i
196	82	5.2	584	2	T19061	hypothetical prote
197	82	5.2	693	2	T19551	mucin-like protein
198	82	5.2	720	2	S51340	nucleoporin NUP2 -
199	82	5.2	894	2	B96557	probable receptor
200	82	5.2	911	2	E86438	hypothetical prote
201	82	5.2	926	2	T38198	COPII coated vesic
202	82	5.2	973	2	A97522	ribonuclease E, RN
203	82	5.2	977	2	AC2741	ribonuclease E [im
204	82	5.2	1023	2	JC4013	major acidic nucle
205	82	5.2	1083	2	S59780	hypothetical prote
206	82	5.2	1127	2	T25804	hypothetical prote
207	82	5.2	1672	2	C81675	polymorphic membra
208	82	5.2	2738	2	E88320	protein F07A11.6 [
209	82	5.2	26926	1	I38344	titin, cardiac mus
210	81.5	5.2	235	2	T47379	hypothetical prote
211	81.5	5.2	386	2	B97212	protein containing
212	81.5	5.2	463	2	B81228	sodium/alanine sym
213	81.5	5.2	636	2	S63131	probable membrane
214	81.5	5.2	687	2	A40711	RNA polymerase II
215	81.5	5.2	860	2	AG1612	DNA mismatch repai
216	81.5	5.2	869	2	T22422	hypothetical prote
217	81.5	5.2	1151	2	T18297	zinc-finger protei
218	81.5	5.2	1212	2	T13804	shs protein - frui
219	81.5	5.2	1216	2	F88473	protein F40H6.5 [i
220	81.5	5.2	1445	1	A48148	protein-tyrosine-p
221	81.5	5.2	1513	2	T23681	hypothetical prote
222	81.5	5.2	2282	2	T42717	DNA-binding protei
223	81.5	5.2	3175	1	RRWVEV	genome polyprotein
224	81	5.1	339	2	T25562	hypothetical prote
225	81	5.1	369	2	T01196	transcription fact
226	81	5.1	422	1	BMRT2Y	synaptotagmin II -
227	81	5.1	683	2	T10720	NADPH-ferrihemopro
228	81	5.1	683	2	E86358	F12K8.13 protein -
229	81	5.1	911	2	S46497	aspartate kinase (
230	81	5.1	967	2	S66852	hypothetical prote
231	81	5.1	1047	2	A55617	masquerade precurs
232	81	5.1	1128	2	A49960	bud emergence prot
233	81	5.1	1169	2	S38181	flocculation prote
234	81	5.1	1367	2	S51959	hypothetical prote
235	81	5.1	1609	2	S25345	probable membrane
236	81	5.1	1726	2	A39401	merozoite surface
237	81	5.1	6642	2	T29757	protein UNC-89 - C
238	80.5	5.1	148	1	S07723	immediate-early se
239	80.5	5.1	391	1	S15617	E2 protein - human
240	80.5	5.1	441	2	T31482	hypothetical prote
241	80.5	5.1	543	2	T22585	hypothetical prote
242	80.5	5.1	592	2	T34446	hypothetical prote
243	80.5	5.1	595	2	A42086	CD30 antigen precu
244	80.5	5.1	742	2	T33514	hypothetical prote
245	80.5	5.1	798	2	T34248	hypothetical prote
246	80.5	5.1	1159	1	A44280	inner layer protei
247	80.5	5.1	2225	2	T26063	hypothetical prote
248	80	5.1	153	2	S67294	hypothetical prote

249	80	5.1	177	1	RGBYGI	regulatory protein
250	80	5.1	345	2	T21776	hypothetical prote
251	80	5.1	415	2	AE2237	hypothetical prote
252	80	5.1	451	2	S71754	cellular hepatitis
253	80	5.1	468	2	A55116	vacuolar ATPase (E
254	80	5.1	650	2	T41681	probable serine/th
255	80	5.1	667	2	A40713	cylicin I - bovine
256	80	5.1	688	2	T18263	S-layer protein -
257	80	5.1	702	2	T34313	hypothetical prote
258	80	5.1	725	2	A41258	a-agglutinin core
259	80	5.1	738	2	T44194	hypothetical prote
260	80	5.1	881	2	S56032	probable membrane
261	80	5.1	1013	1	S04200	NAD ADP-ribosyltra
262	80	5.1	1348	2	S27812	probable epidermal
263	79.5	5.0	152	2	T15170	hypothetical prote
264	79.5	5.0	165	2	A27195	histone H1 - Tetra
265	79.5	5.0	194	2	F72525	hypothetical prote
266	79.5	5.0	354	2	T46740	microfilarial shea
267	79.5	5.0	461	1	A35356	tumor necrosis fac
268	79.5	5.0	510	2	B72007	conserved hypothet
269	79.5	5.0	510	2	A86618	CT861 hypothetical
270	79.5	5.0	534	2	G84713	hypothetical prote
271	79.5	5.0	554	2	JW0094	neurofilament prot
272	79.5	5.0	580	2	T20716	hypothetical prote
273	79.5	5.0	693	2	T25878	hypothetical prote
274	79.5	5.0	827	2	T04789	hypothetical prote
275	79.5	5.0	860	2	AC1250	DNA mismatch repai
276	79.5	5.0	998	2	S31735	NAD ADP-ribosyltra
277	79.5	5.0	1011	2	T20785	hypothetical prote
278	79.5	5.0	1021	2	S64506	protein kinase BUB
279	79.5	5.0	1280	2	E95031	alkaline amylopull
280	79.5	5.0	1365	2	S14871	suppressor two of
281	79.5	5.0	2817	2	B97033	uncharacterized pr
282	79	5.0	215	2	S26363	histone H1.1 - hum
283	79	5.0	249	2	G84781	hypothetical prote
284	79	5.0	352	2	T51659	myb-related transc
285	79	5.0	359	2	T13478	hypothetical prote
286	79	5.0	410	1	B31959	lysosome-associate
287	79	5.0	410	1	JC4317	lysosome-associate
288	79	5.0	534	2	T39903	serine-rich protei
289	79	5.0	575	2	T21775	hypothetical prote
290	79	5.0	611	2	AB1497	internalin protein
291	79	5.0	710	2	S67098	probable membrane
292	79	5.0	739	2	T49456	hypothetical prote
293	79	5.0	761	2	A96810	probable Mutator-l
294	79	5.0	822	2	JC4076	dextranase (EC 3.2
295	79	5.0	836	2	S49940	cell division cont
296	79	5.0	1098	2	T08599	probable transcrip
297	79	5.0	1849	2	C41859	IgA-specific metal
298	79	5.0	1904	2	T13256	tail-host specific
299	78.5	5.0	152	2	T28759	hypothetical prote
300	78.5	5.0	164	2	I53641	mucin 5AC - human
301	78.5	5.0	232	2	A60095	larval glue protei
302	78.5	5.0	294	2	A37232	mucin, tracheal (A
303	78.5	5.0	314	1	HNVZVW	hemagglutinin prec
304	78.5	5.0	314	1	JQ1793	hemagglutinin prec
305	78.5	5.0	322	2	A53715	apomucin precursor
306	78.5	5.0	387	2	A53586	albumin-binding pr
307	78.5	5.0	413	2	S55890	plasma protein rec
308	78.5	5.0	423	2	S69583	hypothetical prote
309	78.5	5.0	542	2	S64030	probable membrane
310	78.5	5.0	591	1	WMBPQ2	gene P2 protein -
311	78.5	5.0	599	2	S46630	hypothetical prote
312	78.5	5.0	688	2	B42161	cGMP-gated cation
313	78.5	5.0	815	2	JG0197	myosin-light-chain
314	78.5	5.0	825	2	T29634	hypothetical prote
315	78.5	5.0	919	1	PXZP1P	H+-exporting ATPas
316	78.5	5.0	1011	1	JH0581	NAD ADP-ribosyltra
317	78.5	5.0	1356	2	T16754	hypothetical prote
318	78.5	5.0	1420	2	T17158	CL2AB protein - ra
319	78.5	5.0	1435	2	T46611	CL2BB protein - ra
320	78.5	5.0	1452	2	T17157	CL2AA protein - ra
321	78.5	5.0	1463	2	T17159	CL2AC protein - ra
322	78.5	5.0	1467	2	T17160	CL2BA protein - ra
323	78.5	5.0	1478	2	T17185	CL2BC protein - ra
324	78.5	5.0	1487	2	T14324	alpha-latrotoxin r
325	78.5	5.0	1876	2	E97944	zinc metalloprotei
326	78	5.0	253	2	S76719	hypothetical prote
327	78	5.0	260	2	AG2238	hypothetical prote
328	78	5.0	266	2	T30919	hypothetical prote
329	78	5.0	287	2	T12471	hypothetical prote
330	78	5.0	293	2	G87018	probable membrane
331	78	5.0	372	2	T48660	heat shock protein
332	78	5.0	373	2	F81333	chaperone DnaJ Cj1
333	78	5.0	425	2	T48724	hypothetical prote
334	78	5.0	434	2	B84684	hypothetical prote
335	78	5.0	521	2	S69559	hypothetical prote
336	78	5.0	530	2	A45690	transactivator EBN
337	78	5.0	627	1	VCVWM2	env polyprotein -
338	78	5.0	655	2	T30044	hypothetical prote
339	78	5.0	786	1	A47547	serine proteinease
340	78	5.0	1050	2	T31853	hypothetical prote
341	78	5.0	1337	2	T30291	dextranase - Strep
342	78	5.0	1360	2	T33922	hypothetical prote
343	78	5.0	1442	1	B48148	protein-tyrosine-p
344	78	5.0	1634	2	T26517	hypothetical prote
345	78	5.0	1723	2	H86557	polymorphic membra
346	78	5.0	1723	2	E72067	polymorphic membra
347	78	5.0	1732	2	C81601	polymorphic membra
348	78	5.0	1955	1	AGCH	agrin precursor -
349	78	5.0	1995	2	T08166	probable membrane
350	78	5.0	5327	2	T13564	microtubule-associ
351	77.5	4.9	396	2	F83130	probable MFS trans
352	77.5	4.9	401	2	AG3552	brancheD-chain ami
353	77.5	4.9	474	1	BMFFSY	synaptotagmin - fr
354	77.5	4.9	514	2	JQ1317	activin receptor p
355	77.5	4.9	519	2	T45764	hypothetical prote
356	77.5	4.9	526	2	A56573	nuclear pore compl
357	77.5	4.9	607	2	S01939	hypothetical prote
358	77.5	4.9	623	2	T18892	hypothetical prote
359	77.5	4.9	816	2	S64439	hypothetical prote
360	77.5	4.9	860	2	JC4566	chitinase (EC 3.2.
361	77.5	4.9	906	2	G90281	conserved hypothet
362	77.5	4.9	938	2	A56731	chromatin assembly
363	77.5	4.9	975	2	T08606	protein phosphatas
364	77.5	4.9	1127	2	E86386	probable mutator-l
365	77.5	4.9	1156	2	T23748	hypothetical prote
366	77.5	4.9	1312	2	A97879	beta-N-acetylhexos
367	77.5	4.9	1475	2	S42718	nuclear pore compl
368	77.5	4.9	2761	2	T21064	hypothetical prote
369	77.5	4.9	3968	2	A44265	trithorax homolog
370	77	4.9	350	2	E75341	peptidyl-prolyl ci
371	77	4.9	353	2	S22805	env polyprotein -
372	77	4.9	453	2	F75206	maltose-binding pe
373	77	4.9	553	2	T19894	hypothetical prote
374	77	4.9	598	2	T22610	hypothetical prote
375	77	4.9	623	2	A48123	cell cycle regulat
376	77	4.9	639	2	T33166	hypothetical prote
377	77	4.9	669	1	VCVWEK	env polyprotein -
378	77	4.9	734	2	B42680	nucleolus-cytoplas
379	77	4.9	750	2	T42614	probable envelope
380	77	4.9	771	2	JC7388	M83 protein - huma
381	77	4.9	861	2	T23810	hypothetical prote
382	77	4.9	892	2	T09193	ataxin 7 - human
383	77	4.9	897	2	S50550	SIN1-associated pr
384	77	4.9	977	2	S49004	tyrosine kinase Mp
385	77	4.9	1237	2	T14633	hypothetical prote
386	77	4.9	1401	2	T30247	Werner syndrome pr
387	77	4.9	1513	2	A54895	mucin 2, intestina
388	77	4.9	2187	2	T30826	nascent polypeptid
389	76.5	4.9	284	2	T42367	a-agglutinin core
390	76.5	4.9	349	2	T43457	hypothetical prote
391	76.5	4.9	382	2	S27388	neuropeptide Y rec
392	76.5	4.9	391	2	C69673	penicillin-binding
393	76.5	4.9	421	2	A60058	neural cell adhesi
394	76.5	4.9	433	2	H84120	methyl-accepting c

395	76.5	4.9	505	2	B46629	mucin 6, gastric (
396	76.5	4.9	518	2	G88961	protein F59A7.8 [i
397	76.5	4.9	542	2	I39540	chitinase (EC 3.2.
398	76.5	4.9	549	2	S04845	Ig heavy chain pre
399	76.5	4.9	640	1	VCVWM1	env polyprotein -
400	76.5	4.9	651	2	C56653	membrane glycoprot
401	76.5	4.9	718	2	T29708	hypothetical prote
402	76.5	4.9	727	2	A88131	protein F10G7.9 [i
403	76.5	4.9	749	2	B86403	probable mutator-l
404	76.5	4.9	773	2	T00502	probable receptor-
405	76.5	4.9	806	2	E69424	hypothetical prote
406	76.5	4.9	990	2	T16554	hypothetical prote
407	76.5	4.9	1154	1	VGIHIB	E2 glycoprotein pr
408	76.5	4.9	1379	2	T45119	FIM protein [impor
409	76.5	4.9	1946	2	JC6032	lactocepin (EC 3.4
410	76.5	4.9	3869	2	A48205	All-1 protein +GTE
411	76.5	4.9	5037	2	B35041	ryanodine receptor
412	76	4.8	167	2	A33532	mucin SMUC-40 - hu
413	76	4.8	172	2	T21753	hypothetical prote
414	76	4.8	243	2	B41710	promastigote surfa
415	76	4.8	340	2	AH0940	probable ABC trans
416	76	4.8	356	2	D88979	protein F37B4.9 [i
417	76	4.8	368	2	S36564	E2 protein - human
418	76	4.8	378	2	AI2180	hypothetical prote
419	76	4.8	382	2	B88561	protein F58A4.7b [
420	76	4.8	384	2	A41710	promastigote surfa
421	76	4.8	389	2	E97305	NADH-dependent but
422	76	4.8	389	2	A47013	butanol dehydrogen
423	76	4.8	499	2	T47722	probable protein k
424	76	4.8	515	2	AD1162	flagellar motor sw
425	76	4.8	532	2	T28784	hypothetical prote
426	76	4.8	536	2	T37544	hypothetical serin
427	76	4.8	539	2	T02512	hypothetical prote
428	76	4.8	549	2	T49298	hypothetical prote
429	76	4.8	592	2	T16725	hypothetical prote
430	76	4.8	615	2	T47395	hypothetical prote
431	76	4.8	699	2	I38073	nucleolar phosphop
432	76	4.8	700	2	A54641	interspersed repea
433	76	4.8	738	2	T44007	hypothetical prote
434	76	4.8	763	2	T08929	hypothetical prote
435	76	4.8	766	2	B85440	receptor kinase-li
436	76	4.8	824	2	T23923	hypothetical prote
437	76	4.8	929	2	G72677	hypothetical prote
438	76	4.8	940	2	AD1374	internalin protein
439	76	4.8	960	1	JN0677	protein-tyrosine k
440	76	4.8	967	2	G86229	hypothetical prote
441	76	4.8	994	1	MNWVM	nonstructural prot
442	76	4.8	1014	1	A29725	NAD ADP-ribosyltra
443	76	4.8	1041	2	H71617	SERA antigen/papai
444	76	4.8	1046	2	T29776	hypothetical prote
445	76	4.8	1263	2	AH2011	heterocyst glycoli
446	76	4.8	1348	2	A43917	probable epidermal
447	76	4.8	1401	2	T17452	Werner syndrome pr
448	76	4.8	1422	2	T42636	protein-tyrosine-p
449	76	4.8	1438	2	B71610	WD40 WEB-1 homolog
450	76	4.8	1489	2	G71406	probable retroviru
451	76	4.8	1513	2	T44045	hypothetical prote
452	76	4.8	1890	2	T04556	hypothetical prote
453	76	4.8	2570	2	T17451	fimbriae-associate
454	75.5	4.8	260	1	G69223	molybdate-binding
455	75.5	4.8	261	2	T30170	hypothetical prote
456	75.5	4.8	273	2	T44657	protein GP80 [impo
457	75.5	4.8	319	1	A35163	carbonate dehydrat
458	75.5	4.8	321	2	T26152	hypothetical prote
459	75.5	4.8	343	2	T40306	hypothetical prote
460	75.5	4.8	348	1	B46216	transcription fact
461	75.5	4.8	387	2	A86302	hypothetical prote
462	75.5	4.8	412	2	E97279	TPR-repeat-contain
463	75.5	4.8	430	1	A46216	transcription fact
464	75.5	4.8	435	2	S40993	hypothetical prote
465	75.5	4.8	443	2	D72383	NADH oxidase - The
466	75.5	4.8	445	2	I38521	inwardly rectifyin
467	75.5	4.8	448	2	S17370	DNA-binding protei
468	75.5	4.8	482	2	AG1147	P60 extracellular
469	75.5	4.8	484	2	A41487	protein P60 precur
470	75.5	4.8	496	2	B41322	N-acetylmuramoyl-L
471	75.5	4.8	511	1	VGBEF4	glycoprotein C - h
472	75.5	4.8	609	2	G87496	peptidase, M23/M37
473	75.5	4.8	639	2	T13151	adapter protein CM
474	75.5	4.8	665	2	G97213	probable membrane-
475	75.5	4.8	709	2	T32089	hypothetical prote
476	75.5	4.8	778	2	T43223	hypothetical prote
477	75.5	4.8	780	2	A48143	HF-1 regulatory el
478	75.5	4.8	963	2	T40290	hypothetical prote
479	75.5	4.8	1131	2	T41144	hypothetical serin
480	75.5	4.8	1166	2	S37692	probable tumor sup
481	75.5	4.8	1235	2	T13710	protein-tyrosine k
482	75.5	4.8	1237	2	E86457	probable RNA helic
483	75.5	4.8	1473	2	T31422	C-terminal domain-
484	75.5	4.8	1655	2	T32633	hypothetical prote
485	75.5	4.8	1737	2	A59235	unconventional myo
486	75.5	4.8	1881	2	H95076	zinc metalloprotei
487	75.5	4.8	2526	2	T20531	hypothetical prote
488	75.5	4.8	3176	2	CGHU3A	collagen alpha 3(V
489	75	4.8	94	2	S53365	mucin 5AC (clone C
490	75	4.8	128	2	T05035	hypothetical prote
491	75	4.8	205	2	S55670	hypothetical prote
492	75	4.8	248	2	AF1914	carbon dioxide con
493	75	4.8	256	2	T09034	hypothetical prote
494	75	4.8	310	1	H71054	hypothetical prote
495	75	4.8	313	2	AH0734	probable bacteriop
496	75	4.8	388	2	T16861	hypothetical prote
497	75	4.8	390	2	A72108	hypothetical prote
498	75	4.8	390	2	B86514	hypothetical prote
499	75	4.8	418	2	T16713	hypothetical prote
500	75	4.8	425	1	A26431	nerve growth facto
501	75	4.8	453	2	C40511	hypothetical prote
502	75	4.8	475	2	E84745	probable splicing
503	75	4.8	477	2	T32938	hypothetical prote
504	75	4.8	481	2	T38149	pre-mrna splicing
505	75	4.8	528	2	S69589	hypothetical prote
506	75	4.8	554	2	A56596	chitinase (EC 3.2.
507	75	4.8	604	2	T37994	probable splicing
508	75	4.8	607	2	S63395	probable membrane
509	75	4.8	651	2	T16450	hypothetical prote
510	75	4.8	679	2	T19703	hypothetical prote
511	75	4.8	739	2	I56187	transcription fact
512	75	4.8	778	2	T45221	DNA damage checkpo
513	75	4.8	796	2	E96654	hypothetical prote
514	75	4.8	858	1	IJRTNC	neural cell adhesi
515	75	4.8	904	2	T03806	hypothetical prote
516	75	4.8	916	2	T20909	hypothetical prote
517	75	4.8	940	2	D89723	protein F39D8.1b [
518	75	4.8	945	2	T21998	hypothetical prote
519	75	4.8	993	2	F97717	hypothetical prote
520	75	4.8	1048	1	S61388	dotA protein - Leg
521	75	4.8	1118	2	A48292	mucin, tracheobron
522	75	4.8	1253	2	T18528	probable pyruvate
523	75	4.8	1419	2	T30531	agglutinin-like ad
524	75	4.8	1741	2	T13610	parallel sister ch
525	75	4.8	1768	2	T13349	parallel sister ch
526	75	4.8	1838	1	CGHU1V	collagen alpha 1(V
527	75	4.8	1979	2	C71622	hypothetical prote
528	75	4.8	3375	2	T19821	hypothetical prote
529	74.5	4.7	148	2	S50653	hypothetical prote
530	74.5	4.7	211	2	S28046	TUB8 protein - pot
531	74.5	4.7	254	2	D88560	protein F58A4.1 [i
532	74.5	4.7	262	2	T33597	hypothetical prote
533	74.5	4.7	276	2	T51685	myb-related transc
534	74.5	4.7	281	2	T49537	hypothetical prote
535	74.5	4.7	294	2	AI2016	hypothetical prote
536	74.5	4.7	310	1	YAZQ31	300K antigen Ag231
537	74.5	4.7	321	2	T50966	hypothetical prote
538	74.5	4.7	382	2	T25280	hypothetical prote
539	74.5	4.7	396	2	T50229	probable transmemb
540	74.5	4.7	407	2	T26938	hypothetical prote

541	74.5	4.7	429	2	S29044	endoglucanase A pr
542	74.5	4.7	432	2	T08771	hypothetical prote
543	74.5	4.7	478	2	A32555	major merozoite su
544	74.5	4.7	482	2	T22754	hypothetical prote
545	74.5	4.7	520	2	S14598	E2 glycoprotein -
546	74.5	4.7	531	2	S09859	hypothetical prote
547	74.5	4.7	551	2	S52287	urbain - silkworm
548	74.5	4.7	636	2	T23232	hypothetical prote
549	74.5	4.7	713	2	JE0230	NADPH-cytochrome P
550	74.5	4.7	802	2	T21315	hypothetical prote
551	74.5	4.7	808	2	T23129	hypothetical prote
552	74.5	4.7	862	2	B36786	hypothetical prote
553	74.5	4.7	884	2	AE3166	ATP-dependent DNA
554	74.5	4.7	998	2	S37627	protein-tyrosine k
555	74.5	4.7	1388	2	A53317	collagen alpha 1(X
556	74.5	4.7	1595	2	T31082	endo-1,4-beta-xyla
557	74.5	4.7	1630	2	A53577	ascites sialoglyco
558	74.5	4.7	1902	2	C97702	cell surface antig
559	74.5	4.7	1965	2	T33216	hypothetical prote
560	74.5	4.7	2688	2	I49477	alpha-A-crystallin
561	74.5	4.7	3828	2	T13857	trithorax protein
562	74.5	4.7	3944	2	T19997	hypothetical prote
563	74	4.7	147	2	S09762	hypothetical prote
564	74	4.7	223	2	T21930	hypothetical prote
565	74	4.7	257	1	MGNZBR	major surface glyc
566	74	4.7	264	2	A49149	mesoderm developme
567	74	4.7	286	2	S44835	F54H12.3 protein -
568	74	4.7	317	2	C85432	hypothetical prote
569	74	4.7	332	2	T31928	hypothetical prote
570	74	4.7	339	1	JT0756	group-V allergen i
571	74	4.7	339	2	A56274	sulfur-regulated 3
572	74	4.7	384	2	T21929	hypothetical prote
573	74	4.7	390	2	C97889	UDPglucose 6-dehyd
574	74	4.7	397	2	E97176	N-terminal domain
575	74	4.7	412	1	AJBORS	argininosuccinate
576	74	4.7	413	2	S28066	sexual differentia
577	74	4.7	417	2	T20327	hypothetical prote
578	74	4.7	435	2	AG1028	prepilin [imported
579	74	4.7	454	2	T02100	hypothetical prote
580	74	4.7	540	1	FOMVHL	gag polyprotein -
581	74	4.7	575	2	S39484	DNA-binding protei
582	74	4.7	586	2	S66697	probable membrane
583	74	4.7	600	2	T06292	hypothetical prote
584	74	4.7	621	2	T20307	hypothetical prote
585	74	4.7	665	1	VCMVKA	env polyprotein pr
586	74	4.7	672	2	T20310	hypothetical prote
587	74	4.7	689	2	B43491	env polyprotein -
588	74	4.7	731	2	T04455	hypothetical prote
589	74	4.7	739	1	A34873	transcription fact
590	74	4.7	775	2	A32494	transposable eleme
591	74	4.7	823	2	G90848	probable exonuclea
592	74	4.7	823	2	E85706	probable exonuclea
593	74	4.7	852	2	T06310	hypothetical prote
594	74	4.7	903	2	T00705	N-chimerin homolog
595	74	4.7	1018	2	T40253	hypothetical prote
596	74	4.7	1099	2	G90546	conserved hypothet
597	74	4.7	1104	2	S59310	probable membrane
598	74	4.7	1110	2	I51116	NF-180 - sea lampr
599	74	4.7	1115	1	IJMSNL	neural cell adhesi
600	74	4.7	1159	2	S62562	probable nuclear p
601	74	4.7	1216	2	B90580	hypothetical prote
602	74	4.7	1390	2	T14004	trfA protein - sli
603	74	4.7	1694	2	H64106	IgA-specific metal
604	74	4.7	1828	2	A40115	microtubule-associ
605	74	4.7	1938	1	MWKW1	myosin heavy chain
606	74	4.7	2414	2	A54277	transcription adap
607	74	4.7	3224	1	S58884	Ran-binding protei
608	73.5	4.7	168	2	A31196	prespore-specific
609	73.5	4.7	182	2	T30078	hypothetical prote
610	73.5	4.7	253	2	T32879	hypothetical prote
611	73.5	4.7	263	2	T38003	hypothetical ser-t
612	73.5	4.7	290	2	S66355	lectin-related sto
613	73.5	4.7	292	2	S24169	mucin - rat
614	73.5	4.7	345	2	D91201	type III secretion
615	73.5	4.7	345	2	H86047	escU [imported] -
616	73.5	4.7	358	2	AD2378	hypothetical prote
617	73.5	4.7	371	2	S20075	promastigote surfa
618	73.5	4.7	376	2	T48245	hypothetical prote
619	73.5	4.7	381	2	E69862	hypothetical prote
620	73.5	4.7	397	2	G69287	hypothetical prote
621	73.5	4.7	405	2	A60534	P2B/LAMP-1 precurs
622	73.5	4.7	445	2	A54852	potassium rectifie
623	73.5	4.7	447	2	A39321	mucin - rat (fragm
624	73.5	4.7	457	2	T20884	hypothetical prote
625	73.5	4.7	458	2	T31631	hypothetical prote
626	73.5	4.7	459	2	I48854	gene murine tumour
627	73.5	4.7	484	1	A24994	cellulose 1,4-beta
628	73.5	4.7	511	1	VGBE1K	glycoprotein C - h
629	73.5	4.7	542	2	T19952	hypothetical prote
630	73.5	4.7	550	1	VGIHD6	E2 glycoprotein pr
631	73.5	4.7	555	2	T26413	hypothetical prote
632	73.5	4.7	569	2	A46462	T cell activation
633	73.5	4.7	601	2	H90270	hypothetical prote
634	73.5	4.7	603	2	T39866	hypothetical prote
635	73.5	4.7	626	2	AB1328	probable peptidogl
636	73.5	4.7	654	2	T33044	hypothetical prote
637	73.5	4.7	696	2	G81262	probable integral
638	73.5	4.7	708	2	F87245	penicillin-bonding
639	73.5	4.7	713	2	T44447	neuregulin-3 [impo
640	73.5	4.7	756	2	JC5886	signaling mediator
641	73.5	4.7	819	2	B95136	conserved domain p
642	73.5	4.7	901	2	A44825	phosphoprotein, sy
643	73.5	4.7	905	2	T02205	Lu-ECAM-1 protein
644	73.5	4.7	976	2	A87576	peptidase, M16 fam
645	73.5	4.7	990	2	H88733	protein F32E10.3 [
646	73.5	4.7	1004	2	T38074	hypothetical prote
647	73.5	4.7	1016	2	T19006	ankyrin related pr
648	73.5	4.7	1139	1	E64234	cytadherence-acces
649	73.5	4.7	1291	2	T22382	hypothetical prote
650	73.5	4.7	2232	2	T34434	hypothetical prote
651	73	4.6	188	2	C96593	unknown protein, 9
652	73	4.6	198	2	E71837	protein-export mem
653	73	4.6	213	2	S43949	histone H1 - mouse
654	73	4.6	260	2	I50109	gastrulation prote
655	73	4.6	288	2	JQ2365	polyprotein - Bean
656	73	4.6	315	1	HNVZVV	hemagglutinin prec
657	73	4.6	316	2	G86333	hypothetical prote
658	73	4.6	327	2	S20074	promastigote surfa
659	73	4.6	359	2	S42787	serine/threonine-r
660	73	4.6	369	2	E84291	iron (III) ABC tra
661	73	4.6	422	2	A55417	synaptotagmin II -
662	73	4.6	428	1	Q4ECAD	damX protein (aroB
663	73	4.6	441	2	A43555	GAP-43-related pro
664	73	4.6	461	2	T51044	related to spore c
665	73	4.6	469	2	E64456	hypothetical prote
666	73	4.6	486	2	S66097	cell-cycle protein
667	73	4.6	486	2	A89927	elastin binding pr
668	73	4.6	492	1	CHBOA3	gamma-aminobutyric
669	73	4.6	496	2	E90181	hypothetical prote
670	73	4.6	550	2	C75557	hypothetical prote
671	73	4.6	558	2	A98199	translocated intim
672	73	4.6	558	2	E86045	probable transloca
673	73	4.6	600	2	E72027	phosphoenolpyruvat
674	73	4.6	600	2	A86597	phosphoenolpyruvat
675	73	4.6	669	2	A46511	envelope protein -
676	73	4.6	688	2	A43491	env polyprotein -
677	73	4.6	720	2	T51007	hypothetical prote
678	73	4.6	728	2	T20561	hypothetical prote
679	73	4.6	771	2	T34376	hypothetical prote
680	73	4.6	781	2	T49472	hormone-sensitive
681	73	4.6	814	2	T33140	hypothetical prote
682	73	4.6	918	2	A36337	membrane glycoprot
683	73	4.6	932	1	VGBEBC	glycoprotein gI pr
684	73	4.6	958	2	T10679	hypothetical prote
685	73	4.6	1016	2	T41720	hypothetical prote
686	73	4.6	1055	2	H90023	hypothetical prote

687	73	4.6	1071	2	T22327	hypothetical prote
688	73	4.6	1256	1	A43829	muramidase-release
689	73	4.6	1320	2	JC5630	TCOF1 protein - mo
690	73	4.6	1345	2	S46817	hypothetical prote
691	73	4.6	1702	2	A41859	IgA-specific metal
692	73	4.6	1993	2	AF1450	probable peptidogl
693	73	4.6	2179	1	GNNYH4	genome polyprotein
694	73	4.6	2285	2	T12796	probable transglyc
695	73	4.6	2416	2	T13825	adenomatous polypo
696	73	4.6	2468	2	A83412	hypothetical prote
697	73	4.6	2722	2	T20532	hypothetical prote
698	72.5	4.6	263	2	I51225	snail1 protein - z
699	72.5	4.6	314	2	B95034	dihydropteroate sy
700	72.5	4.6	321	2	T26153	hypothetical prote
701	72.5	4.6	328	2	S35336	transcription fact
702	72.5	4.6	382	2	T27058	hypothetical prote
703	72.5	4.6	391	2	T35470	probable integral
704	72.5	4.6	406	2	T23934	hypothetical prote
705	72.5	4.6	415	2	T32490	hypothetical prote
706	72.5	4.6	463	1	A36479	milk fat globule m
707	72.5	4.6	487	2	S40820	probable permease
708	72.5	4.6	498	1	VGXPLM	surface glycoprote
709	72.5	4.6	499	2	AI2449	hypothetical prote
710	72.5	4.6	507	2	S05542	hypothetical prote
711	72.5	4.6	511	2	T35194	transcription init
712	72.5	4.6	560	2	T32661	hypothetical prote
713	72.5	4.6	580	2	B38418	jockey protein 1 -
714	72.5	4.6	610	2	S35049	mucin JER57 - huma
715	72.5	4.6	642	2	T39607	fork head protein
716	72.5	4.6	648	2	PC4395	mucin 3 - human (f
717	72.5	4.6	657	2	A82415	conserved hypothet
718	72.5	4.6	663	2	T18631	hypothetical prote
719	72.5	4.6	687	2	A49636	soluble vascular e
720	72.5	4.6	710	2	A99486	ABC transporter, b
721	72.5	4.6	728	2	F72693	probable phosphoes
722	72.5	4.6	729	2	G96559	hypothetical prote
723	72.5	4.6	743	2	D86888	penicillin-binding
724	72.5	4.6	765	1	T44946	transducer protein
725	72.5	4.6	896	2	S36326	clathrin assembly
726	72.5	4.6	907	1	QQBE21	membrane antigen g
727	72.5	4.6	915	2	S36327	clathrin assembly
728	72.5	4.6	944	2	C70839	probable mmpL3 pro
729	72.5	4.6	982	2	A53253	microtubule-associ
730	72.5	4.6	1016	1	JS0428	NAD ADP-ribosyltra
731	72.5	4.6	1036	2	S73601	protein P200 - Myc
732	72.5	4.6	1148	2	T09073	splicing factor Si
733	72.5	4.6	1152	2	A33183	microtubule-associ
734	72.5	4.6	1180	2	E86719	hypothetical prote
735	72.5	4.6	1199	2	A40670	nuclear envelope p
736	72.5	4.6	1219	2	T14578	nucleoporin Nup153
737	72.5	4.6	1222	2	T22490	hypothetical prote
738	72.5	4.6	1309	1	BVBYD9	RAD9 protein - yea
739	72.5	4.6	1312	2	E95006	beta-N-acetylhexos
740	72.5	4.6	1338	2	S09982	protein-tyrosine k
741	72.5	4.6	1555	2	T18688	hypothetical prote
742	72.5	4.6	1635	2	T14075	chitinase (EC 3.2.
743	72.5	4.6	1736	2	F86178	hypothetical prote
744	72.5	4.6	1847	2	T18308	probable vitelloge
745	72.5	4.6	1973	2	G89608	protein B0272.5 [i
746	72.5	4.6	1973	2	T18686	hypothetical prote
747	72.5	4.6	2305	2	B89608	protein C23F12.1 [
748	72.5	4.6	2305	2	T15571	hypothetical prote
749	72.5	4.6	2314	1	A46151	protein-tyrosine-p
750	72.5	4.6	2897	2	B48666	cell proliferation
751	72.5	4.6	3069	2	H70656	fatty-acid synthas
752	72.5	4.6	3256	2	A48666	cell proliferation
753	72	4.6	139	2	G98226	hypothetical prote
754	72	4.6	139	2	AI3059	hypothetical prote
755	72	4.6	159	2	F72758	hypothetical prote
756	72	4.6	197	2	T33525	hypothetical prote
757	72	4.6	199	2	JE0351	OX40 ligand protei
758	72	4.6	236	2	T03041	hypothetical prote
759	72	4.6	246	2	PC4397	mucin 3 T10 - huma
760	72	4.6	282	2	B37994	RF2 protein - saim
761	72	4.6	303	2	S40973	hypothetical prote
762	72	4.6	317	1	GEHUS	bone sialoprotein
763	72	4.6	322	2	G69946	phage-related prot
764	72	4.6	324	2	S36646	integrin-associate
765	72	4.6	330	2	T49644	hypothetical prote
766	72	4.6	334	2	T19637	hypothetical prote
767	72	4.6	411	2	T03154	DNA polymerase pro
768	72	4.6	428	2	D86003	hypothetical prote
769	72	4.6	428	2	F91157	probable membrane
770	72	4.6	460	2	A84154	amino acid transpo
771	72	4.6	468	2	S70297	SPS2 protein homol
772	72	4.6	482	2	A44997	merozoite surface
773	72	4.6	508	2	A33378	fasciclin III prec
774	72	4.6	509	2	A96563	probable protein k
775	72	4.6	544	2	S07144	neurofilament trip
776	72	4.6	548	1	QFPGL	neurofilament trip
777	72	4.6	576	2	T38293	hypothetical serin
778	72	4.6	587	2	S38634	chaperonin, mitoch
779	72	4.6	592	2	D70863	hypothetical prote
780	72	4.6	622	2	A90570	lipoprotein [impor
781	72	4.6	674	2	S74506	ribonuclease E - S
782	72	4.6	677	2	T00369	hypothetical prote
783	72	4.6	679	2	S64258	hypothetical prote
784	72	4.6	736	2	T41259	hypothetical prote
785	72	4.6	770	1	S30293	transcription fact
786	72	4.6	855	2	D98004	histidine Motif-Co
787	72	4.6	876	2	T49801	hypothetical prote
788	72	4.6	884	2	T20405	hypothetical prote
789	72	4.6	958	2	T26258	hypothetical prote
790	72	4.6	993	1	P1VXTA	RNA 1 protein - to
791	72	4.6	1034	2	S49947	SMT4 protein - yea
792	72	4.6	1038	2	AG2187	hypothetical prote
793	72	4.6	1146	2	S46837	hypothetical prote
794	72	4.6	1176	2	T49482	hypothetical prote
795	72	4.6	1196	2	H85061	hypothetical prote
796	72	4.6	1203	2	T17415	mycelial surface a
797	72	4.6	1388	2	A57655	tim (timeless) pro
798	72	4.6	1489	2	T31108	cyst germination s
799	72	4.6	1547	2	T28657	blackjack protein,
800	72	4.6	1570	2	T18272	1-phosphatidylinos
801	72	4.6	1778	2	T50074	probable nucleopor
802	72	4.6	1829	2	T24583	hypothetical prote
803	72	4.6	2441	2	S39161	CREB-binding prote
804	72	4.6	2578	2	A56922	transcription fact
805	72	4.6	2971	2	T08026	hypothetical prote
806	71.5	4.5	141	2	A38196	non-structural hyp
807	71.5	4.5	146	2	S52800	hypothetical prote
808	71.5	4.5	162	2	C84948	NADH2 dehydrogenas
809	71.5	4.5	164	2	A26490	histone H1, macron
810	71.5	4.5	178	2	JQ1547	stripe disease-spe
811	71.5	4.5	231	2	F84311	hypothetical prote
812	71.5	4.5	263	2	S01360	salivary glue prot
813	71.5	4.5	305	2	AB2149	hypothetical prote
814	71.5	4.5	313	2	JQ1862	31R protein - vari
815	71.5	4.5	313	2	T28598	hypothetical prote
816	71.5	4.5	363	2	T25278	hypothetical prote
817	71.5	4.5	372	2	F43674	US7 protein - huma
818	71.5	4.5	373	2	S43455	hypothetical prote
819	71.5	4.5	381	2	S65212	hypothetical prote
820	71.5	4.5	385	2	T38113	hypothetical serin
821	71.5	4.5	392	2	T49471	mucin (muc3) relat
822	71.5	4.5	393	2	T49578	hypothetical prote
823	71.5	4.5	395	2	I52842	CD43 Lp-3 antigen
824	71.5	4.5	395	2	A43545	leukosialin CD43 p
825	71.5	4.5	408	2	A46712	glycoprotein IIa -
826	71.5	4.5	414	2	B84600	hypothetical prote
827	71.5	4.5	442	1	S11712	transcription init
828	71.5	4.5	443	1	D64584	heat shock protein
829	71.5	4.5	466	2	AI0957	chromosomal replic
830	71.5	4.5	503	2	G75262	hypothetical prote
831	71.5	4.5	507	2	T50398	hypothetical serin
832	71.5	4.5	540	1	A55145	thiamine-phosphate

833	71.5	4.5	540	2	H98086	chaperonin GroEL [
834	71.5	4.5	540	2	G95222	chaperonin, 60 kDa
835	71.5	4.5	584	2	T19565	hypothetical prote
836	71.5	4.5	631	2	I52257	episialin - mouse
837	71.5	4.5	661	1	VCMVCB	env polyprotein -
838	71.5	4.5	675	2	T47378	probable transposa
839	71.5	4.5	681	2	A45705	type I transmembra
840	71.5	4.5	755	2	T20950	hypothetical prote
841	71.5	4.5	760	1	S07896	transcription fact
842	71.5	4.5	882	2	T01168	hypothetical prote
843	71.5	4.5	918	2	I58178	glutamate receptor
844	71.5	4.5	1042	2	T48801	hypothetical prote
845	71.5	4.5	1043	2	T23875	hypothetical prote
846	71.5	4.5	1121	2	T02764	myosin-I binding p
847	71.5	4.5	1156	2	T43326	germline RNA helic
848	71.5	4.5	1172	2	T32759	hypothetical prote
849	71.5	4.5	1234	2	T31623	hypothetical prote
850	71.5	4.5	1260	2	A87046	hypothetical prote
851	71.5	4.5	1297	2	T30274	proteoliaisin - se
852	71.5	4.5	1459	2	T32271	hypothetical prote
853	71.5	4.5	1557	2	D41214	protein-tyrosine-p
854	71.5	4.5	1566	2	T20058	hypothetical prote
855	71.5	4.5	1630	2	C41214	protein-tyrosine-p
856	71	4.5	98	2	S53367	mucin 5AC (clone M
857	71	4.5	135	2	T49996	AtAGP4 - Arabidops
858	71	4.5	168	2	JN0073	glycophorin A - mo
859	71	4.5	177	2	G75285	hypothetical prote
860	71	4.5	213	2	A86228	hypothetical prote
861	71	4.5	240	2	T33698	hypothetical prote
862	71	4.5	242	2	T27226	hypothetical prote
863	71	4.5	304	2	T15922	hypothetical prote
864	71	4.5	310	2	T20535	hypothetical prote
865	71	4.5	329	2	T43012	conserved hypothet
866	71	4.5	343	2	S75435	hypothetical prote
867	71	4.5	349	2	T05857	hypothetical prote
868	71	4.5	370	2	S49008	fork head protein
869	71	4.5	378	2	S00842	leukosialin precur
870	71	4.5	379	1	S71571	alcohol dehydrogen
871	71	4.5	394	2	T21752	hypothetical prote
872	71	4.5	410	1	S68153	cellulase (EC 3.2.
873	71	4.5	415	2	A35560	lysosomal membrane
874	71	4.5	416	2	T20448	hypothetical prote
875	71	4.5	455	2	A87913	protein B0205.10 [
876	71	4.5	462	2	T32751	hypothetical prote
877	71	4.5	474	1	TVRTC4	Ca2+/calmodulin-de
878	71	4.5	476	2	B44997	merozoite surface
879	71	4.5	496	2	T30976	hypothetical prote
880	71	4.5	502	2	I52637	Ca2+/calmodulin-de
881	71	4.5	530	2	S62439	hypothetical serin
882	71	4.5	534	2	G97703	hypothetical prote
883	71	4.5	622	2	T15467	hypothetical prote
884	71	4.5	626	1	NBHUIA	platelet glycoprot
885	71	4.5	665	1	VCMVVR	env polyprotein pr
886	71	4.5	669	2	T08827	hypothetical prote
887	71	4.5	670	2	T13739	probable hormone r
888	71	4.5	711	2	T48335	receptor like prot
889	71	4.5	719	2	T27977	lin-15A protein -
890	71	4.5	738	2	I40719	isocitrate dehydro
891	71	4.5	751	2	T21967	hypothetical prote
892	71	4.5	767	1	JU0474	glucan 1,4-alpha-g
893	71	4.5	778	1	ALBYG	glucan 1,4-alpha-g
894	71	4.5	784	2	AH2560	hypothetical prote
895	71	4.5	791	2	T39924	hypothetical prote
896	71	4.5	880	2	D89756	protein T23E7.2b [
897	71	4.5	968	2	T00353	hypothetical prote
898	71	4.5	977	2	H84469	hypothetical prote
899	71	4.5	982	2	T19171	hypothetical prote
900	71	4.5	1032	2	T18293	guanylate kinase-i
901	71	4.5	1164	2	B71429	phytochrome D - Ar
902	71	4.5	1200	1	SNPSO	ice nucleation pro
903	71	4.5	1244	2	T19615	hypothetical prote
904	71	4.5	1256	2	G97902	alpha-amylase (EC
905	71	4.5	1302	2	T23236	hypothetical prote
906	71	4.5	1326	2	H89134	protein F25G6.9 [i
907	71	4.5	1367	2	T33819	hypothetical prote
908	71	4.5	1533	2	T00344	hypothetical prote
909	71	4.5	1583	2	S59644	sister chromatid c
910	71	4.5	1751	2	A45604	major blood-stage
911	71	4.5	1819	2	T32008	hypothetical prote
912	71	4.5	1842	2	T43409	probable fatty-aci
913	71	4.5	1842	2	T38781	fatty acid synthas
914	71	4.5	2035	2	A40718	host cell factor C
915	71	4.5	2090	2	S26058	probable transform
916	71	4.5	2848	2	T32550	hypothetical prote
917	71	4.5	2957	2	T33152	hypothetical prote
918	71	4.5	5035	1	I46646	ryanodine receptor
919	70.5	4.5	118	2	S49913	cryptogein - Phyto
920	70.5	4.5	128	2	A35690	mucin 3 (clone SIB
921	70.5	4.5	146	1	ERAD32	early E3 16K glyco
922	70.5	4.5	172	2	F49247	merozoite surface
923	70.5	4.5	174	2	E49247	merozoite surface
924	70.5	4.5	193	2	G90125	hypothetical prote
925	70.5	4.5	204	2	S67295	probable membrane
926	70.5	4.5	209	2	C89850	conserved hypothet
927	70.5	4.5	211	2	C71482	probable endonucle
928	70.5	4.5	212	2	F86545	hypothetical prote
929	70.5	4.5	212	2	F72077	hypothetical prote
930	70.5	4.5	236	2	PC4396	mucin 3 T9 - human
931	70.5	4.5	255	2	I46606	MHC SLA-DQ alpha c
932	70.5	4.5	264	2	T09377	hypothetical prote
933	70.5	4.5	275	2	T21933	hypothetical prote
934	70.5	4.5	284	2	T28018	hypothetical prote
935	70.5	4.5	288	2	T41112	hypothetical prote
936	70.5	4.5	308	2	T29756	hypothetical prote
937	70.5	4.5	312	2	T25994	hypothetical prote
938	70.5	4.5	314	2	B97905	dihydropteroate sy
939	70.5	4.5	316	1	A43661	dihydropteroate sy
940	70.5	4.5	321	2	T19259	hypothetical prote
941	70.5	4.5	330	2	S28102	rlx protein - Stap
942	70.5	4.5	350	2	AI0139	UTP-hexose-1-phosp
943	70.5	4.5	380	1	D34285	ubiquinol-cytochro
944	70.5	4.5	382	2	A28067	lysosomal membrane
945	70.5	4.5	385	2	F70591	probable kefB prot
946	70.5	4.5	393	2	S62335	I71-7 protein - fr
947	70.5	4.5	402	2	E86185	hypothetical prote
948	70.5	4.5	403	1	S35541	transcription fact
949	70.5	4.5	427	2	C88883	protein JC8.10 [im
950	70.5	4.5	431	1	JC2002	transcription fact
951	70.5	4.5	433	2	S37790	probable serine/th
952	70.5	4.5	445	2	T23199	hypothetical prote
953	70.5	4.5	462	2	A48933	gamma-aminobutyric
954	70.5	4.5	465	2	H82345	mannose-1-phosphat
955	70.5	4.5	522	2	S41819	nucleoporin p62 -
956	70.5	4.5	526	2	A34896	adenylate cyclase-
957	70.5	4.5	526	2	C84552	hypothetical prote
958	70.5	4.5	562	2	A85042	hypothetical prote
959	70.5	4.5	608	2	A46312	gag polyprotein -
960	70.5	4.5	616	2	T29234	hypothetical prote
961	70.5	4.5	629	2	AE1525	probable peptidogl
962	70.5	4.5	649	2	T24505	hypothetical prote
963	70.5	4.5	716	2	T26998	hypothetical prote
964	70.5	4.5	814	2	F59430	GTPase regulator a
965	70.5	4.5	846	2	T38840	hypothetical trp-a
966	70.5	4.5	874	2	B86322	F6A14.8 protein -
967	70.5	4.5	893	2	T18271	hypothetical prote
968	70.5	4.5	899	2	C84765	hypothetical prote
969	70.5	4.5	910	1	S73361	dnaJ homolog prote
970	70.5	4.5	979	2	A35913	regulatory factor
971	70.5	4.5	999	1	IJHUG3	desmoglein 3 precu
972	70.5	4.5	1015	2	JC6552	DNA topoisomerase
973	70.5	4.5	1028	2	E85089	probable transposo
974	70.5	4.5	1032	2	G89427	protein T08D2.3 [i
975	70.5	4.5	1052	2	C64221	hypothetical 114K
976	70.5	4.5	1106	2	T31742	hypothetical prote
977	70.5	4.5	1115	2	A47541	protein kinase IRE
978	70.5	4.5	1123	2	T18270	hypothetical prote

979	70.5	4.5	1131	2	T15787	hypothetical prote
980	70.5	4.5	1204	2	C75015	probable pyrolysin
981	70.5	4.5	1221	2	AI0193	ribonuclease E (EC
982	70.5	4.5	1520	2	T44231	hypothetical prote
983	70.5	4.5	1603	2	S17983	gene posterior sex
984	70.5	4.5	1742	2	T17120	cellulase (EC 3.2.
985	70.5	4.5	1872	2	T00339	hypothetical prote
986	70.5	4.5	2717	2	A34203	DNA-binding protei
987	70.5	4.5	3054	1	GNBVEV	genome polyprotein
988	70	4.4	147	2	JC7938	type II antifreeze
989	70	4.4	148	2	T32622	hypothetical prote
990	70	4.4	150	2	T52587	probable arabinoga
991	70	4.4	150	2	T48611	agp6 protein - Ara
992	70	4.4	209	2	AB2218	hypothetical prote
993	70	4.4	210	2	JC7830	cytokine-inducible
994	70	4.4	214	2	A46629	mucin 6, gastric (
995	70	4.4	221	2	T47592	hypothetical prote
996	70	4.4	234	2	G64858	probable membrane
997	70	4.4	239	2	B83709	hypothetical prote
998	70	4.4	298	2	C55223	minor tail protein
999	70	4.4	310	2	T26267	hypothetical prote
1000	70	4.4	311	2	H96002	probable sugar kin
1001	70	4.4	321	2	T42750	hypothetical prote
1002	70	4.4	329	2	S38082	pathogenesis-relat
1003	70	4.4	333	2	G98297	ribose ABC transpo
1004	70	4.4	333	2	AH2985	ABC transporter, m
1005	70	4.4	340	2	C90894	probable LACI-type
1006	70	4.4	340	2	F85723	probable LACI-type
1007	70	4.4	340	2	G64905	sugar-binding prot
1008	70	4.4	350	2	S22456	hydroxyproline-ric
1009	70	4.4	350	2	AH3043	dehydrogenase Atu3
1010	70	4.4	350	2	D98242	lipopolysaccharide
1011	70	4.4	355	2	B26883	neural cell adhesi
1012	70	4.4	357	2	E72245	hydrolase, ama/hip
1013	70	4.4	358	2	A88082	protein T05A8.7 [i
1014	70	4.4	360	2	T33835	hypothetical prote
1015	70	4.4	360	2	T08673	hypothetical prote
1016	70	4.4	409	2	T18726	hypothetical prote
1017	70	4.4	424	2	I51210	synaptotagmin p65
1018	70	4.4	425	2	T18723	hypothetical prote
1019	70	4.4	426	2	T04985	probable transamin
1020	70	4.4	433	2	S19996	hypothetical prote
1021	70	4.4	445	2	S45713	potassium channel
1022	70	4.4	446	2	S66268	inward rectifier p
1023	70	4.4	456	2	T38221	hypothetical serin
1024	70	4.4	458	2	T26630	hypothetical prote
1025	70	4.4	461	2	T38698	noc1 protein - fis
1026	70	4.4	462	2	T19830	hypothetical prote
1027	70	4.4	487	2	AI1505	hypothetical cell
1028	70	4.4	497	2	T51195	hypothetical prote
1029	70	4.4	529	2	S18453	variant surface gl
1030	70	4.4	542	2	B47022	chitinase (EC 3.2.
1031	70	4.4	589	2	AI0684	hypothetical prote
1032	70	4.4	599	2	G71481	probable phosphoen
1033	70	4.4	611	2	T22456	hypothetical prote
1034	70	4.4	613	2	B90294	hypothetical prote
1035	70	4.4	617	2	T15408	hypothetical prote
1036	70	4.4	622	2	AC1236	acyltransferase (t
1037	70	4.4	625	2	S34035	hypothetical prote
1038	70	4.4	651	2	S18874	nucleolin - Africa
1039	70	4.4	653	2	E86787	hypothetical prote
1040	70	4.4	662	2	T50464	glucose-regulated
1041	70	4.4	697	2	E96752	hypothetical prote
1042	70	4.4	706	2	S33761	transferrin precur
1043	70	4.4	714	2	T22454	hypothetical prote
1044	70	4.4	753	2	T24869	hypothetical prote
1045	70	4.4	768	2	E86417	unknown protein, 5
1046	70	4.4	770	2	T51024	related to C2H2 zi
1047	70	4.4	822	2	T51049	related to nucleol
1048	70	4.4	823	2	F90914	hypothetical prote
1049	70	4.4	835	2	JC6140	cell surface-assoc
1050	70	4.4	937	2	A56517	nucleoporin Nup98
1051	70	4.4	949	2	S19808	glutamate receptor
1052	70	4.4	971	2	T19431	hypothetical prote
1053	70	4.4	971	2	F88448	protein C45G9.10 [
1054	70	4.4	1004	2	A55142	myosin-light-chain
1055	70	4.4	1186	2	T19050	hypothetical prote
1056	70	4.4	1213	2	A41724	limb deformity (ld
1057	70	4.4	1274	2	JN0015	trp protein - frui
1058	70	4.4	1275	2	JU0092	trp protein - frui
1059	70	4.4	1415	2	T08945	hypothetical prote
1060	70	4.4	1420	1	A44361	amiloride-sensitiv
1061	70	4.4	1589	2	C44766	defective chorion-
1062	70	4.4	1868	2	S48938	hypothetical prote
1063	70	4.4	2440	2	S39162	transcription coac
1064	70	4.4	3163	1	JQ1895	genome polyprotein
1065	69.5	4.4	120	1	W4WL42	E4 protein - human
1066	69.5	4.4	124	2	E84613	hypothetical prote
1067	69.5	4.4	146	2	S52810	hypothetical prote
1068	69.5	4.4	202	2	AB2378	hypothetical prote
1069	69.5	4.4	217	2	S01358	salivary glue prot
1070	69.5	4.4	219	2	B72291	hypothetical prote
1071	69.5	4.4	266	2	H55590	hypothetical prote
1072	69.5	4.4	271	2	B96773	hypothetical prote
1073	69.5	4.4	299	2	G70784	probable mmpS3 pro
1074	69.5	4.4	313	2	H36854	hemagglutinin - va
1075	69.5	4.4	316	2	S58719	probable membrane
1076	69.5	4.4	326	2	I48351	fos-related antige
1077	69.5	4.4	338	2	S28004	probable cell surf
1078	69.5	4.4	364	2	T32589	hypothetical prote
1079	69.5	4.4	372	1	QQBE88	glycoprotein I pre
1080	69.5	4.4	400	2	T32705	hypothetical prote
1081	69.5	4.4	417	2	AD0200	isocitrate dehydro
1082	69.5	4.4	423	2	T24383	hypothetical prote
1083	69.5	4.4	425	1	FOMVGC	gag polyprotein -
1084	69.5	4.4	425	2	T24111	hypothetical prote
1085	69.5	4.4	427	2	T38526	ubiquitin regulato
1086	69.5	4.4	441	2	C75076	heme biosynthesis
1087	69.5	4.4	450	2	C90608	hypothetical prote
1088	69.5	4.4	458	2	F86433	protein T17H7.5 [i
1089	69.5	4.4	514	2	A44100	cell adhesion mole
1090	69.5	4.4	514	2	A31643	cell adhesion 80K
1091	69.5	4.4	519	2	S69989	unspecific monooxy
1092	69.5	4.4	520	2	S14600	E2 glycoprotein pr
1093	69.5	4.4	538	2	AG2902	conserved hypothet
1094	69.5	4.4	550	2	H97677	hypothetical prote
1095	69.5	4.4	551	2	G95176	conserved hypothet
1096	69.5	4.4	552	2	T25593	hypothetical prote
1097	69.5	4.4	568	2	A34891	Ig heavy chain pre
1098	69.5	4.4	593	2	S55189	hypothetical prote
1099	69.5	4.4	610	2	S59394	protein kinase RCK
1100	69.5	4.4	611	2	A54086	calnexin-t - mouse
1101	69.5	4.4	629	2	S20516	dnaK-type molecula
1102	69.5	4.4	640	2	T25367	hypothetical prote
1103	69.5	4.4	645	2	S41372	dnaK-type molecula
1104	69.5	4.4	646	2	T19206	hypothetical prote
1105	69.5	4.4	658	2	JC8011	G protein-coupled
1106	69.5	4.4	675	2	T03744	myoD protein inhib
1107	69.5	4.4	736	2	T19366	hypothetical prote
1108	69.5	4.4	782	2	A82940	hypothetical prote
1109	69.5	4.4	833	2	AF2089	hypothetical prote
1110	69.5	4.4	844	2	B64678	NADH2 dehydrogenas
1111	69.5	4.4	850	1	MMHUE4	erythrocyte membra
1112	69.5	4.4	852	2	T46091	hypothetical prote
1113	69.5	4.4	862	2	T46289	hypothetical prote
1114	69.5	4.4	871	2	S47518	cadherin - African
1115	69.5	4.4	942	2	T19553	hypothetical prote
1116	69.5	4.4	993	2	AE1905	outer membrane sec
1117	69.5	4.4	1051	2	JC4091	glycoprotein A - P
1118	69.5	4.4	1087	1	QFMSH	neurofilament trip
1119	69.5	4.4	1132	2	T43483	translation initia
1120	69.5	4.4	1460	2	S48457	nucleoporin RAT7 -
1121	69.5	4.4	1502	2	S45429	probable membrane
1122	69.5	4.4	1522	2	S48904	probable purine nu
1123	69.5	4.4	1870	2	D88486	protein F20H11.2 [
1124	69.5	4.4	1875	2	S38173	myosin-like protei

1125	69.5	4.4	1957	2	A45627	myosin heavy chain
1126	69.5	4.4	2271	2	F90073	hypothetical prote
1127	69.5	4.4	2894	2	C64474	hypothetical prote
1128	69.5	4.4	4199	2	S76412	hypothetical prote
1129	69	4.4	171	2	T31478	hypothetical prote
1130	69	4.4	234	2	T35448	hypothetical prote
1131	69	4.4	255	2	T22429	hypothetical prote
1132	69	4.4	258	2	S23106	priA protein - shi
1133	69	4.4	284	2	T06241	histone H1 (clone
1134	69	4.4	299	2	S44554	citrate transport
1135	69	4.4	303	2	S29185	sodium channel pro
1136	69	4.4	338	2	F69437	hypothetical prote
1137	69	4.4	339	2	S08981	malate dehydrogena
1138	69	4.4	344	1	RWRTC2	T-cell surface gly
1139	69	4.4	344	2	T13975	NADH2 dehydrogenas
1140	69	4.4	356	2	S73315	protoporphyrin IX
1141	69	4.4	382	2	S71669	finger protein MIG
1142	69	4.4	396	2	T26987	hypothetical prote
1143	69	4.4	400	1	A39822	leukosialin precur
1144	69	4.4	416	2	T34279	hypothetical prote
1145	69	4.4	423	2	T44258	transducer protein
1146	69	4.4	431	2	G86277	F14L17.11 protein
1147	69	4.4	443	2	T14916	mitosis-specific c
1148	69	4.4	467	2	T26195	hypothetical prote
1149	69	4.4	482	2	T48397	S-receptor kinase-
1150	69	4.4	483	2	G86902	dextransucrase (EC
1151	69	4.4	486	2	D64474	hypothetical prote
1152	69	4.4	490	1	C57150	NADP-reducing hydr
1153	69	4.4	495	2	T38959	hypothetical prote
1154	69	4.4	511	2	I50114	early growth respo
1155	69	4.4	513	2	S50915	SIN3 protein-bindi
1156	69	4.4	525	2	A35596	nuclear pore glyco
1157	69	4.4	555	2	B41492	58K antigen - Rick
1158	69	4.4	556	2	S06838	gamma-aminobutyric
1159	69	4.4	556	2	S51892	probable membrane
1160	69	4.4	583	2	T18999	hypothetical prote
1161	69	4.4	609	2	S62518	hypothetical prote
1162	69	4.4	610	1	I46001	C4b-binding protei
1163	69	4.4	611	2	A53418	calmegin precursor
1164	69	4.4	647	2	B34457	204 protein - mous
1165	69	4.4	650	2	S22835	alpha-agglutinin -
1166	69	4.4	651	2	T21175	hypothetical prote
1167	69	4.4	652	2	S50210	surface layer prot
1168	69	4.4	658	2	T41309	hypothetical threo
1169	69	4.4	670	2	F84540	hypothetical prote
1170	69	4.4	677	2	S54561	RNA14 protein - ye
1171	69	4.4	739	2	H72364	aspartokinase II -
1172	69	4.4	790	2	T34293	hypothetical prote
1173	69	4.4	793	1	KXRTF	furin (EC 3.4.21.7
1174	69	4.4	814	2	T49207	receptor kinase-li
1175	69	4.4	825	2	S26706	transcription fact
1176	69	4.4	836	2	T21631	hypothetical prote
1177	69	4.4	854	1	QRHYLD	LDL receptor precu
1178	69	4.4	871	2	T28706	hypothetical prote
1179	69	4.4	879	1	QRRTLD	LDL receptor precu
1180	69	4.4	903	1	VGBEK1	glycoprotein B pre
1181	69	4.4	942	2	S53963	MCS1 protein - yea
1182	69	4.4	988	2	A40628	probable transposa
1183	69	4.4	995	2	T27327	hypothetical prote
1184	69	4.4	1007	2	JC8066	138K protein - Tet
1185	69	4.4	1203	2	T04294	hypothetical prote
1186	69	4.4	1215	2	S60904	hypothetical prote
1187	69	4.4	1360	2	T34302	cell polarity prot
1188	69	4.4	1385	2	T13415	hypothetical prote
1189	69	4.4	1455	1	A48925	mannose receptor p
1190	69	4.4	1624	2	T25592	hypothetical prote
1191	69	4.4	1633	2	T01879	hypothetical prote
1192	69	4.4	1680	2	T41628	probable transcrip
1193	69	4.4	1758	2	S57015	probable purine nu
1194	69	4.4	1804	2	H96597	hypothetical prote
1195	69	4.4	1819	2	D97033	uncharacterized pr
1196	69	4.4	1963	1	MWKW	myosin heavy chain
1197	69	4.4	2067	2	A42854	probable spindle p
1198	69	4.4	2329	2	S44625	C50C3.6 protein -
1199	69	4.4	2361	2	T25752	hypothetical prote
1200	69	4.4	2464	1	QRMSP1	microtubule-associ
1201	69	4.4	3122	2	T17202	DNA-directed DNA p
1202	68.5	4.3	168	2	S52994	arabinogalactan-li
1203	68.5	4.3	189	1	ERAD75	early E3 20.6K gly
1204	68.5	4.3	189	2	JX0235	core protein MGC-2
1205	68.5	4.3	204	2	S51232	gibberellin-respon
1206	68.5	4.3	218	2	AH1837	hypothetical prote
1207	68.5	4.3	246	2	S47805	hypothetical 27.4K
1208	68.5	4.3	246	2	D91186	probable outer mem
1209	68.5	4.3	246	2	C86033	probable outer mem
1210	68.5	4.3	257	2	C84890	hypothetical prote
1211	68.5	4.3	261	2	D84262	hypothetical prote
1212	68.5	4.3	280	2	AE2031	gamma-tocopherol m
1213	68.5	4.3	287	2	S45662	histone H1 - tomat
1214	68.5	4.3	288	2	T22846	hypothetical prote
1215	68.5	4.3	318	2	T20063	hypothetical prote
1216	68.5	4.3	349	2	T42965	glycoprotein - ate
1217	68.5	4.3	359	2	G70814	probable far prote
1218	68.5	4.3	378	2	T35403	probable polypreny
1219	68.5	4.3	385	2	H97239	polyferredoxin [im
1220	68.5	4.3	385	2	JC7783	RAD 23B protein -
1221	68.5	4.3	394	2	G84206	hypothetical prote
1222	68.5	4.3	412	1	AJMSRS	argininosuccinate
1223	68.5	4.3	412	1	AJRTRS	argininosuccinate
1224	68.5	4.3	413	2	T04520	hypothetical prote
1225	68.5	4.3	414	2	G64091	cell division prot
1226	68.5	4.3	420	2	A88962	protein F59A7.1 [i
1227	68.5	4.3	421	2	S09595	synaptotagmin P65
1228	68.5	4.3	426	2	A35641	5-aminoimidazole r
1229	68.5	4.3	435	2	C86340	protein F2D10.28 [
1230	68.5	4.3	435	2	T25350	hypothetical prote
1231	68.5	4.3	443	2	F71929	heat shock protein
1232	68.5	4.3	458	2	AC0121	probable exported
1233	68.5	4.3	498	1	VGXPLA	surface glycoprote
1234	68.5	4.3	500	1	S60929	probable aldehyde
1235	68.5	4.3	509	2	T48459	cytochrome P450-li
1236	68.5	4.3	514	1	A47692	fumarate hydratase
1237	68.5	4.3	527	2	T26732	hypothetical prote
1238	68.5	4.3	535	2	B84443	hypothetical prote
1239	68.5	4.3	536	2	AG1482	hypothetical prote
1240	68.5	4.3	553	2	A49364	59 protein, brain
1241	68.5	4.3	573	2	H96744	probable cytosolic
1242	68.5	4.3	588	2	JC8021	chitinase (EC 3.2.
1243	68.5	4.3	592	2	T32402	hypothetical prote
1244	68.5	4.3	594	2	S51412	hypothetical prote
1245	68.5	4.3	630	2	A39344	tumor-associated m
1246	68.5	4.3	637	2	T20981	hypothetical prote
1247	68.5	4.3	647	2	S26386	transcription fact
1248	68.5	4.3	659	2	T40383	hypothetical prote
1249	68.5	4.3	670	2	S22293	zinc finger protei
1250	68.5	4.3	696	2	G71829	probable outer mem
1251	68.5	4.3	697	2	A86402	protein T22C5.17 [
1252	68.5	4.3	699	2	T09483	Cys-rich protein R
1253	68.5	4.3	721	2	E70766	hypothetical prote
1254	68.5	4.3	725	2	T01268	leucine-rich repea
1255	68.5	4.3	737	2	AG2156	hypothetical prote
1256	68.5	4.3	751	2	AC2098	hypothetical prote
1257	68.5	4.3	763	2	S55616	glycoprotein H - e
1258	68.5	4.3	770	2	G88445	protein C26E6.2 [i
1259	68.5	4.3	795	2	T20609	hypothetical prote
1260	68.5	4.3	798	2	T50514	hypothetical prote
1261	68.5	4.3	825	1	GLHQ	beta-glucosidase (
1262	68.5	4.3	839	2	I50590	class I INCENP pro
1263	68.5	4.3	846	2	S52418	GTP-binding regula
1264	68.5	4.3	865	2	AC1966	hypothetical prote
1265	68.5	4.3	877	2	I50591	class II INCENP pr
1266	68.5	4.3	914	2	T25220	hypothetical prote
1267	68.5	4.3	952	2	T18837	hypothetical prote
1268	68.5	4.3	1043	2	T13172	gag-like protein p
1269	68.5	4.3	1278	2	A71609	probable secreted
1270	68.5	4.3	1285	2	H85041	hypothetical prote

1271	68.5	4.3	1311	2	A56390	mannosyl-glycoprot
1272	68.5	4.3	1435	2	S69632	regulatory protein
1273	68.5	4.3	1438	2	A48216	neurexin III-alpha
1274	68.5	4.3	1444	1	A30588	140K adhesin precu
1275	68.5	4.3	1541	2	S46686	hypothetical prote
1276	68.5	4.3	1791	2	T24089	hypothetical prote
1277	68.5	4.3	2114	2	E96505	hypothetical prote
1278	68.5	4.3	2292	1	GNNYEB	genome polyprotein
1279	68.5	4.3	2292	1	GNNYED	genome polyprotein
1280	68.5	4.3	2292	2	S55401	capsid polyprotein
1281	68	4.3	62	2	S53366	mucin 5AC (clone M
1282	68	4.3	208	1	HSRT1T	histone H1t - rat
1283	68	4.3	211	2	H72608	hypothetical prote
1284	68	4.3	228	2	T33579	hypothetical prote
1285	68	4.3	245	2	D81977	hypothetical prote
1286	68	4.3	246	2	H90833	major tail protein
1287	68	4.3	256	2	B85691	probable tail comp
1288	68	4.3	268	2	T32740	hypothetical prote
1289	68	4.3	288	2	T21790	hypothetical prote
1290	68	4.3	295	2	S50316	CIN5 protein - yea
1291	68	4.3	301	2	H70644	hypothetical prote
1292	68	4.3	333	2	T15367	hypothetical prote
1293	68	4.3	339	2	AH0050	probable periplasm
1294	68	4.3	360	2	S69063	probable membrane
1295	68	4.3	372	2	T45628	glycerophosphodies
1296	68	4.3	378	2	S61992	SLG1 protein - yea
1297	68	4.3	380	1	S51826	alcohol dehydrogen
1298	68	4.3	384	2	H64161	hypothetical prote
1299	68	4.3	387	2	A56275	1,3-propanediol de
1300	68	4.3	388	2	T43019	probable DNA-bindi
1301	68	4.3	402	2	T20595	hypothetical prote
1302	68	4.3	416	2	T19149	hypothetical prote
1303	68	4.3	420	2	T42616	envelope protein -
1304	68	4.3	422	1	BMHU1Y	synaptotagmin I -
1305	68	4.3	423	2	T14531	S-locus-specific g
1306	68	4.3	423	2	H84257	Htr13 transducer [
1307	68	4.3	426	2	I48379	gene hb protein -
1308	68	4.3	427	2	JH0413	synaptotagmin o-p6
1309	68	4.3	452	2	T46147	zinc finger protei
1310	68	4.3	479	2	A84588	probable tyrosine
1311	68	4.3	487	1	S07061	glutamate receptor
1312	68	4.3	500	2	AI1913	apolipoprotein N-a
1313	68	4.3	502	2	T21935	hypothetical prote
1314	68	4.3	503	2	T51782	hypothetical prote
1315	68	4.3	515	2	B84406	TRK potassium upta
1316	68	4.3	516	2	A31270	radial spoke prote
1317	68	4.3	537	1	FOMVM7	gag polyprotein -
1318	68	4.3	543	2	A38093	transformation-sen
1319	68	4.3	550	2	T06379	SAR DNA-binding pr
1320	68	4.3	573	2	S50661	hypothetical prote
1321	68	4.3	576	2	S75958	hypothetical prote
1322	68	4.3	581	2	T22455	hypothetical prote
1323	68	4.3	590	2	S66956	hypothetical prote
1324	68	4.3	599	1	A54906	afamin precursor -
1325	68	4.3	600	2	S56744	mucin (clone pGM7-
1326	68	4.3	610	2	T22909	hypothetical prote
1327	68	4.3	621	1	YRNC	monophenol monooxy
1328	68	4.3	630	2	S77346	hypothetical prote
1329	68	4.3	632	2	T48616	hypothetical prote
1330	68	4.3	638	2	S36723	FUN36 protein - ye
1331	68	4.3	645	2	T16078	hypothetical prote
1332	68	4.3	647	2	T39141	hypothetical prote
1333	68	4.3	648	2	T04837	probable serine/th
1334	68	4.3	655	1	A55726	RNA-binding protei
1335	68	4.3	659	2	H81431	methyl-accepting c
1336	68	4.3	659	2	A98085	hypothetical prote
1337	68	4.3	662	2	B81251	probable methyl-ac
1338	68	4.3	665	2	E81444	probable methyl-ac
1339	68	4.3	668	2	B86831	hypothetical prote
1340	68	4.3	669	2	B70186	translation elonga
1341	68	4.3	686	2	S66693	hypothetical prote
1342	68	4.3	695	2	I51652	dsRNA-binding prot
1343	68	4.3	709	2	S51793	dibasic processing
1344	68	4.3	730	2	A75486	hypothetical prote
1345	68	4.3	733	2	T01875	probable long-chai
1346	68	4.3	752	2	T34355	hypothetical prote
1347	68	4.3	761	2	T03719	probable thyroid r
1348	68	4.3	775	1	WMBE19	ribonucleoside-dip
1349	68	4.3	784	2	C82679	cell division prot
1350	68	4.3	785	2	S54016	SOK2 protein - yea
1351	68	4.3	793	2	S65240	probable membrane
1352	68	4.3	809	2	T18970	hypothetical prote
1353	68	4.3	817	2	T21336	hypothetical prote
1354	68	4.3	833	2	G75621	arylesterase/monox
1355	68	4.3	859	2	S66827	aluminium resistan
1356	68	4.3	899	1	GNMVMM	pol polyprotein -
1357	68	4.3	903	2	T00074	hypothetical prote
1358	68	4.3	923	2	A86334	T20H2.17 protein -
1359	68	4.3	971	2	T10678	hypothetical prote
1360	68	4.3	974	2	S34189	starch phosphoryla
1361	68	4.3	991	2	S43891	dna exoribonucleas
1362	68	4.3	1010	2	T16616	hypothetical prote
1363	68	4.3	1018	2	T18249	conserved hypothet
1364	68	4.3	1052	2	T14343	zinc finger RNA bi
1365	68	4.3	1072	2	A37127	microtubule-associ
1366	68	4.3	1117	2	S63399	probable membrane
1367	68	4.3	1173	2	S48877	Ca2+-transporting
1368	68	4.3	1196	2	S35994	DNA repair protein
1369	68	4.3	1203	2	T51029	related to pathway
1370	68	4.3	1204	2	F81158	exodeoxyribonuclea
1371	68	4.3	1230	2	T22458	hypothetical prote
1372	68	4.3	1275	2	T33369	hypothetical prote
1373	68	4.3	1279	2	T13613	hypothetical prote
1374	68	4.3	1280	2	T00365	hypothetical prote
1375	68	4.3	1338	2	T40993	protein kinase cek
1376	68	4.3	1371	2	T29019	hypothetical prote
1377	68	4.3	1541	2	A37023	IgA-specific metal
1378	68	4.3	1545	2	B41859	IgA-specific metal
1379	68	4.3	1578	2	I48216	neurexin III-alpha
1380	68	4.3	1711	2	T31337	1,4-beta-glucanase
1381	68	4.3	1772	2	A45532	major merozoite su
1382	68	4.3	1968	1	S05697	myosin heavy chain
1383	68	4.3	2228	2	T14029	variant-specific s
1384	68	4.3	2810	2	T22298	hypothetical prote
1385	68	4.3	3191	2	T22945	hypothetical prote
1386	68	4.3	3712	2	S18253	laminin alpha-1 ch
1387	67.5	4.3	127	2	T30102	hypothetical prote
1388	67.5	4.3	137	2	F95239	conserved domain p
1389	67.5	4.3	137	2	H98103	hypothetical prote
1390	67.5	4.3	159	2	T31598	hypothetical prote
1391	67.5	4.3	180	2	T31974	hypothetical prote
1392	67.5	4.3	191	2	S38117	hypothetical prote
1393	67.5	4.3	210	2	B88082	protein T05A8.6 [i
1394	67.5	4.3	232	1	WMADC2	early E1A 25K prot
1395	67.5	4.3	235	2	T02598	probable replicati
1396	67.5	4.3	238	2	T07921	probable starch sy
1397	67.5	4.3	240	2	H69932	hypothetical prote
1398	67.5	4.3	248	2	PQ0769	glycoprotein G - b
1399	67.5	4.3	252	2	AG1423	hypothetical prote
1400	67.5	4.3	256	2	H36857	B26R protein - var
1401	67.5	4.3	297	2	S55063	conserved hypothet
1402	67.5	4.3	311	2	T40921	hypothetical prote
1403	67.5	4.3	326	2	S15749	transforming prote
1404	67.5	4.3	327	2	D90530	hypothetical prote
1405	67.5	4.3	345	2	E88103	protein W10G11.5 [
1406	67.5	4.3	346	2	T46916	hypothetical prote
1407	67.5	4.3	348	2	T40623	probable polyA-bin
1408	67.5	4.3	355	2	T15526	hypothetical prote
1409	67.5	4.3	358	2	T01296	leucine-rich repea
1410	67.5	4.3	369	2	AG1950	hypothetical prote
1411	67.5	4.3	383	2	E96972	riboflavin biosynt
1412	67.5	4.3	387	2	T15462	hypothetical prote
1413	67.5	4.3	391	2	A44063	paired box transcr
1414	67.5	4.3	399	2	T42242	hypothetical 44.2K
1415	67.5	4.3	410	2	C84638	probable WRKY-type
1416	67.5	4.3	426	2	AI1920	ABC transporter AT

1417	67.5	4.3	467	2	B86225	protein T12M4.6 [i
1418	67.5	4.3	476	2	T32032	hypothetical prote
1419	67.5	4.3	476	2	T27051	hypothetical prote
1420	67.5	4.3	482	2	AI2094	hypothetical prote
1421	67.5	4.3	487	2	T49424	hypothetical prote
1422	67.5	4.3	493	2	A34130	gamma-aminobutyric
1423	67.5	4.3	506	2	S47439	I2 protein - Trypa
1424	67.5	4.3	527	2	T28878	hypothetical prote
1425	67.5	4.3	530	2	T32812	hypothetical prote
1426	67.5	4.3	532	2	G70986	probable coA ligas
1427	67.5	4.3	532	2	T49467	related to COP1-in
1428	67.5	4.3	538	2	S65764	chitinase (EC 3.2.
1429	67.5	4.3	540	2	T00646	hypothetical prote
1430	67.5	4.3	577	2	S20876	chaperonin hsp60 p
1431	67.5	4.3	582	2	H70426	neutral proteinase
1432	67.5	4.3	583	2	G84829	probable PTR2 fami
1433	67.5	4.3	593	2	T26865	hypothetical prote
1434	67.5	4.3	595	2	F85438	nucleoporin-like p
1435	67.5	4.3	601	2	S47896	probable molybdopt
1436	67.5	4.3	601	2	S56144	SH3 domain binding
1437	67.5	4.3	619	2	A43361	Ets-related transc
1438	67.5	4.3	631	2	JC6031	scaffoldin dockeri
1439	67.5	4.3	632	1	VGVNSY	surface glycoprote
1440	67.5	4.3	644	2	H75141	oligopeptide-bindi
1441	67.5	4.3	648	2	T43337	polo-like kinase-1
1442	67.5	4.3	656	1	A49358	RNA-binding protei
1443	67.5	4.3	670	2	T49510	fibroin-3 related
1444	67.5	4.3	686	2	F96542	probable protein k
1445	67.5	4.3	713	2	B75489	hypothetical prote
1446	67.5	4.3	714	1	S31502	NADPH-ferrihemopro
1447	67.5	4.3	715	2	D84480	Mutator-like trans
1448	67.5	4.3	733	1	HHMS86	heat shock protein
1449	67.5	4.3	749	2	T50397	probable serine/th
1450	67.5	4.3	792	2	S70305	hypothetical prote
1451	67.5	4.3	802	1	B44390	protein-tyrosine-p
1452	67.5	4.3	812	2	T48016	probable zinc-fing
1453	67.5	4.3	812	2	T03659	phospholipase D (E
1454	67.5	4.3	815	2	A64048	aspartate kinase (
1455	67.5	4.3	815	2	C84287	hypothetical prote
1456	67.5	4.3	826	2	G90283	hypothetical prote
1457	67.5	4.3	839	2	T41826	P95 orf83 - Bombyx
1458	67.5	4.3	872	2	JH0561	metabotropic gluta
1459	67.5	4.3	882	2	T23807	hypothetical prote
1460	67.5	4.3	886	2	S29605	glycoprotein 350/2
1461	67.5	4.3	912	2	T01769	hypothetical prote
1462	67.5	4.3	915	2	T16623	hypothetical prote
1463	67.5	4.3	928	1	VGBEBG	glycoprotein gI pr
1464	67.5	4.3	936	2	S43738	transcription acti
1465	67.5	4.3	955	2	F84914	hypothetical prote
1466	67.5	4.3	969	2	T15446	hypothetical prote
1467	67.5	4.3	973	2	B86547	polymorphic outer
1468	67.5	4.3	973	2	F72076	polymorphic outer
1469	67.5	4.3	984	2	A41996	NF-kappa-B p50 sub
1470	67.5	4.3	995	2	C81593	polymorphic membra
1471	67.5	4.3	1020	1	QFHUH	neurofilament trip
1472	67.5	4.3	1026	2	T34506	hypothetical prote
1473	67.5	4.3	1051	2	T51904	hypothetical prote
1474	67.5	4.3	1097	2	T13033	cyclin T - fruit f
1475	67.5	4.3	1106	2	T29496	hypothetical prote
1476	67.5	4.3	1120	2	H88449	protein F54D8.1 [i
1477	67.5	4.3	1219	2	H84464	probable helicase
1478	67.5	4.3	1257	2	T13957	period protein PER
1479	67.5	4.3	1282	2	JE0120	glycoprotein A - m
1480	67.5	4.3	1296	1	HMSO1F	aggregation protei
1481	67.5	4.3	1328	2	T43060	agrin - electric r
1482	67.5	4.3	1348	2	AH1115	cell surface prote
1483	67.5	4.3	1425	2	E89303	protein C47E8.8 [i
1484	67.5	4.3	1501	2	C84512	probable retroelem
1485	67.5	4.3	1675	2	T31473	hypothetical prote
1486	67.5	4.3	1784	2	T43167	sodium channel pro
1487	67.5	4.3	1784	2	T10532	gag-pol polyprotei
1488	67.5	4.3	1843	2	S18803	collagen alpha 1(V
1489	67.5	4.3	1896	2	B72175	D15R protein - var
1490	67.5	4.3	1897	2	T28621	hypothetical prote
1491	67.5	4.3	1975	2	B81192	hemagglutinin/hemo
1492	67.5	4.3	1995	2	G81044	hemagglutinin/hemo
1493	67.5	4.3	2044	2	AB1180	probable peptidogl
1494	67.5	4.3	2380	2	E71604	hypothetical prote
1495	67.5	4.3	2401	2	T28676	rhoptry protein -
1496	67.5	4.3	2453	2	S60254	nuclear receptor c
1497	67.5	4.3	2559	2	T09144	probable guanine n
1498	67.5	4.3	3005	2	S33642	homeotic protein z
1499	67.5	4.3	3345	2	T13423	hypothetical prote
1500	67.5	4.3	4385	2	T29042	hypothetical prote

ALIGNMENTS

RESULT 1
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CA
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <ZHO>
A;Cross-references: UNIPROT:P15379; UNIPARC:UPI000002A5F4; GB:M30655; NID:g200332; PIDN
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 14.5%; Score 229; DB 2; Length 363;
Best Local Similarity 24.9%; Pred. No. 6.4e-11;
Matches 87; Conservative 57; Mismatches 145; Indels 60; Gaps 13;

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Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              |:| ||  ::: : |:|| |:  | |     :: ||| : |:    :|   ||:: ||
Db         14 LLQLSLAHQQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMKLALS 73

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
               |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|     |
Db         74 KGFETCRYGFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCFNASAPPEEDC 132

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------------ 166
                 |:   : |:          |   :  | | ||    | |    | |
Db        133 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDDDVSSGSTI 187

Qy        167 --TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPPVENKAAFK-----NEAAGF 217
                :||      | :|  :      : |   ||::| : :   ::: : :      :| ||
Db        188 EKSTPEGYILHTYLPTEQPTGDQDDSFFIRSTLATRDRDSSKDSRGSSRTVTHGSELAGH 247

Qy        218 GG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQK 259
                                  :|  |::||| |    | | |  |    :          |:|
Db        248 SSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKK 301

Qy        260 EMI---ETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 305
              :::      |:: | :: |  | ||  :     :| ||:|  :|: |:
Db        302 KLVINGGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 349
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RESULT 2
A30901
lymphocyte adhesion receptor precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 21-Jul-2000
C;Accession: A33935; A30901
R;Idzerda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John,
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion rece
A;Reference number: A33935; MUID:89282830; PMID:2471974

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A;Accession: A33935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <IDZ>
A;Cross-references: UNIPARC:UPI000012736C; GB:M22452; NID:g176576; PID:g176577
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD44; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antig
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>
F;21-270/Domain: extracellular #status predicted <EXT>
F;271-290/Domain: transmembrane #status predicted <TMM>
F;291-362/Domain: intracellular #status predicted <CYT>
F;25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             14.1%;  Score 222.5;  DB 2;  Length 362;
  Best Local Similarity   25.5%;  Pred. No. 2.1e-10;
  Matches   92;  Conservative   43;  Mismatches  127;  Indels   99;  Gaps   16;

Qy           4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
               ||| ||   :: : ::||  ||  | |     :: ||| : |:    :|    |:| ||
Db          14 LVQLSL--AQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS 71

Qy          64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
                |||| ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db          72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPGEDC 129

Qy         124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP------APT---------- 166
                 |:   : |      |   :  | | |     | | |      :||
Db         130 -----TSVTDLPNAFDGPITITIVNRDGTRYVKKGEYRTNPEDINPSSPTDDDVSSGSSS 184

Qy         167 ----------------TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAF 210
                             |:|| |                  | ||:  |   :: ||
Db         185 ERSSTLGGYIFYNHFSTSPPIPDEDG---------------PWITDSTDRTPATRDQGAF 229

Qy         211 K----------NEAAGF------GG------------VPTALLVLALLFFGAAAGLGFCY 242
                       :|:||       ||            :|  |::|| |    |  |  |
Db         230 DPSGGSHTTHGSESAGHSHGSREGGANTTSGPLRTPQIPEWLIILASL-LALALILAVC- 287

Qy         243 VKRYVKAFPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----NPEESKSPS 295
                 :          |:|:::       |:: |::  |  | ||  :     | | |::|
Db         288 ----IAVNSRRRCGQKKKLVINNGNGAVEDRKSSGLN-GEASKSQEMVHLVNKESSETPD 342

Qy         296 K 296
               :
Db         343 Q 343


RESULT 3
A34424
CD44 membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
A;Reference number: A34424; MUID:90046829; PMID:2682651
A;Accession: A34424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <NOT>
A;Cross-references: UNIPARC:UPI00000E88CD; GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:
R;Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antige
A;Reference number: A34907; MUID:90094420; PMID:2403559
A;Accession: A34907
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 8-195,'G',197-365 <WOL>
A;Cross-references: UNIPARC:UPI000016CFB0; GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

  Query Match             14.1%;  Score 222;  DB 2;  Length 365;
  Best Local Similarity   24.0%;  Pred. No. 2.4e-10;
  Matches   82;  Conservative   55;  Mismatches  144;  Indels   60;  Gaps   12;

Qy          12 EELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSY 71
               ::: : |:||  |:  | |     :: ||| : |:    :|   ||:: ||   |||| |
Db          24 QQIDLNVTCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMKLALSKGFETCRY 83

Qy          72 GWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEIITTK 131
               |:: :| ||| || ||  |  | || |     :  :  ||:|:|      |     |:
Db          84 GFI-EGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTYCFNASAPPEEDC-----TSV 137

Qy         132 DPIFNTQTATQTTEFIVSDST-YSVASPYST---------------IPAPTTTPPAPAS- 174
                 : |:     |   :  | | ||    | |                      |     | |
Db         138 TDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDDDVSSGSTIEKSTPESY 197

Qy         175 ---TSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFK-----NEAAGFGG------ 219
                  | :|  :      : |   ||::| : :   ::: : :     :| ||
Db         198 ILHTYLPTEQPTGDQDDSFFIRSTLATRDRDSSKDSRGSSRTVTHGSELAGHSSANQDSG 257

Qy         220 ------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMI---ET 264
                         :|  |::|| |    |  |  |     :          |:|:::
Db         258 VTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKKKLVINGGN 311

Qy         265 KVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 305
                 |:: | :: |  | ||  :     :| ||:|  :|: |:
Db         312 GTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 351


RESULT 4
A35616
T-cell surface glycoprotein CD44 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A35616
R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A;Title: CD44 is the principal cell surface receptor for hyaluronate.
A;Reference number: A35616; MUID:90304889; PMID:1694723
A;Accession: A35616
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-362 <ARU>
A;Cross-references: UNIPROT:P20944; UNIPARC:UPI0000179518
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein

  Query Match             13.8%;  Score 217.5;  DB 2;  Length 362;
  Best Local Similarity   25.4%;  Pred. No. 5.4e-10;
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Qy           8 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFE 67
               ||  |:: : ::||  |:  | |     :: ||| : |:    :|   ||:  ||   ||
Db          18 SLAHEQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVMALSKGFE 77

Qy          68 TCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI 127
               || ||:: :| ||| || ||  |  |  || |     |  :  ||:|:|      |
Db          78 TCRYGFI-EGHVVIPRIQPNAICAANHTGVYILTSNTS-HYDTYCFNASAPLEEDC---- 131

Qy         128 ITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPTTTPPAPAS-------- 174
                :|:   : |:      |   :  | | ||    | |     | |  ||    :|
Db         132 -TSVTDLPNSFEGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNTTDDDVSSGSSSEKST 190

Qy         175 -------TSIPRRKKLICVTEVFMETSTMSTE--------------------TEPFVEN 206
                    | :|         : :   |||:|                        |     |
Db         191 SGGYVFHTYLPTIHSTADQDDPYFIGSTMATRDQDSSMDPRGNSLTVTDGSKLTGHSSGN 250

Qy         207 KAAFKNEAAGFG---GVPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 263
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                : :  |  :  |    :|  |:||| |    |  |  |     :         |:|:::
Db        251 QDSGANTTSRPGRKPQIPEWLIVLASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 304

Qy        264 TKVVKEEKANDSNPNEESKKTDKNPE----ESKSPSKTTVRCLEAE 305
                  |  |  |:| : :  |: |     :| ||:|  : : |:
Db        305 NS--GNGKVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQFMTAD 348


RESULT 5
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.; Matzku, S.
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinom
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: UNIPROT:P26051; UNIPARC:UPI000012736D; GB:M61874; NID:g576534; PIDN:
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: UNIPARC:UPI0000179A9B; GB:M61875
C;Keywords: cell adhesion

  Query Match             13.8%;  Score 217;  DB 2;  Length 503;
  Best Local Similarity   25.8%;  Pred. No. 9e-10;
  Matches   83;  Conservative   40;  Mismatches  161;  Indels   38;  Gaps   11;

Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
               |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|       |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------------ 166
                  |:   : |:      |   :  | | ||    | |     | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVSSGSTI 188

Qy        167 --TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFKNEAAGFGGV-- 220
                :||      | :|  :      : |   ||::|  | |:|        |   :  :
Db        189 EKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATIATTPWVSAHTKQNQERTQWNPIHS 248

Qy        221 -PTALLVLALLFFGAAAGLGFCYVKRYVK--AFPFTNKNQQKEMIETKVVKEEKANDSNP 277
               |  ||                : : : :    || |   | |  ||         | |
Db        249 NPEVLLQTTTRMTDIDRNSTSAHGENWTQEPQPPFNNHEYQDEE-ETPHATSTTWADPNS 307

Qy        278 NEESKKTDK-----NPEESKSP 294
                |   | |      |  : |:|
Db        308 TTEEAATQKEKWFENEWQGKNP 329


RESULT 6
A53286
cell-surface glycoprotein CD44 precursor - bovine
N;Alternate names: CD44 protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53286; S22123
R;Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A;Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A;Reference number: A53286; MUID:92017904; PMID:1922105
A;Accession: A53286
A;Molecule type: mRNA
A;Residues: 1-366 <BOS>
A;Cross-references: UNIPROT:Q29423; UNIPARC:UPI0000127366; EMBL:X62881; NID:g186; PIDN:C
A;Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F;274-294/Domain: transmembrane #status predicted <TMM>
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicte

  Query Match             13.2%;  Score 208.5;  DB 2;  Length 366;
  Best Local Similarity   23.8%;  Pred. No. 2.9e-09;
  Matches   81;  Conservative   44;  Mismatches  142;  Indels   73;  Gaps   11;

Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              ||| ||   :: : ::||  |:  | |     :: ||| : |:     :|    |:| |
Db         14 LVQLSL--AQIDLNITCRYAGVFHVEKNGRYSISKTEAADLCKAFNSTLPTMAQMEAARN 71

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
               |||| ||:: :| ||| || ||  |  |  || |     | |:   |:|:|       |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTICFNASAPPGEDC 129

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP--------APTTTPPAPAS 174
                  |:   : |       |   :  | | |:    | | |       :|:: |    |
Db        130 -----TSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSVVSPSSPPDDEMS 184

Qy        175 TSIPRRKKLICVTEVF----------------------METSTMSTETEPFVENKAAFK 211
              : |  :      :|                      :|    :  :| :
Db        185 SGSPSERSTSGGYSIFHTHLPTVHPSRPRRPWSQRAENTSDTRDYGSSHDPSGRSYTTHA 244

Qy        212 NEAAGFGG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPPT 253
              :|:||                   :|  |::|| |     |  |  |     :
Db        245 SESAGHSSGSEEHGANTTSGPMRKPQIPEWLIILASL-LALALILAVC-----IAVNSRR 298

Qy        254 NKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKS 293
                |:|:::          | :   || | :  | | |||
Db        299 RCGQKKKLVIN--------NGNGTMEERKPSGLNGEASKS 330


RESULT 7
JH0417
cell adhesion molecule CD44 - human
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 31-Dec-2004
C;Accession: JH0417; A32376; G02251; A32377
R;Harn, H.J.; Isola, N.; Cooper, D.L.
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991
A;Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte cD
A;Reference number: JH0417; MUID:91337049; PMID:1840487
A;Accession: JH0417
A;Molecule type: mRNA
A;Residues: 1-361 <HAR>
A;Cross-references: UNIPROT:Q92493; UNIPARC:UPI000016A68F; GB:M59040; NID:g180129; PIDN
A;Experimental source: reticulocyte
A;Note: the authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA
R;Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.
Cell 56, 1057-1062, 1989
A;Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil
A;Reference number: A32376; MUID:89168434; PMID:2466575
A;Accession: A32376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238,'E',240-361 <STA>
A;Cross-references: UNIPARC:UPI0000143A5B; GB:M24915; NID:g180196; PIDN:AAA35674.1; PID
R;Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.
submitted to the EMBL Data Library, November 1995
A;Reference number: H00921
A;Accession: G02251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-25,'M',27-108,'S',110-361 <BOS>
A;Cross-references: UNIPARC:UPI000016A285; EMBL:U40373; NID:g1101785; PID:g1101786
R;Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.;
Cell 56, 1063-1072, 1989
```

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A;Title: A human lymphocyte homing receptor, the hermes antigen, is related to cartilage
A;Reference number: A32377; MUID:89168435; PMID:2466576
A;Accession: A32377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108,'S',110-293,'S' <GOL>
A;Cross-references: UNIPARC:UPI0000070BED; GB:M25078; NID:g186660; PIDN:AAA36138.1; PID:
C;Keywords: alternative splicing; cell adhesion; surface antigen; transmembrane protein
F;269-285/Domain: transmembrane #status predicted <TMM>

  Query Match             13.0%;  Score 205;  DB 2;  Length 361;
  Best Local Similarity   24.4%;  Pred. No. 5.5e-09;
  Matches   83;  Conservative   46;  Mismatches  145;  Indels   66;  Gaps   14;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 128
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDC----- 129

Qy        129 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA---PTTTPPAPASTSIPRRKKLI 184
              |:   : |      |   :  | | |     | | |     |:       |:     :
Db        130 TSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSST 189

Qy        185 CVTEVFMETSTM------------STETEPPFVENKAAFK----------NEAAGF---- 217
                 :|   ||:             ||:  |   ::  |            :|: |
Db        190 SGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATRDQDTFHPSGGSHTTHGSESDGHSHGS 249

Qy        218 --GG------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 263
                ||            :|  |::|| |     |  |  |     :           |:|:::
Db        250 QEGGANTTSGPIRTPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 303

Qy        264 TK---VVKEEKANDSNPNEESKKTDK----NPEESKSPSK 296
                 |:: | :  |  | ||  :     | | |::| :
Db        304 NSGNGAVEDRKPSGLN-GEASKSQEMVHLVNKESSETPDQ 342


RESULT 8
S45305
CD44 antigen precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S45305
R;Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.
Biochim. Biophys. Acta 1218, 112-114, 1994
A;Title: Molecular cloning of the canine CD44 antigen cDNA.
A;Reference number: S45305; MUID:94250687; PMID:7514890
A;Accession: S45305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <MIL>
A;Cross-references: UNIPROT:Q28284; UNIPARC:UPI0000127367; EMBL:Z27115; NID:g473226; PID
C;Superfamily: human cell adhesion protein CD44

  Query Match             12.8%;  Score 202;  DB 2;  Length 351;
  Best Local Similarity   23.2%;  Pred. No. 9.3e-09;
  Matches   81;  Conservative   49;  Mismatches  141;  Indels   78;  Gaps   14;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: | | : |:    :|    |:| ||   |||
Db         10 LSLAQIDLNITCRYAGVFHVEKNGRYSISRTAAADLCKAFNSTLPTMAQMERALSVGFET 69

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEII 128
              | ||:: :| ||| || ||  |  |  || | |  :  : |:  ||:|:|      |
Db         70 CRYGFI-EGHVVIPRIQPNAICAANHTGVYI-LISNTSQYDTYCFNASAPPEEDC----- 122

Qy        129 TTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIPA---PTTTPPAPASTSIPRRKKLI 184
              |:   : |      |   :  | | ||    | | |     |:       |:     :
Db        123 TSVTHLPNAFDGPITITIVNRDGTRYSQKGEYRTNPEDINPSNPTDDDVSSGSSSERSTS 182

Qy        185 CVTEVF------------METSTMSTETE-------------PFVENKAAFKNEAAGF-- 217
                 :|   :|:  |  |  |  |  |  |             |  |  |  |  |
Db        183 AGYNIFHTHLPTAYPTEDQDSSRVSSNSDHTPITKDHDSSVHPSERSHTTHGSESAGHSS 242

Qy        218 ----GG------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEM 261
                  ||            :|  |::|| |     |  |  |     :           | ::
Db        243 GSQEGGANTTSGPMRKPQIPEWLIILASL-LALALILAVCIA-----------VNSRRRC 290

Qy        262 IETKVVKEEKAN----DSNP---NEESKKTDK-----NPEESKSPSKTT 298
                : | :      |     |  |   | |: |: :     | | |::| : |
Db        291 GQKKKLVINNGNGAVGDRKPSGINGEASKSQEMVHLVNKEPSETPDQYT 339


RESULT 9
A47195
lymphocyte homing receptor isoform CD44 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47195
R;Screaton, G.R.; Bell, M.V.; Jackson, D.G.; Cornelis, F.B.; Gerth, U.; Bell, J.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 12160-12164, 1992
A;Title: Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals at
A;Reference number: A47195; MUID:93101687; PMID:1465456
A;Accession: A47195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-742 <SCR>
A;Cross-references: UNIPROT:Q9UJ36; UNIPARC:UPI000017C297
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120739,
, NCBIN:120764, NCBIN:120766, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:120776, NCI

  Query Match             12.8%;  Score 202;  DB 2;  Length 742;
  Best Local Similarity   26.0%;  Pred. No. 2.4e-08;
  Matches   61;  Conservative   30;  Mismatches   84;  Indels   60;  Gaps    7;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 ------------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 154
                                           || |   :|  :  ::  ::|   :  |
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        155 VASPYSTI-PAPTTTPP--------APASTSIPRRKKLICVTEVFMETSTMSTET 200
              :   :||: | |     |         ||:|               | ||  :|||
Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATT-------------LMSTSATATET 234


RESULT 10
JH0518
lymphocyte homing receptor CD44, splice form CD44R1 - human
N;Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface
N;Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing recept
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R;Dougherty, G.J.; Lansdorp, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A;Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 lyr
A;Reference number: JH0518; MUID:91277598; PMID:2056274
A;Accession: JH0518
A;Molecule type: mRNA
A;Residues: 1-426 <DOU>
A;Cross-references: UNIPROT:Q9UCB0; UNIPARC:UPI0000179519
A;Experimental source: lymphocytes, cell line KG1a
A;Accession: JH0519
A;Molecule type: mRNA
A;Residues: 1-223,288-426 <DO2>
A;Cross-references: UNIPARC:UPI000017951A
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A;Experimental source: lymphocyte, cell line KG1a
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta,
Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal e
A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
A;Molecule type: DNA
A;Residues: 223-357 <COO>
A;Cross-references: UNIPARC:UPI000017951B
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat
A;Reference number: A39209; MUID:91177958; PMID:2007624
A;Accession: A39209
A;Molecule type: mRNA
A;Residues: 184-376 <BRO>
A;Cross-references: UNIPARC:UPI000016A690; GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:g
R;Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by ins
A;Reference number: A42402; MUID:92165834; PMID:1537855
A;Accession: A42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-223,288-359 <JAC>
A;Cross-references: UNIPARC:UPI000017951C
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
A;Note: variant B
A;Accession: C42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-320 <JA2>
A;Cross-references: UNIPARC:UPI000017951D
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
A;Note: variant D
R;Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy
A;Reference number: A53029; MUID:94149816; PMID:7508992
A;Accession: A53029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76,'X',78-89 <SHE>
A;Cross-references: UNIPARC:UPI000006D03F
C;Genetics:
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 35/1; 65/1; 133/1
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycc
F;1-426/Product: lymphocyte homing receptor CD44, splice form CD44R1 #status predicted <
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

  Query Match             12.7%;  Score 199.5;  DB 2;  Length 426;
  Best Local Similarity   22.2%;  Pred. No. 1.9e-08;
  Matches   83;  Conservative   48;  Mismatches  138;  Indels  105;  Gaps   12;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |    :: : ::||   |:  | |      :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              | ||:: :| ||| || ||  |  |  || |      | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 ------------------------------PEIITTKDPIFNTQTATQTTE-------FI 147
                                           || |   :|  :  ::  ::|       :|
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        148 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 185
                              ::|||      :: | :||   ||  |       : |. |

Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        186 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAGFGGVP------TALLVLALL 230
              |:    : : ||  |   |:|          :: :|:  |    |       | ||
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLL----- 308

Qy        231 FFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKV-----VKEEKANDSNPN-EESKKT 284
                          : |   :| | :::    : :       |       ||| |   |
Db        309 ------------EGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSG 355

Qy        285 DKNPEESKSPSKTT 298
              |::       | ||
Db        356 DQDTFHPSGGSHTT 369


RESULT 11
S13530
CD44E protein, epithelial - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S13530
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with
A;Reference number: S13530; MUID:91122041; PMID:1991450
A;Accession: S13530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-493 <STA>
A;Cross-references: UNIPARC:UPI0000159271; EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PI
C;Keywords: transmembrane protein

  Query Match             12.7%;  Score 199.5;  DB 2;  Length 493;
  Best Local Similarity   23.6%;  Pred. No. 2.3e-08;
  Matches   66;  Conservative   39;  Mismatches  100;  Indels   75;  Gaps    8;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |    :: : ::||   |:  | |      :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              | ||:: :| ||| || ||  |  |  || |      | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTYNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 ------------------------------PEIITTKDPIFNTQTATQTTE-------FI 147
                                           || |   :|  :  ::  ::|       :|
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        148 -----------------VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 185
                              ::|||      :: | :||   ||  |       : |. |
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        186 VTEVFMETSTMSTETEPFVENK---------AAFKNEAAG 216
              |:    : : ||  |   |:|          :: :|:  |
Db        255 TTQQ-SNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTG 293


RESULT 12
I77371
CD44R5 - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I77371
R;Tanabe, K.K.; Nishi, T.; Saya, H.
Mol. Carcinog. 7, 212-220, 1993
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44
A;Reference number: I57483; MUID:93356912; PMID:8352881
A;Accession: I77371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-395 <RES>
A;Cross-references: UNIPARC:UPI000016B3F6; GB:S66400; NID:g435697; PIDN:AAB27919.1; PID
C;Genetics:
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A;Gene: GDB:CD44
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 257/1
C;Superfamily: human cell adhesion protein CD44

  Query Match            12.6%;  Score 198;  DB 2;  Length 395;
  Best Local Similarity   23.0%;  Pred. No. 2.3e-08;
  Matches   85;  Conservative   49;  Mismatches  145;  Indels   90;  Gaps   14;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 ----------------------------PEIITTKDPIFNTQTATQTTEFIVSDS--- 151
                                         || |   :|  :  ::  ::|   :
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYI 194

Qy        152 --TYSVASPY----------STIPAPTTTPPAPASTSI-PRRKKLICVTEVFMETSTMST 198
                |:|   |          ||   | |   :  ||:: |       : |    |  :|
Db        195 FYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSM 254

Qy        199 ET------EPFVENKAAFKNEAAGF------GG------------VPTALLVLALLFFGA 234
              |       |   :     :|: |       ||             :|  |::|| |
Db        255 TTRDQDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASL-LAL 313

Qy        235 AAGLGFCYVKRYVKAFPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----N 287
              | | |     :          |:|:::       |:: | :  |  | ||  :     |
Db        314 ALILAVC-----IAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLN-GEASKSQEMVHLVN 367

Qy        288 PEESKSPSK 296
              | |::| :
Db        368 KESSETPDQ 376


RESULT 13
I37369
epican - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: I37369; S24631
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.
J. Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is
A;Reference number: I37369; PMID:1281868
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Accession: I37369
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-699 <RES>
A;Cross-references: UNIPARC:UPI000016A89D; EMBL:X66733; NID:g31190; PID:g31191

  Query Match            12.5%;  Score 196.5;  DB 2;  Length 699;
  Best Local Similarity   25.4%;  Pred. No. 6.1e-08;
  Matches   60;  Conservative   34;  Mismatches   93;  Indels   49;  Gaps    7;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:| ||   |||
Db         17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              | ||:: :| ||| || ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 ----------------------------PEIITTKDPIFNTQTATQTTEFIVSDSTYS 154
                                         || |   :|  :  ::  ::|   :   |
Db        135 LPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGY- 193

Qy        155 VASPYSTI-PAPTTTPP--APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENK 207
                :   :||: | |    |    ::  ||              ::|:|   ||  ||:
Db        194 IFYTFSTVHPIPDEDSPWITDSTDRIPATS---------TSSNTISAGWEPNEENE 240


RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butch
Immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <TA2>
A;Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NID:g1059; PIDN:C
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

  Query Match            11.8%;  Score 186;  DB 2;  Length 359;
  Best Local Similarity   24.6%;  Pred. No. 1.9e-07;
  Matches   84;  Conservative   42;  Mismatches  159;  Indels   56;  Gaps   11;

Qy          9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFET 68
              |   :: : ::||  |:  | |     :: ||| : |:    :|    |:: ||   |||
Db         17 LSLAQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMQKALNIGFET 76

Qy         69 CSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
              |  |:: :| |||  | ||  |  |  || |     | |:  ||:|:|      |
Db         77 CRIGFI-EGHVVIPPIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy        125 -------PEIIT----------------TKDPIFNTQTATQTTEFIVSDSTYSVASPYST 161
                     |  ||                |     |  |         | |  |  : ||
Db        135 LPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSTPADDDVSSGSSSERSTSGGYSI 194

Qy        162 IPA--PTTTP------------PAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENK 207
                  ||| |             |    |:  |       |    |||  || ::   |
Db        195 FHTHLPTTRPTQDQSSPWVSDSPEKTPTTKDRASGGRAQTTHGSETSGHSTGSQ---EGG 251

Qy        208 AAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETK-- 265
              |:  :       :|  |::|| |     |  |  |     :          |:|:::
Db        252 ASTTSGPIRRPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKKKLVINNGN 305

Qy        266 -VVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 305
               | : ||:  |  | |:  :     :|  |:|  : : |:
Db        306 GAVDDRKASGLN-GEASRSQEMVHLVNKESSETQDQFMTAD 345


RESULT 15
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2109 <LIX>
A;Cross-references: UNIPROT:P07898; UNIPARC:UPI000013177F; GB:L21913; NID:g416133; PIDN:
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
A;Accession: S39796
A;Molecule type: mRNA
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A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,'A'
A;Cross-references: UNIPARC:UPI0000173C73; GB:M88101
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.
A;Reference number: S27356; MUID:93111968; PMID:1339285
A;Accession: S27356
A;Molecule type: mRNA
A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1549,'T'
A;Cross-references: UNIPARC:UPI0000173C74; UNIPARC:UPI0000173C75; EMBL:M88101
R;Sai, S.; Tanaka, T.; Kosher, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A;Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly
A;Reference number: A25442; MUID:86259736; PMID:3460082
A;Accession: A25442
A;Molecule type: mRNA
A;Residues: 1693-1795,'G',1797-1855,1894-2109 <SAI>
A;Cross-references: UNIPARC:UPI00001712F6; GB:M13993; NID:g211654; PIDN:AAA48720.1; PID:
A;Experimental source: sternal cartilage
R;Tanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A;Reference number: A32002; MUID:89008500; PMID:3170613
A;Accession: A32002
A;Molecule type: DNA
A;Residues: 1893-1987,'S',1989-2022 <TAN>
A;Cross-references: UNIPARC:UPI0000173C76
A;Note: the authors translated the codon TCC for residue 1787 as Phe
R;Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s
A;Reference number: I50216; MUID:90307744; PMID:1694853
A;Accession: I50216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PA',1044-1559 <KRU>
A;Cross-references: UNIPARC:UPI00001712FB; GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:
R;Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an
A;Reference number: A37072; MUID:90307743; PMID:2365711
A;Accession: A37072
A;Molecule type: protein
A;Residues: 998-1015,'X',1017-1019,'X',1021-1023 <KR2>
A;Cross-references: UNIPARC:UPI0000173C77
A;Note: amino end of 86K core peptide CS-A
A;Accession: B37072
A;Molecule type: protein
A;Residues: 1247-1250,'D',1252-1272,'X',1274-1275 <KR3>
A;Cross-references: UNIPARC:UPI0000173C78
A;Note: amino end of 75K core peptide CS-B
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: alternative splicing
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2109/Product: aggrecan #status predicted <MAT>
F;44-131/Domain: immunoglobulin homology <IMM>
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-346/Domain: link protein repeat homology <LNK2>
F;537-614/Domain: link protein repeat homology <LNK3>
F;635-716/Domain: link protein repeat homology <LNK4>
F;1859-1890/Domain: EGF homology <EGF>
F;1897-2017/Domain: C-type lectin homology <LCH>
F;2024-2080/Domain: complement factor H repeat homology <FHD>

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  Best Local Similarity   27.0%;  Pred. No. 0.0018;
  Matches   74;  Conservative   27;  Mismatches  104;  Indels   69;  Gaps   13;

Qy         34 QQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDGFV--VISRISPNPKCG 91
              ::  | || : |  ||  ||   ::  | |   : || ||: |  |   |||  ||  ||
Db        258 EKFTFQEAFDKCHSLGARLATTGELYLAWKDGMDMCSAGWLADRSVRYPISRARPN--CG 315

Qy         92 KNGVGV-LIWKVPV--------SRQFAAYCYNSSDTWTNSCIP-----EIITTKDPIFNT 137
                 | |||  ::  |         | :: | ||:  |    : :|     |: |     |
Db        316 GNLVGVRTVYLNPANQTGYPHPSSRYDAICYSGDD--FEALVPGLFTDEVGTELGSAFTI 373

Qy        138 QTATQT----------TEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRRKKLICVT 187
              || |||           ||    ::  |:|:        | |    | | :|     :  |
Db        374 QTVTQTEVELPLPRNVTE---EEARGSIATLEPMEITATATELYEAFTVLPD----LFAT 426

Qy        188 EVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVKRYV 247
              | :||::      |  ||    : |  |   ||                    |   |
Db        427 SVTVETAS------PREEN--VTREEITGIWAVPEE------------------VTTSV 459

Qy        248 KAFPFTNKNQQKEMIETKVVKEEKANDSNPNEES 281
                ||       | |   |:|  |  : |  ||
Db        460 SGTAFTT-----GMAEVSSVEEAIAVTATPGLES 488


Search completed: March 20, 2006, 14:09:54
Job time : 16.7123 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:48 ; Search time 66.0354 Seconds
(without alignments)
3269.333 Million cell updates/sec

Title: US-10-063-510-6_COPY_17_322
Perfect score: 1575
Sequence: 1 TRLLVQGSLRAEELSIQVSC.....NPEESKSPSKTTVRCLEAEV 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1575	100.0	322	2	Q9UNF4_HUMAN	Q9unf4 homo sapien
2	1561	99.1	322	2	Q8TC18_HUMAN	Q8tc18 homo sapien
3	1556	98.8	322	2	Q9Y5Y7_HUMAN	Q9y5y7 homo sapien
4	1118	71.0	322	2	Q6UC88_BOVIN	Q6uc88 bos taurus
5	1055	67.0	318	2	Q8BHC0_MOUSE	Q8bhc0 mus musculu
6	1055	67.0	318	2	Q99NE4_MOUSE	Q99ne4 mus musculu
7	726.5	46.1	201	2	Q7YS22_PIG	Q7ys22 sus scrofa
8	245	15.6	392	2	Q58E15_XENLA	Q58e15 xenopus lae
9	241	15.3	441	2	Q6GM56_XENLA	Q6gm56 xenopus lae
10	233.5	14.8	362	1	CD44_CRIGR	P20944 cricetulus
11	229.5	14.6	437	2	Q6P8A2_XENTR	Q6p8a2 xenopus tro
12	222.5	14.1	362	1	CD44_PAPHA	P14745 papio hamad
13	222	14.1	364	2	O70509_RAT	O70509 rattus norv
14	217	13.8	503	1	CD44_RAT	P26051 rattus norv
15	214.5	13.6	780	2	O08779_RAT	O08779 rattus norv
16	212.5	13.5	431	1	CD44_MESAU	Q60522 m cd44 anti
17	211	13.4	265	2	Q98SR5_ANAPL	Q98sr5 anas platyr
18	209.5	13.3	398	2	Q90ZL8_ANAPL	Q90zl8 anas platyr
19	209.5	13.3	778	1	CD44_MOUSE	P15379 mus musculu
20	208.5	13.2	366	1	CD44_BOVIN	Q29423 bos taurus
21	204	13.0	361	2	Q86T72_HUMAN	Q86t72 homo sapien
22	203.5	12.9	364	2	O97569_CERSI	O97569 ceratotheri
23	203.5	12.9	396	2	Q9W6S4_CHICK	Q9w6s4 gallus gall
24	203	12.9	742	2	Q9UJ36_HUMAN	Q9uj36 homo sapien
25	202	12.8	351	1	CD44_CANFA	Q28284 canis famil
26	202	12.8	361	2	Q8N694_HUMAN	Q8n694 homo sapien
27	202	12.8	742	1	CD44_HUMAN	P16070 h cd44 anti
28	200.5	12.7	580	2	Q80X37_MOUSE	Q80x37 mus musculu
29	199.5	12.7	493	2	Q86Z27_HUMAN	Q86z27 homo sapien
30	199.5	12.7	493	2	Q5R9V4_PONPY	Q5r9v4 pongo pygma
31	199	12.6	338	2	Q9H5A4_HUMAN	Q9h5a4 homo sapien
32	198.5	12.6	168	2	Q90ZL6_ANAPL	Q90zl6 anas platyr
33	197	12.5	719	2	Q9H5A5_HUMAN	Q9h5a5 homo sapien
34	196	12.4	294	2	Q92493_HUMAN	Q92493 homo sapien
35	191.5	12.2	676	2	Q9H5A7_HUMAN	Q9h5a7 homo sapien
36	191	12.1	271	2	Q9H5A3_HUMAN	Q9h5a3 homo sapien
37	191	12.1	470	2	Q9H5A6_HUMAN	Q9h5a6 homo sapien
38	186	11.8	359	1	CD44_HORSE	Q05078 equus cabal
39	173.5	11.0	153	2	Q4SI95_TETNG	Q4si95 tetraodon n
40	150	9.5	537	1	PGCA_PIG	Q29011 sus scrofa
41	149.5	9.5	2109	2	P79787_CHICK	P79787 gallus gall
42	148.5	9.4	2109	1	PGCA_CHICK	P07898 gallus gall
43	145.5	9.2	494	2	Q9BGH3_PIG	Q9bgh3 sus scrofa
44	145.5	9.2	3562	1	CSPG2_CHICK	Q90953 gallus gall
45	145	9.2	277	1	TSG6_HUMAN	P98066 homo sapien
46	145	9.2	277	2	Q53TI7_HUMAN	Q53ti7 homo sapien
47	144	9.1	275	1	TSG6_MOUSE	O08859 mus musculu
48	144	9.1	280	2	Q5W1C4_BOVIN	Q5w1c4 bos taurus
49	143	9.1	2149	2	Q6XL68_BOVIN	Q6xl68 bos taurus
50	143	9.1	2327	2	Q6XL66_BOVIN	Q6xl66 bos taurus
51	143	9.1	2364	1	PGCA_BOVIN	P13608 bos taurus
52	143	9.1	2365	2	Q6XL67_BOVIN	Q6xl67 bos taurus
53	141.5	9.0	243	2	Q4S9S8_TETNG	Q4s9s8 tetraodon n
54	140.5	8.9	2571	1	STAB1_MOUSE	Q8r4y4 mus musculu
55	139.5	8.9	2333	1	PGCA_CANFA	Q28343 canis famil
56	137	8.7	276	1	TSG6_RABIT	P98065 oryctolagus
57	136	8.6	2559	1	STAB2_MOUSE	Q8r4u0 mus musculu
58	133	8.4	514	2	Q62913_RAT	Q62913 rattus norv
59	133	8.4	1431	1	STAB2_RAT	Q8cfm6 rattus norv
60	133	8.4	2551	1	STAB2_HUMAN	Q8wwq8 h stabilin-
61	132.5	8.4	721	2	Q6PID9_HUMAN	Q6pid9 homo sapien
62	132	8.4	1046	2	Q4S1V9_TETNG	Q4s1v9 tetraodon n
63	131.5	8.3	2124	1	PGCA_RAT	P07897 rattus norv
64	131	8.3	314	2	Q4SE78_TETNG	Q4se78 tetraodon n
65	131	8.3	2132	1	PGCA_MOUSE	Q61282 mus musculu
66	130.5	8.3	883	1	PGCB_MOUSE	Q61361 mus musculu
67	130.5	8.3	883	1	PGCB_RAT	P55068 rattus norv
68	130.5	8.3	883	2	Q80WT7_MOUSE	Q80wt7 mus musculu
69	130.5	8.3	1152	2	Q90WM2_XENLA	Q90wm2 xenopus lae
70	130.5	8.3	2415	1	PGCA_HUMAN	P16112 homo sapien
71	130.5	8.3	2570	1	STAB1_HUMAN	Q9ny15 homo sapien
72	128.5	8.2	912	1	PGCB_BOVIN	Q28062 bos taurus
73	128	8.1	845	2	Q4RV64_TETNG	Q4rv64 tetraodon n
74	127.5	8.1	671	2	Q5T3I5_HUMAN	Q5t3i5 homo sapien
75	127.5	8.1	850	2	Q59F90_HUMAN	Q59f90 homo sapien
76	127.5	8.1	911	1	PGCB_HUMAN	Q96gw7 homo sapien
77	127.5	8.1	911	2	Q5SZ10_HUMAN	Q5sz10 homo sapien
78	127	8.1	266	2	Q5I051_XENLA	Q5i051 xenopus lae
79	126	8.0	3358	1	CSPG2_MOUSE	Q62059 mus musculu
80	125.5	8.0	536	2	Q5RG03_BRARE	Q5rg03 brachydanio
81	124.5	7.9	1515	2	Q4T6A4_TETNG	Q4t6a4 tetraodon n
82	124	7.9	2586	2	Q4RUP1_TETNG	Q4rup1 tetraodon n
83	123.5	7.8	386	2	Q4S472_TETNG	Q4s472 tetraodon n
84	123.5	7.8	2760	2	Q4T8G9_TETNG	Q4t8g9 tetraodon n
85	122	7.7	383	2	Q5BJ60_XENTR	Q5bj60 xenopus tro
86	122	7.7	394	1	PGCA_RABIT	Q28670 oryctolagus
87	121.5	7.7	360	1	HPLN3_HUMAN	Q96s86 homo sapien
88	121.5	7.7	1091	2	Q4SE77_TETNG	Q4se77 tetraodon n
89	121	7.7	516	2	Q8IWX2_HUMAN	Q8iwx2 homo sapien
90	120.5	7.7	1570	2	Q75ZI3_BRARE	Q75zi3 brachydanio
91	120	7.6	313	2	Q4SHL9_TETNG	Q4shl9 tetraodon n
92	119.5	7.6	411	2	Q702X4_HHV1	Q702x4 human herpe
93	119	7.6	359	2	Q7ZX17_XENLA	Q7zx17 xenopus lae
94	118.5	7.5	3396	1	CSPG2_HUMAN	P13611 homo sapien
95	118.5	7.5	3410	2	Q59FG9_HUMAN	Q59fg9 homo sapien
96	117.5	7.5	397	2	Q702X3_HHV1	Q702x3 human herpe
97	117	7.4	537	2	Q4IQU7_GIBZE	Q4iqu7 gibberella
98	117	7.4	1452	2	Q55DV2_DICDI	Q55dv2 dictyosteli
99	116	7.4	368	2	Q8BS97_MOUSE	Q8bs97 mus musculu
100	116	7.4	368	2	Q4VA91_MOUSE	Q4va91 mus musculu
101	116	7.4	2738	1	CSPG2_RAT	Q9erb4 rattus norv
102	115.5	7.3	744	2	Q4RLD6_TETNG	Q4rld6 tetraodon n
103	115	7.3	370	2	Q7M2W7_PIG	Q7m2w7 sus scrofa
104	115	7.3	394	2	Q6DCI6_XENLA	Q6dci6 xenopus lae

105	115	7.3	3381	1	CSPG2_BOVIN	P81282	bos taurus
106	114.5	7.3	1039	2	Q4S473_TETNG	Q4s473	tetraodon n
107	114.5	7.3	1257	1	CSPG3_RAT	P55067	rattus norv
108	114	7.2	610	2	Q9N3C0_CAEEL	Q9n3c0	caenorhabdi
109	113.5	7.2	289	2	Q60TZ2_CAEBR	Q60tz2	caenorhabdi
110	113.5	7.2	341	1	HPLN2_MOUSE	Q9esm3	mus musculu
111	113.5	7.2	1290	2	Q9W6E1_CHICK	Q9w6e1	gallus gall
112	113	7.2	459	2	Q54G90_DICDI	Q54g90	dictyosteli
113	113	7.2	892	1	LDLR2_XENLA	Q99088	xenopus lae
114	112.5	7.1	340	1	HPLN2_HUMAN	Q9gzv7	homo sapien
115	112.5	7.1	340	2	Q5T3J0_HUMAN	Q5t3j0	homo sapien
116	112.5	7.1	417	1	PGCB_FELCA	P41725	felis silve
117	112	7.1	210	2	Q8C9U7_MOUSE	Q8c9u7	mus musculu
118	112	7.1	390	1	VGLI_HHV11	P06487	human herpe
119	112	7.1	390	2	Q702X7_HHV1	Q702x7	human herpe
120	111.5	7.1	402	1	ODP2_MYCPN	P75392	mycoplasma
121	111	7.0	354	2	Q86W61_HUMAN	Q86w61	homo sapien
122	111	7.0	359	2	Q5R1X6_RAT	Q5r1x6	rattus norv
123	110	7.0	363	2	Q6NV41_BRARE	Q6nv41	brachydanio
124	109	6.9	816	2	O70474_RAT	O70474	rattus norv
125	109	6.9	1321	1	CSPG3_HUMAN	O14594	homo sapien
126	109	6.9	1335	2	Q4LE67_HUMAN	Q4le67	homo sapien
127	108.5	6.9	341	1	HPLN2_RAT	Q9esm2	rattus norv
128	108.5	6.9	397	2	Q702X6_HHV1	Q702x6	human herpe
129	108.5	6.9	1441	2	Q4S3C4_TETNG	Q4s3c4	tetraodon n
130	108	6.9	354	1	HPLN1_HUMAN	P10915	homo sapien
131	108	6.9	359	1	HPLN3_MOUSE	Q80wm5	mus musculu
132	108	6.9	624	2	Q19780_CAEEL	Q19780	caenorhabdi
133	107.5	6.8	739	2	O02360_CAEEL	O02360	caenorhabdi
134	107	6.8	354	1	HPLN1_RAT	P03994	rattus norv
135	107	6.8	355	1	HPLN1_CHICK	P07354	gallus gall
136	107	6.8	356	1	HPLN1_MOUSE	Q9qup5	mus musculu
137	107	6.8	543	2	Q4YVC9_PLABE	Q4yvc9	plasmodium
138	107	6.8	862	2	Q9UF98_HUMAN	Q9uf98	homo sapien
139	107	6.8	956	2	Q60MG7_CAEBR	Q60mg7	caenorhabdi
140	107	6.8	1268	1	CSPG3_MOUSE	P55066	mus musculu
141	107	6.8	1321	1	CSPG3_PANTR	Q5is41	pan troglod
142	107	6.8	1795	2	O76894_DROME	O76894	drosophila
143	106.5	6.8	1390	2	Q54GX9_DICDI	Q54gx9	dictyosteli
144	106	6.7	1059	2	Q5ISN4_MACFA	Q5isn4	macaca fasc
145	106	6.7	1153	2	Q4IAN9_GIBZE	Q4ian9	gibberella
146	105.5	6.7	374	2	Q9Z209_CRIGR	Q9z209	cricetulus
147	105.5	6.7	573	2	Q8CJD9_RAT	Q8cjd9	rattus norv
148	105.5	6.7	830	2	Q6CAY0_YARLI	Q6cay0	yarrowia li
149	105	6.7	354	1	HPLN1_BOVIN	P55252	bos taurus
150	105	6.7	438	2	Q4X548_PLACH	Q4x548	plasmodium
151	105	6.7	463	2	Q7RNE3_PLAYO	Q7rne3	plasmodium
152	105	6.7	480	2	Q5CGY9_CRYHO	Q5cgy9	cryptospori
153	105	6.7	612	2	Q6CD44_YARLI	Q6cd44	yarrowia li
154	104.5	6.6	862	1	CSPG2_MACNE	Q28858	macaca neme
155	104	6.6	139	2	O95370_HUMAN	O95370	homo sapien
156	104	6.6	354	1	HPLN1_HORSE	Q28381	equus cabal
157	104	6.6	354	1	HPLN1_PIG	P10859	sus scrofa
158	104	6.6	627	2	Q8MP19_DICDI	Q8mp19	dictyosteli
159	104	6.6	681	2	Q555L9_DICDI	Q55519	dictyosteli
160	104	6.6	1716	2	Q9I7Q8_DROME	Q9i7q8	drosophila
161	104	6.6	1912	2	Q9VS99_DROME	Q9vs99	drosophila
162	103.5	6.6	288	2	Q6QPC9_9ADEN	Q6qpc9	simian aden
163	103.5	6.6	616	2	Q58EE4_BRARE	Q58ee4	brachydanio
164	103.5	6.6	952	2	Q86AH0_DICDI	Q86ah0	dictyosteli
165	103.5	6.6	1197	2	Q5IS86_9PRIM	Q5is86	saimiri bol
166	103.5	6.6	1254	2	Q94185_CAEEL	Q94185	caenorhabdi
167	103.5	6.6	1592	2	Q5AWR8_EMENI	Q5awr8	aspergillus
168	103	6.5	80	2	Q86UZ1_HUMAN	Q86uz1	homo sapien
169	103	6.5	231	2	Q5T3I6_HUMAN	Q5t3i6	homo sapien
170	103	6.5	232	2	Q5BDD1_EMENI	Q5bdd1	aspergillus
171	102.5	6.5	182	2	Q8I0D8_DROME	Q8i0d8	drosophila
172	102.5	6.5	183	2	Q9VT37_DROME	Q9vt37	drosophila
173	102.5	6.5	497	2	Q8QVC4_9REOV	Q8qvc4	eyach virus
174	102.5	6.5	590	2	Q5BG25_EMENI	Q5bg25	aspergillus
175	102.5	6.5	595	2	Q5UPW9_MIMIV	Q5upw9	mimivirus.
176	102.5	6.5	699	2	Q8QVE9_9REOV	Q8qve9	eyach virus
177	102	6.5	391	2	Q753G3_ASHGO	Q753g3	ashbya goss
178	102	6.5	404	2	Q702X0_HHV1	Q702x0	human herpe
179	102	6.5	404	2	Q702Y3_HHV1	Q702y3	human herpe
180	102	6.5	527	2	Q54VQ0_DICDI	Q54vq0	dictyosteli
181	102	6.5	1879	2	Q4VZL0_CUCSA	Q4vzl0	cucumis sat
182	101.5	6.4	380	2	O02343_CAEEL	O02343	caenorhabdi
183	101.5	6.4	1853	2	Q7KT96_DROME	Q7kt96	drosophila
184	101.5	6.4	1893	2	Q9NKC9_DROME	Q9nkc9	drosophila
185	101.5	6.4	4370	2	Q4Q1Q2_LEIMA	Q4q1q2	leishmania
186	101	6.4	700	2	Q8TG00_ASPFU	Q8tg00	aspergillus
187	101	6.4	700	2	Q4WS89_ASPFU	Q4ws89	aspergillus
188	101	6.4	708	2	Q18175_CAEEL	Q18175	caenorhabdi
189	101	6.4	1777	2	Q54FB8_DICDI	Q54fb8	dictyosteli
190	101	6.4	2535	2	Q755B8_ASHGO	Q755b8	ashbya goss
191	100.5	6.4	353	2	Q4IH62_GIBZE	Q4ih62	gibberella
192	100.5	6.4	402	1	HPLN4_HUMAN	Q86uw8	homo sapien
193	100.5	6.4	411	2	Q702X9_HHV1	Q702x9	human herpe
194	100.5	6.4	841	2	Q4Q5Z4_LEIMA	Q4q5z4	leishmania
195	100.5	6.4	1121	2	Q59YM6_CANAL	Q59ym6	candida alb
196	100.5	6.4	1121	2	Q7Z884_CANAL	Q7z884	candida alb
197	100	6.3	319	2	Q4S1V7_TETNG	Q4s1v7	tetraodon n
198	100	6.3	403	2	Q702W8_HHV1	Q702w8	human herpe
199	100	6.3	404	2	Q702W6_HHV1	Q702w6	human herpe
200	100	6.3	404	2	Q702Y0_HHV1	Q702y0	human herpe
201	100	6.3	441	2	Q5BA48_EMENI	Q5ba48	aspergillus
202	100	6.3	486	2	Q8FRY2_COREF	Q8fry2	corynebacte
203	100	6.3	738	2	Q5WN81_CAEBR	Q5wn81	caenorhabdi
204	99.5	6.3	335	2	Q60H44_BRARE	Q60h44	brachydanio
205	99.5	6.3	478	2	Q7YX15_CAEEL	Q7yx15	caenorhabdi
206	99.5	6.3	577	2	Q52GY0_CAEEL	Q52gy0	caenorhabdi
207	99.5	6.3	1092	1	NCA12_XENLA	P36335	xenopus lae
208	99.5	6.3	1117	2	Q54SZ6_DICDI	Q54sz6	dictyosteli
209	99.5	6.3	1165	2	Q60NC3_CAEBR	Q60nc3	caenorhabdi
210	99.5	6.3	2297	2	Q5PZ43_BRARE	Q5pz43	brachydanio
211	99	6.3	178	2	Q8FQU3_COREF	Q8fqu3	corynebacte
212	99	6.3	388	2	Q4H2F0_HPV27	Q4h2f0	human papil
213	99	6.3	604	2	Q6E9B8_LISMO	Q6e9b8	listeria mo
214	99	6.3	896	2	Q20253_CAEEL	Q20253	caenorhabdi
215	99	6.3	1100	2	Q8CCT8_MOUSE	Q8cct8	mus musculu
216	99	6.3	5376	1	ZAN_MOUSE	O88799	mus musculu
217	98.5	6.3	204	2	Q9N5Z8_CAEEL	Q9n5z8	caenorhabdi
218	98.5	6.3	346	2	Q7S973_NEUCR	Q7s973	neurospora
219	98.5	6.3	397	2	Q702W7_HHV1	Q702w7	human herpe
220	98.5	6.3	397	2	Q702X1_HHV1	Q702x1	human herpe
221	98.5	6.3	425	2	Q702W3_HHV1	Q702w3	human herpe
222	98.5	6.3	578	2	Q63ZX6_MOUSE	Q63zx6	mus musculu
223	98.5	6.3	1126	2	Q9VGK5_DROME	Q9vgk5	drosophila
224	98.5	6.3	1203	2	Q6ZQ56_MOUSE	Q6zq56	mus musculu
225	98	6.2	390	2	Q702W4_HHV1	Q702w4	human herpe
226	98	6.2	604	2	Q8GNR7_LISMO	Q8gnr7	listeria mo
227	98	6.2	604	2	Q6E9T6_LISMO	Q6e9t6	listeria mo
228	98	6.2	604	2	Q8GNR1_LISMO	Q8gnr1	listeria mo
229	98	6.2	1015	2	Q54V57_DICDI	Q54v57	dictyosteli
230	98	6.2	2112	2	Q9VEL9_DROME	Q9vel9	drosophila
231	97.5	6.2	297	2	Q7PR65_ANOGA	Q7pr65	anopheles g
232	97.5	6.2	385	2	Q9NHU9_DROMI	Q9nhu9	drosophila
233	97.5	6.2	505	2	Q4FYQ6_LEIMA	Q4fyq6	leishmania
234	97.5	6.2	553	2	Q8F932_LEPIN	Q8f932	leptospira
235	97.5	6.2	557	2	Q72VI3_LEPIC	Q72vi3	leptospira
236	97.5	6.2	836	2	Q55DF3_DICDI	Q55df3	dictyosteli
237	97.5	6.2	909	1	LDLR1_XENLA	Q99087	xenopus lae
238	97	6.2	294	2	Q54FY4_DICDI	Q54fy4	dictyosteli
239	97	6.2	404	2	Q702Y6_HHV1	Q702y6	human herpe
240	97	6.2	604	2	Q6E9K8_LISMO	Q6e9k8	listeria mo
241	97	6.2	604	2	Q6E9X2_LISMO	Q6e9x2	listeria mo
242	97	6.2	604	2	Q6EAI6_LISMO	Q6eai6	listeria mo
243	97	6.2	889	2	Q4RUP0_TETNG	Q4rup0	tetraodon n
244	97	6.2	1159	2	Q55GQ9_DICDI	Q55gq9	dictyosteli
245	97	6.2	1604	2	Q4SNA3_TETNG	Q4sna3	tetraodon n
246	96.5	6.1	268	2	Q5ATR9_EMENI	Q5atr9	aspergillus
247	96.5	6.1	276	2	Q54NG3_DICDI	Q54ng3	dictyosteli
248	96.5	6.1	385	2	Q9N666_DROMI	Q9n666	drosophila
249	96.5	6.1	385	2	Q9NHU6_DROMI	Q9nhu6	drosophila
250	96.5	6.1	397	2	Q702Y5_HHV1	Q702y5	human herpe

251	96.5	6.1	407	2	Q564S9_CAEEL	Q564s9	caenorhabdi
252	96.5	6.1	465	1	YHU6_YEAST	P38845	saccharomyc
253	96.5	6.1	604	2	Q8GNS1_LISMO	Q8gns1	listeria mo
254	96.5	6.1	731	1	NOG2_CRYGA	Q6tgj8	cryptococcu
255	96.5	6.1	961	2	Q5ATY9_EMENI	Q5aty9	aspergillus
256	96.5	6.1	961	2	Q92223_EMENI	Q92223	emericella
257	96.5	6.1	1065	2	Q50ZF1_ENTHI	Q50zf1	entamoeba h
258	96.5	6.1	1403	1	LARP_DROME	Q9vaw5	drosophila
259	96	6.1	173	2	Q4KTX2_CEREL	Q4ktx2	cervus elap
260	96	6.1	232	2	Q4V3Z2_DROME	Q4v3z2	drosophila
261	96	6.1	236	2	Q4V400_DROME	Q4v400	drosophila
262	96	6.1	429	2	O76430_CAEEL	O76430	caenorhabdi
263	96	6.1	449	2	Q71UN8_CAEEL	Q71un8	caenorhabdi
264	96	6.1	481	2	Q9XUF4_CAEEL	Q9xuf4	caenorhabdi
265	96	6.1	545	2	Q5A7A3_CANAL	Q5a7a3	candida alb
266	96	6.1	549	2	Q54WC8_DICDI	Q54wc8	dictyosteli
267	96	6.1	555	2	Q95XI3_CAEEL	Q95xi3	caenorhabdi
268	96	6.1	604	2	Q6E9R2_LISMO	Q6e9r2	listeria mo
269	96	6.1	604	2	Q6E9R8_LISMO	Q6e9r8	listeria mo
270	96	6.1	604	2	Q6EAJ7_LISMO	Q6eaj7	listeria mo
271	96	6.1	604	2	Q724K9_LISMF	Q724k9	listeria mo
272	96	6.1	620	2	Q5A7H9_CANAL	Q5a7h9	candida alb
273	96	6.1	625	2	Q58SF3_DROSI	Q58sf3	drosophila
274	96	6.1	625	2	Q58SH8_DROSI	Q58sh8	drosophila
275	96	6.1	625	2	Q5ELN3_DROSI	Q5eln3	drosophila
276	96	6.1	625	2	Q6V6E1_DROSI	Q6v6e1	drosophila
277	96	6.1	732	2	Q54FU3_DICDI	Q54fu3	dictyosteli
278	96	6.1	804	2	Q54L26_DICDI	Q54l26	dictyosteli
279	96	6.1	1038	2	Q4T3K8_TETNG	Q4t3k8	tetraodon n
280	96	6.1	1088	1	NCA11_XENLA	P16170	xenopus lae
281	96	6.1	1155	2	Q4JA20_SULAC	Q4ja20	sulfolobus
282	96	6.1	1569	2	Q54DM4_DICDI	Q54dm4	dictyosteli
283	96	6.1	3178	1	YS89_CAEEL	Q09624	caenorhabdi
284	95.5	6.1	266	2	Q4HZD3_GIBZE	Q4hzd3	gibberella
285	95.5	6.1	385	2	Q9NHU5_DROMI	Q9nhu5	drosophila
286	95.5	6.1	385	2	Q9NHU7_DROMI	Q9nhu7	drosophila
287	95.5	6.1	469	2	Q54P62_DICDI	Q54p62	dictyosteli
288	95.5	6.1	585	2	Q5SE79_9MONO	Q5se79	avian pneum
289	95.5	6.1	996	2	Q5BF33_EMENI	Q5bf33	aspergillus
290	95.5	6.1	1259	2	Q869X4_DICDI	Q869x4	dictyosteli
291	95.5	6.1	5374	2	Q99ND0_MOUSE	Q99nd0	mus musculu
292	95	6.0	273	2	Q61002_MOUSE	Q61002	mus musculu
293	95	6.0	281	2	Q4KSI9_9ADEN	Q4ksi9	human adeno
294	95	6.0	390	2	Q702W9_HHV1	Q702w9	human herpe
295	95	6.0	424	2	Q9FGW0_ARATH	Q9fgw0	arabidopsis
296	95	6.0	538	2	O69379_LISMO	O69379	listeria mo
297	95	6.0	601	2	Q5ZKL1_CHICK	Q5zkl1	gallus gall
298	95	6.0	604	2	Q9RQI3_LISMO	Q9rqi3	listeria mo
299	95	6.0	604	2	Q6EAD8_LISMO	Q6ead8	listeria mo
300	95	6.0	639	2	Q8GNR2_LISMO	Q8gnr2	listeria mo
301	95	6.0	639	2	Q6E904_LISMO	Q6e904	listeria mo
302	95	6.0	639	2	Q6E982_LISMO	Q6e982	listeria mo
303	95	6.0	639	2	Q6E9Q6_LISMO	Q6e9q6	listeria mo
304	95	6.0	753	2	Q6PFP4_BRARE	Q6pfp4	brachydanio
305	95	6.0	1203	2	Q6C028_YARLI	Q6c028	yarrowia li
306	95	6.0	1317	1	YQU3_CAEEL	Q09550	caenorhabdi
307	95	6.0	1578	2	Q55C84_DICDI	Q55c84	dictyosteli
308	95	6.0	1748	2	Q54FL9_DICDI	Q54fl9	dictyosteli
309	94.5	6.0	359	1	TIMD1_HUMAN	Q96d42	homo sapien
310	94.5	6.0	383	2	Q702X5_HHV1	Q702x5	human herpe
311	94.5	6.0	383	2	Q702Y4_HHV1	Q702y4	human herpe
312	94.5	6.0	395	2	Q702Z0_HHV1	Q702z0	human herpe
313	94.5	6.0	405	2	Q4INQ5_GIBZE	Q4inq5	gibberella
314	94.5	6.0	494	2	Q4WG24_ASPFU	Q4wg24	aspergillus
315	94.5	6.0	510	2	Q5YFP0_9VIRU	Q5yfp0	singapore g
316	94.5	6.0	519	2	Q7YTR7_CAEEL	Q7ytr7	caenorhabdi
317	94.5	6.0	539	2	Q54GL8_DICDI	Q54gl8	dictyosteli
318	94.5	6.0	698	2	Q61SH2_CAEBR	Q61sh2	caenorhabdi
319	94.5	6.0	814	2	Q5AG78_CANAL	Q5ag78	candida alb
320	94.5	6.0	1007	2	Q55CR8_DICDI	Q55cr8	dictyosteli
321	94.5	6.0	1007	2	Q5P0E5_AZOSE	Q5p0e5	azoarcus sp
322	94.5	6.0	1066	2	Q76NW3_DICDI	Q76nw3	dictyosteli
323	94.5	6.0	1079	2	Q9N4S7_CAEEL	Q9n4s7	caenorhabdi
324	94.5	6.0	1390	2	Q17602_CAEEL	Q17602	caenorhabdi
325	94.5	6.0	1622	2	Q54G21_DICDI	Q54g21	dictyosteli
326	94.5	6.0	1942	2	Q8GIZ7_LACDL	Q8giz7	lactobacill
327	94.5	6.0	3370	2	Q8I1N9_PLAF7	Q8i1n9	plasmodium
328	94	6.0	239	2	Q55C69_DICDI	Q55c69	dictyosteli
329	94	6.0	639	2	Q8GNR8_LISMO	Q8gnr8	listeria mo
330	94	6.0	639	2	Q6E8W8_LISMO	Q6e8w8	listeria mo
331	94	6.0	639	2	Q6E922_LISMO	Q6e922	listeria mo
332	94	6.0	639	2	Q6E9G6_LISMO	Q6e9g6	listeria mo
333	94	6.0	639	2	Q6EA26_LISMO	Q6ea26	listeria mo
334	94	6.0	639	2	Q6EA68_LISMO	Q6ea68	listeria mo
335	94	6.0	639	2	Q6EAF0_LISMO	Q6eaf0	listeria mo
336	94	6.0	769	2	O00816_TOXGO	O00816	toxoplasma
337	94	6.0	989	2	Q83U76_CHLTR	Q83u76	chlamydia t
338	94	6.0	989	2	Q84FU9_CHLTR	Q84fu9	chlamydia t
339	94	6.0	1067	2	Q5BGE6_EMENI	Q5bge6	aspergillus
340	94	6.0	1241	1	PER_DROPS	P12348	drosophila
341	93.5	5.9	278	2	Q4WIP3_ASPFU	Q4wip3	aspergillus
342	93.5	5.9	383	2	Q702W5_HHV1	Q702w5	human herpe
343	93.5	5.9	385	2	Q9NHU8_DROMI	Q9nhu8	drosophila
344	93.5	5.9	498	2	Q6FWR9_CANGA	Q6fwr9	candida gla
345	93.5	5.9	556	2	Q6DEK7_BRARE	Q6dek7	brachydanio
346	93.5	5.9	607	2	Q8GNS0_LISMO	Q8gns0	listeria mo
347	93.5	5.9	613	2	Q51TE4_MAGGR	Q51te4	magnaporthe
348	93.5	5.9	802	2	Q60LR3_CAEBR	Q60lr3	caenorhabdi
349	93.5	5.9	980	2	Q54TI9_DICDI	Q54ti9	dictyosteli
350	93.5	5.9	1033	2	Q4HYJ6_GIBZE	Q4hyj6	gibberella
351	93.5	5.9	1595	2	Q5SBM3_LACSK	Q5sbm3	lactobacill
352	93	5.9	261	2	Q70CC2_EIMTE	Q70cc2	eimeria ten
353	93	5.9	385	2	Q8T8I7_DROPS	Q8t8i7	drosophila
354	93	5.9	385	2	Q8T8I9_DROPS	Q8t8i9	drosophila
355	93	5.9	405	2	Q66HZ2_BRARE	Q66hz2	brachydanio
356	93	5.9	448	2	Q5EFZ7_CHICK	Q5efz7	gallus gall
357	93	5.9	572	2	Q58SM0_DROME	Q58sm0	drosophila
358	93	5.9	572	2	Q58SM7_DROME	Q58sm7	drosophila
359	93	5.9	608	2	Q50MX9_ENTHI	Q50mx9	entamoeba h
360	93	5.9	629	2	Q24017_DROME	Q24017	drosophila
361	93	5.9	629	2	Q5ELT0_DROME	Q5elt0	drosophila
362	93	5.9	629	2	Q5ELT4_DROME	Q5elt4	drosophila
363	93	5.9	629	2	Q5ELV0_DROME	Q5elv0	drosophila
364	93	5.9	639	2	Q8GNR5_LISMO	Q8gnr5	listeria mo
365	93	5.9	639	2	Q8GNR6_LISMO	Q8gnr6	listeria mo
366	93	5.9	639	2	Q6E8X4_LISMO	Q6e8x4	listeria mo
367	93	5.9	758	2	Q54UR7_DICDI	Q54ur7	dictyosteli
368	93	5.9	791	2	Q51UQ4_MAGGR	Q51uq4	magnaporthe
369	93	5.9	916	2	Q7YZI0_MONBE	Q7yzi0	monosiga br
370	93	5.9	928	2	Q4SL40_TETNG	Q4sl40	tetraodon n
371	93	5.9	1034	2	Q613E9_CAEBR	Q613e9	caenorhabdi
372	93	5.9	1285	2	Q4RXD7_TETNG	Q4rxd7	tetraodon n
373	93	5.9	1349	2	Q8WWQ4_HUMAN	Q8wwq4	homo sapien
374	93	5.9	1413	2	Q54FI2_DICDI	Q54fi2	dictyosteli
375	92.5	5.9	215	2	Q614I3_CAEBR	Q614i3	caenorhabdi
376	92.5	5.9	247	2	Q8MKY7_DROME	Q8mky7	drosophila
377	92.5	5.9	299	2	Q4HYT1_GIBZE	Q4hyt1	gibberella
378	92.5	5.9	300	1	JAM1_MOUSE	O88792	mus musculu
379	92.5	5.9	318	2	Q86HN3_DICDI	Q86hn3	dictyosteli
380	92.5	5.9	385	2	Q9NHV2_DROMI	Q9nhv2	drosophila
381	92.5	5.9	400	1	HPLN4_MOUSE	Q80wm4	mus musculu
382	92.5	5.9	446	2	Q8EMV3_OCEIH	Q8emv3	oceanobacil
383	92.5	5.9	453	2	Q5KCR5_CRYNE	Q5kcr5	cryptococcu
384	92.5	5.9	466	2	Q55IY7_CRYNE	Q55iy7	cryptococcu
385	92.5	5.9	466	2	Q5KCR4_CRYNE	Q5kcr4	cryptococcu
386	92.5	5.9	487	2	Q54G14_DICDI	Q54g14	dictyosteli
387	92.5	5.9	569	2	Q9KGV9_LISMO	Q9kgv9	listeria mo
388	92.5	5.9	604	2	Q6EAE4_LISMO	Q6eae4	listeria mo
389	92.5	5.9	623	2	O57602_ICTPU	O57602	ictalurus p
390	92.5	5.9	638	2	Q55FI4_DICDI	Q55fi4	dictyosteli
391	92.5	5.9	708	2	Q73H41_WOLPM	Q73h41	wolbachia p
392	92.5	5.9	784	2	Q7S3V6_NEUCR	Q7s3v6	neurospora
393	92.5	5.9	812	2	Q55D98_DICDI	Q55d98	dictyosteli
394	92.5	5.9	927	2	Q21811_CAEEL	Q21811	caenorhabdi
395	92.5	5.9	1491	2	Q4QDK4_LEIMA	Q4qdk4	leishmania
396	92.5	5.9	1636	1	BUD3_YEAST	P25558	saccharomyc

397	92.5	5.9	2338	2	Q759S3_ASHGO	Q759s3 ashbya goss
398	92	5.8	347	2	Q8SYW5_DROME	Q8syw5 drosophila
399	92	5.8	500	2	Q864U4_BOVIN	Q864u4 bos taurus
400	92	5.8	504	2	Q54FD8_DICDI	Q54fd8 dictyosteli
401	92	5.8	567	2	Q4P6Q2_USTMA	Q4p6q2 ustilago ma
402	92	5.8	574	2	Q58SM3_DROME	Q58sm3 drosophila
403	92	5.8	586	2	Q5B1Y4_EMENI	Q5b1y4 aspergillus
404	92	5.8	604	2	Q9JNA2_LISMO	Q9jna2 listeria mo
405	92	5.8	629	2	Q5ELR9_DROME	Q5elr9 drosophila
406	92	5.8	629	2	Q5ELS5_DROME	Q5els5 drosophila
407	92	5.8	629	2	Q5ELU4_DROME	Q5elu4 drosophila
408	92	5.8	639	2	Q6EA92_LISMO	Q6ea92 listeria mo
409	92	5.8	644	2	Q6CF33_YARLI	Q6cf33 yarrowia li
410	92	5.8	659	2	Q95XE2_CAEEL	Q95xe2 caenorhabdi
411	92	5.8	741	2	Q6CH88_YARLI	Q6ch88 yarrowia li
412	92	5.8	828	2	Q5B8I9_EMENI	Q5b8i9 aspergillus
413	92	5.8	846	2	O01699_CAEEL	O01699 caenorhabdi
414	92	5.8	907	2	Q6CTD8_KLULA	Q6ctd8 kluyveromyc
415	92	5.8	966	1	SSN6_YEAST	P14922 saccharomyc
416	92	5.8	1170	2	Q54PK2_DICDI	Q54pk2 dictyosteli
417	92	5.8	1241	2	Q75JC0_DICDI	Q75jc0 dictyosteli
418	92	5.8	1269	2	Q54CA1_DICDI	Q54ca1 dictyosteli
419	92	5.8	1343	2	Q54XT5_DICDI	Q54xt5 dictyosteli
420	92	5.8	1720	2	Q8I486_PLAF7	Q8i486 plasmodium
421	91.5	5.8	161	2	Q6CPZ3_KLULA	Q6cpz3 kluyveromyc
422	91.5	5.8	198	2	Q7WRT1_LISMO	Q7wrt1 listeria mo
423	91.5	5.8	198	2	Q7X384_LISMO	Q7x384 listeria mo
424	91.5	5.8	296	2	Q6P9X9_RAT	Q6p9x9 rattus norv
425	91.5	5.8	298	2	Q9Z0P0_RAT	Q9z0p0 rattus norv
426	91.5	5.8	300	2	Q8VC39_MOUSE	Q8vc39 mus musculu
427	91.5	5.8	305	2	Q8R183_MOUSE	Q8r183 mus musculu
428	91.5	5.8	338	2	Q6EAH4_LISMO	Q6eah4 listeria mo
429	91.5	5.8	383	2	Q5I693_HHV1	Q5i693 human herpe
430	91.5	5.8	383	2	Q702X8_HHV1	Q702x8 human herpe
431	91.5	5.8	385	2	Q9NHV1_DROMI	Q9nhv1 drosophila
432	91.5	5.8	497	2	Q8QVC5_9REOV	Q8qvc5 eyach virus
433	91.5	5.8	538	2	Q76H84_STRMU	Q76h84 streptococc
434	91.5	5.8	573	2	O69380_LISMO	O69380 listeria mo
435	91.5	5.8	579	2	Q5CYK7_CRYPV	Q5cyk7 cryptospori
436	91.5	5.8	588	2	Q5ANG0_CANAL	Q5ang0 candida alb
437	91.5	5.8	604	2	Q8GNR3_LISMO	Q8gnr3 listeria mo
438	91.5	5.8	604	2	Q6E8U4_LISMO	Q6e8u4 listeria mo
439	91.5	5.8	633	2	Q9JMY6_LISMO	Q9jmy6 listeria mo
440	91.5	5.8	633	2	Q4TVQ6_LISMO	Q4tvq6 listeria mo
441	91.5	5.8	639	1	ACTA_LISMO	P33379 listeria mo
442	91.5	5.8	639	2	Q8GNR9_LISMO	Q8gnr9 listeria mo
443	91.5	5.8	639	2	Q6E8V0_LISMO	Q6e8v0 listeria mo
444	91.5	5.8	639	2	Q6E9I4_LISMO	Q6e9i4 listeria mo
445	91.5	5.8	639	2	Q6E9X8_LISMO	Q6e9x8 listeria mo
446	91.5	5.8	639	2	Q6EA56_LISMO	Q6ea56 listeria mo
447	91.5	5.8	639	2	Q6EAA4_LISMO	Q6eaa4 listeria mo
448	91.5	5.8	639	2	Q8GNS2_LISMO	Q8gns2 listeria mo
449	91.5	5.8	639	2	Q6E8T8_LISMO	Q6e8t8 listeria mo
450	91.5	5.8	651	2	Q61YZ5_CAEBR	Q61yz5 caenorhabdi
451	91.5	5.8	860	2	Q7RZN3_NEUCR	Q7rzn3 neurospora
452	91.5	5.8	930	2	Q9YBL5_AERPE	Q9ybl5 aeropyrum p
453	91.5	5.8	1148	2	Q6CBJ2_YARLI	Q6cbj2 yarrowia li
454	91.5	5.8	1167	2	Q7RWQ7_NEUCR	Q7rwq7 neurospora
455	91.5	5.8	1481	2	Q4P152_USTMA	Q4p152 ustilago ma
456	91.5	5.8	1783	2	Q51UR4_MAGGR	Q51ur4 magnaporthe
457	91	5.8	174	2	Q7YTP1_CAEEL	Q7ytp1 caenorhabdi
458	91	5.8	198	2	Q7X3M4_LISMO	Q7x3m4 listeria mo
459	91	5.8	213	2	Q5T3I7_HUMAN	Q5t3i7 homo sapien
460	91	5.8	246	2	Q9UAV4_CAEEL	Q9uav4 caenorhabdi
461	91	5.8	316	2	Q9U9J0_TOXCA	Q9u9j0 toxocara ca
462	91	5.8	450	2	Q8CV85_OCEIH	Q8cv85 oceanobacil
463	91	5.8	488	2	Q09586_CAEEL	Q09586 caenorhabdi
464	91	5.8	576	2	Q61MD1_CAEBR	Q61md1 caenorhabdi
465	91	5.8	591	2	Q4WHJ8_ASPFU	Q4whj8 aspergillus
466	91	5.8	596	2	Q6P1T0_XENTR	Q6p1t0 xenopus tro
467	91	5.8	600	2	Q4VBE0_XENTR	Q4vbe0 xenopus tro
468	91	5.8	620	2	Q8SVR3_ENCCU	Q8svr3 encephalito
469	91	5.8	629	2	Q5ELR5_DROME	Q5elr5 drosophila
470	91	5.8	629	2	Q5ELR7_DROME	Q5elr7 drosophila
471	91	5.8	629	2	Q5ELS3_DROME	Q5els3 drosophila
472	91	5.8	639	2	Q6E964_LISMO	Q6e964 listeria mo
473	91	5.8	639	2	Q6EAI0_LISMO	Q6eai0 listeria mo
474	91	5.8	644	2	Q54D31_DICDI	Q54d31 dictyosteli
475	91	5.8	693	2	Q7PYY7_ANOGA	Q7pyy7 anopheles g
476	91	5.8	701	2	Q8ZWG4_PYRAE	Q8zwg4 pyrobaculum
477	91	5.8	730	2	Q86AZ8_DICDI	Q86az8 dictyosteli
478	91	5.8	876	2	Q619L5_CAEBR	Q619l5 caenorhabdi
479	91	5.8	1398	2	Q869T5_DICDI	Q869t5 dictyosteli
480	91	5.8	1842	2	Q4N830_THEPA	Q4n830 theileria p
481	91	5.8	2162	2	Q09515_CAEEL	Q09515 caenorhabdi
482	91	5.8	2176	2	Q54VP0_DICDI	Q54vp0 dictyosteli
483	91	5.8	4262	2	Q685J2_HUMAN	Q685j2 homo sapien
484	91	5.8	4493	2	Q685J3_HUMAN	Q685j3 homo sapien
485	90.5	5.7	306	2	Q54UW3_DICDI	Q54uw3 dictyosteli
486	90.5	5.7	336	2	Q4Z0P5_PLABE	Q4z0p5 plasmodium
487	90.5	5.7	360	2	Q4WG94_ASPFU	Q4wg94 aspergillus
488	90.5	5.7	384	2	Q9DW41_RCMVM	Q9dw41 rat cytomeg
489	90.5	5.7	385	2	Q9NHV0_DROMI	Q9nhv0 drosophila
490	90.5	5.7	385	2	Q9NHV3_DROMI	Q9nhv3 drosophila
491	90.5	5.7	406	2	Q528W4_MAGGR	Q528w4 magnaporthe
492	90.5	5.7	408	2	Q6UDF5_9HERP	Q6udf5 psittacid h
493	90.5	5.7	411	2	Q6P6W1_RAT	Q6p6w1 rattus norv
494	90.5	5.7	461	2	Q6C2X8_YARLI	Q6c2x8 yarrowia li
495	90.5	5.7	496	2	Q55D06_DICDI	Q55d06 dictyosteli
496	90.5	5.7	575	1	CH61_CUCMA	Q05045 cucurbita m
497	90.5	5.7	595	2	Q5ANA0_CANAL	Q5ana0 candida alb
498	90.5	5.7	659	2	Q59R26_CANAL	Q59r26 candida alb
499	90.5	5.7	678	2	Q54U48_DICDI	Q54u48 dictyosteli
500	90.5	5.7	690	2	Q66S18_9UROC	Q66s18 oikopleura
501	90.5	5.7	862	2	Q615W4_CAEBR	Q615w4 caenorhabdi
502	90.5	5.7	972	2	Q60Q42_CAEBR	Q60q42 caenorhabdi
503	90.5	5.7	1084	2	Q55A66_DICDI	Q55a66 dictyosteli
504	90.5	5.7	1084	2	Q86LA6_DICDI	Q86la6 dictyosteli
505	90.5	5.7	1126	2	Q5CIS2_CRYHO	Q5cis2 cryptospori
506	90.5	5.7	1175	2	Q9VRL7_DROME	Q9vrl7 drosophila
507	90.5	5.7	1400	2	Q5FBC4_DICDI	Q5fbc4 dictyosteli
508	90.5	5.7	1505	2	Q54VU4_DICDI	Q54vu4 dictyosteli
509	90.5	5.7	1711	1	NU214_DROME	Q9w1x4 drosophila
510	90.5	5.7	1976	2	Q9V9I8_DROME	Q9v9i8 drosophila
511	90.5	5.7	2300	2	Q7SFP6_NEUCR	Q7sfp6 neurospora
512	90	5.7	294	2	Q4V3X0_DROME	Q4v3x0 drosophila
513	90	5.7	296	2	Q923D3_MOUSE	Q923d3 mus musculu
514	90	5.7	388	1	VE2_HPV27	P36789 human papil
515	90	5.7	448	2	Q61C01_CAEBR	Q61c01 caenorhabdi
516	90	5.7	488	2	Q4V3Z8_DROME	Q4v3z8 drosophila
517	90	5.7	508	2	Q54BP8_DICDI	Q54bp8 dictyosteli
518	90	5.7	511	2	Q5A7R7_CANAL	Q5a7r7 candida alb
519	90	5.7	540	2	Q7SFI7_NEUCR	Q7sfi7 neurospora
520	90	5.7	560	2	Q54LP6_DICDI	Q54lp6 dictyosteli
521	90	5.7	572	2	Q58SM4_DROME	Q58sm4 drosophila
522	90	5.7	572	2	Q58SM6_DROME	Q58sm6 drosophila
523	90	5.7	598	2	Q5ELV8_DROSI	Q5elv8 drosophila
524	90	5.7	604	2	Q6E9Q0_LISMO	Q6e9q0 listeria mo
525	90	5.7	612	2	Q7QJB6_ANOGA	Q7qjb6 anopheles g
526	90	5.7	616	2	Q4WC60_ASPFU	Q4wc60 aspergillus
527	90	5.7	626	2	Q8IQJ5_DROME	Q8iqj5 drosophila
528	90	5.7	629	2	Q5ELS7_DROME	Q5els7 drosophila
529	90	5.7	629	2	Q9V3H7_DROME	Q9v3h7 drosophila
530	90	5.7	630	2	Q5ELS1_DROME	Q5els1 drosophila
531	90	5.7	639	2	Q6E8S6_LISMO	Q6e8s6 listeria mo
532	90	5.7	740	2	Q54H84_DICDI	Q54h84 dictyosteli
533	90	5.7	812	2	Q61KE5_CAEBR	Q61ke5 caenorhabdi
534	90	5.7	823	2	Q54Y28_DICDI	Q54y28 dictyosteli
535	90	5.7	877	2	Q9H3Q6_HUMAN	Q9h3q6 homo sapien
536	90	5.7	878	2	Q9H3Q7_HUMAN	Q9h3q7 homo sapien
537	90	5.7	948	2	Q86AV9_DICDI	Q86av9 d phosphati
538	90	5.7	954	2	Q610Z8_CAEBR	Q610z8 caenorhabdi
539	90	5.7	957	2	O14651_HUMAN	O14651 homo sapien
540	90	5.7	965	2	Q22286_CAEEL	Q22286 caenorhabdi
541	90	5.7	1086	2	Q54X99_DICDI	Q54x99 dictyosteli
542	90	5.7	1170	2	Q4IC26_GIBZE	Q4ic26 gibberella

543	90	5.7	1217	2	Q9UKW9_HUMAN	Q9ukw9	homo sapien
544	90	5.7	1293	2	Q4Q6D9_LEIMA	Q4q6d9	leishmania
545	90	5.7	1367	1	MUC1_YEAST	P08640	saccharomyc
546	90	5.7	1367	2	Q6LCS8_SACDI	Q6lcs8	saccharomyc
547	90	5.7	2282	2	Q9NK56_DROME	Q9nk56	drosophila
548	89.5	5.7	276	2	Q52BL6_MAGGR	Q52bl6	magnaporthe
549	89.5	5.7	305	2	Q8VBW0_MOUSE	Q8vbw0	mus musculu
550	89.5	5.7	319	1	CJ078_MOUSE	Q8bp27	mus musculu
551	89.5	5.7	326	2	Q7SCW5_NEUCR	Q7scw5	neurospora
552	89.5	5.7	359	2	Q5KCB0_CRYNE	Q5kcb0	cryptococcu
553	89.5	5.7	411	1	LAMP2_RAT	P17046	rattus norv
554	89.5	5.7	440	2	Q9P566_NEUCR	Q9p566	neurospora
555	89.5	5.7	443	2	Q6P111_BRARE	Q6p111	brachydanio
556	89.5	5.7	456	2	Q25242_LUCCU	Q25242	lucilia cup
557	89.5	5.7	471	2	Q9VMG7_DROME	Q9vmg7	drosophila
558	89.5	5.7	480	2	Q25241_LUCCU	Q25241	lucilia cup
559	89.5	5.7	492	2	Q6CGC6_YARLI	Q6cgc6	yarrowia li
560	89.5	5.7	510	2	Q6SCJ8_ASPFU	Q6scj8	aspergillus
561	89.5	5.7	548	2	Q61CS6_CAEBR	Q61cs6	caenorhabdi
562	89.5	5.7	558	2	Q4JK70_DERPT	Q4jk70	dermatophag
563	89.5	5.7	604	2	Q6E9W0_LISMO	Q6e9w0	listeria mo
564	89.5	5.7	606	2	Q5ZLR8_CHICK	Q5zlr8	gallus gall
565	89.5	5.7	659	2	Q556Y6_DICDI	Q556y6	dictyosteli
566	89.5	5.7	659	2	Q86AI8_DICDI	Q86ai8	dictyosteli
567	89.5	5.7	917	2	Q7QJI6_ANOGA	Q7qji6	anopheles g
568	89.5	5.7	1145	2	Q8JKT0_9VIRU	Q8jkt0	heliothis z
569	89.5	5.7	1368	2	Q23821_CAEVU	Q23821	caenorhabdi
570	89.5	5.7	1773	2	Q4N437_THEPA	Q4n437	theileria p
571	89.5	5.7	1816	2	Q4N6E9_THEPA	Q4n6e9	theileria p
572	89	5.7	195	2	Q9QX82_RAT	Q9qx82	rattus norv
573	89	5.7	307	1	SGS3_DROME	P02840	drosophila
574	89	5.7	369	2	Q91E39_9ALPH	Q91e39	phocid herp
575	89	5.7	392	2	Q59FZ0_HUMAN	Q59fz0	homo sapien
576	89	5.7	416	1	LAMP1_HUMAN	P11279	homo sapien
577	89	5.7	417	2	Q8WU33_HUMAN	Q8wu33	homo sapien
578	89	5.7	421	2	Q6KCA6_CANDU	Q6kca6	candida dub
579	89	5.7	422	2	Q5CNT4_CRYHO	Q5cnt4	cryptospori
580	89	5.7	429	2	P79046_9ASCO	P79046	humicola gr
581	89	5.7	477	2	Q14887_HUMAN	Q14887	homo sapien
582	89	5.7	482	2	Q6BSZ9_DEBHA	Q6bsz9	debaryomyce
583	89	5.7	503	1	NAS14_CAEEL	Q19269	caenorhabdi
584	89	5.7	589	2	Q4N7T4_THEPA	Q4n7t4	theileria p
585	89	5.7	603	2	Q6CE49_YARLI	Q6ce49	yarrowia li
586	89	5.7	648	2	Q4QGJ2_LEIMA	Q4qgj2	leishmania
587	89	5.7	666	2	Q7QXK0_GIALA	Q7qxk0	giardia lam
588	89	5.7	714	2	Q9NGW9_DICDI	Q9ngw9	dictyosteli
589	89	5.7	770	2	Q55G55_DICDI	Q55g55	dictyosteli
590	89	5.7	833	2	Q8IRC1_DROME	Q8irc1	drosophila
591	89	5.7	851	2	Q9VZI0_DROME	Q9vzi0	drosophila
592	89	5.7	860	2	Q5WNQ1_CAEBR	Q5wnq1	caenorhabdi
593	89	5.7	880	2	Q54UK3_DICDI	Q54uk3	dictyosteli
594	89	5.7	887	2	Q9I7T2_DROME	Q9i7t2	drosophila
595	89	5.7	898	2	Q8IRC0_DROME	Q8irc0	drosophila
596	89	5.7	917	2	Q4X105_ASPFU	Q4x105	aspergillus
597	89	5.7	951	2	Q9FVX8_ORYSA	Q9fvx8	oryza sativ
598	89	5.7	952	2	Q9U3P1_CAEEL	Q9u3p1	caenorhabdi
599	89	5.7	958	2	Q4WTT4_ASPFU	Q4wtt4	aspergillus
600	89	5.7	983	2	Q8IRB9_DROME	Q8irb9	drosophila
601	89	5.7	1081	2	Q59EA1_HUMAN	Q59ea1	homo sapien
602	89	5.7	1116	2	Q5AJH8_CANAL	Q5ajh8	candida alb
603	89	5.7	1473	2	Q54TV0_DICDI	Q54tv0	dictyosteli
604	89	5.7	1483	2	Q7KWU3_DICDI	Q7kwu3	dictyosteli
605	89	5.7	1493	2	Q559I7_DICDI	Q559i7	dictyosteli
606	89	5.7	1521	2	Q7Q1W8_ANOGA	Q7q1w8	anopheles g
607	89	5.7	1708	2	Q7XWZ9_ORYSA	Q7xwz9	oryza sativ
608	89	5.7	2273	2	Q63HU2_BURPS	Q63hu2	burkholderi
609	89	5.7	6994	2	Q17343_CAEEL	Q17343	caenorhabdi
610	89	5.7	6994	2	Q17490_CAEEL	Q17490	caenorhabdi
611	88.5	5.6	193	2	O23366_ARATH	O23366	arabidopsis
612	88.5	5.6	264	2	Q80XS5_MOUSE	Q80xs5	mus musculu
613	88.5	5.6	321	2	Q25939_PLAFA	Q25939	plasmodium
614	88.5	5.6	359	2	Q55JE9_CRYNE	Q55je9	cryptococcu
615	88.5	5.6	376	1	MID2_YEAST	P36027	saccharomyc
616	88.5	5.6	389	2	Q611Z9_CAEBR	Q611z9	caenorhabdi
617	88.5	5.6	448	2	Q6AQD8_DESPS	Q6aqd8	desulfotale
618	88.5	5.6	481	2	Q9VWK3_DROME	Q9vwk3	drosophila
619	88.5	5.6	494	2	Q618M1_CAEBR	Q618m1	caenorhabdi
620	88.5	5.6	518	2	Q8NJS3_CANAL	Q8njs3	candida alb
621	88.5	5.6	569	2	Q71XI0_LISMF	Q71xi0	listeria mo
622	88.5	5.6	582	2	Q8IR74_DROME	Q8ir74	drosophila
623	88.5	5.6	596	1	UBQL4_MOUSE	Q99nb8	mus musculu
624	88.5	5.6	598	2	Q9JMY5_LISMO	Q9jmy5	listeria mo
625	88.5	5.6	615	2	Q9M6E8_PHAVU	Q9m6e8	phaseolus v
626	88.5	5.6	622	2	Q58SF6_DROSI	Q58sf6	drosophila
627	88.5	5.6	653	2	Q8IJX0_PLAF7	Q8ijx0	plasmodium
628	88.5	5.6	699	2	Q6CSM7_KLULA	Q6csm7	kluyveromyc
629	88.5	5.6	721	2	Q97UG7_SULSO	Q97ug7	sulfolobus
630	88.5	5.6	722	2	O59644_SULSO	O59644	sulfolobus
631	88.5	5.6	722	2	Q6FTP4_CANGA	Q6ftp4	candida gla
632	88.5	5.6	752	2	Q52CR1_MAGGR	Q52cr1	magnaporthe
633	88.5	5.6	764	2	Q4WYI0_ASPFU	Q4wyi0	aspergillus
634	88.5	5.6	901	2	Q9H195_HUMAN	Q9h195	homo sapien
635	88.5	5.6	980	2	Q84FU6_CHLTR	Q84fu6	chlamydia t
636	88.5	5.6	980	2	Q84FU8_CHLTR	Q84fu8	chlamydia t
637	88.5	5.6	981	2	Q84FU7_CHLTR	Q84fu7	chlamydia t
638	88.5	5.6	1101	1	GUNC_CELFI	P14090	cellulomona
639	88.5	5.6	1106	2	Q4IAX5_GIBZE	Q4iax5	gibberella
640	88.5	5.6	1224	2	Q54PM6_DICDI	Q54pm6	dictyosteli
641	88.5	5.6	1230	2	Q54JY4_DICDI	Q54jy4	dictyosteli
642	88.5	5.6	1292	2	Q4RHM3_TETNG	Q4rhm3	tetraodon n
643	88.5	5.6	1346	2	Q54SH1_DICDI	Q54sh1	dictyosteli
644	88.5	5.6	2122	2	Q54R92_DICDI	Q54r92	dictyosteli
645	88	5.6	103	2	Q9TTB3_PIG	Q9ttb3	sus scrofa
646	88	5.6	161	2	Q9CVT7_MOUSE	Q9cvt7	mus musculu
647	88	5.6	302	2	Q55XK5_CRYNE	Q55xk5	cryptococcu
648	88	5.6	302	2	Q5KMC9_CRYNE	Q5kmc9	cryptococcu
649	88	5.6	347	2	Q9TZV4_PLAFA	Q9tzv4	plasmodium
650	88	5.6	362	2	Q9TZV3_PLAFA	Q9tzv3	plasmodium
651	88	5.6	382	2	Q6C971_YARLI	Q6c971	yarrowia li
652	88	5.6	385	2	Q8T8I2_DROPB	Q8t8i2	drosophila
653	88	5.6	385	2	Q8T8I4_DROPB	Q8t8i4	drosophila
654	88	5.6	385	2	Q8T8I6_DROPB	Q8t8i6	drosophila
655	88	5.6	385	2	Q8T8J0_DROPB	Q8t8j0	drosophila
656	88	5.6	385	2	Q8T8J1_DROPB	Q8t8j1	drosophila
657	88	5.6	385	2	Q8T8K3_DROPE	Q8t8k3	drosophila
658	88	5.6	447	2	Q6CCR1_YARLI	Q6ccr1	yarrowia li
659	88	5.6	449	2	Q6CWZ6_KLULA	Q6cwz6	kluyveromyc
660	88	5.6	456	2	Q9U2W2_CAEEL	Q9u2w2	caenorhabdi
661	88	5.6	487	2	Q4U479_ANOGA	Q4u479	anopheles g
662	88	5.6	543	2	Q7QK86_ANOGA	Q7qk86	anopheles g
663	88	5.6	564	2	O01627_CAEEL	O01627	caenorhabdi
664	88	5.6	577	2	Q6FSJ1_CANGA	Q6fsj1	candida gla
665	88	5.6	587	2	Q51R09_MAGGR	Q51r09	magnaporthe
666	88	5.6	588	2	Q813F9_BACCR	Q813f9	bacillus ce
667	88	5.6	601	2	Q6V6S2_DROME	Q6v6s2	drosophila
668	88	5.6	602	2	Q8YV91_ANASP	Q8yv91	anabaena sp
669	88	5.6	604	2	Q6E916_LISMO	Q6e916	listeria mo
670	88	5.6	716	2	Q9NYE4_HUMAN	Q9nye4	homo sapien
671	88	5.6	931	2	Q51LJ1_MAGGR	Q51lj1	magnaporthe
672	88	5.6	995	2	Q91638_XENLA	Q91638	xenopus lae
673	88	5.6	1051	2	Q6C1J9_YARLI	Q6c1j9	yarrowia li
674	88	5.6	1409	2	Q5ALT5_CANAL	Q5alt5	candida alb
675	88	5.6	1630	1	MSP1_PLAFK	P04932	plasmodium
676	88	5.6	1790	2	Q8I8I6_APLCA	Q8i8i6	aplysia cal
677	88	5.6	2195	2	Q4SA07_TETNG	Q4sa07	tetraodon n
678	88	5.6	5703	1	MUC5B_HUMAN	Q9hc84	homo sapien
679	87.5	5.6	147	2	O61043_TRYCR	O61043	trypanosoma
680	87.5	5.6	244	2	Q54RQ4_DICDI	Q54rq4	dictyosteli
681	87.5	5.6	283	2	Q5XUY9_ARATH	Q5xuy9	arabidopsis
682	87.5	5.6	283	2	Q9FKU2_ARATH	Q9fku2	arabidopsis
683	87.5	5.6	289	2	Q4IJR0_GIBZE	Q4ijr0	gibberella
684	87.5	5.6	299	2	Q5H2T1_XANOR	Q5h2t1	xanthomonas
685	87.5	5.6	338	2	Q6CY50_KLULA	Q6cy50	kluyveromyc
686	87.5	5.6	345	2	Q56WV8_ARATH	Q56wv8	arabidopsis
687	87.5	5.6	366	2	Q6FSI8_CANGA	Q6fsi8	candida gla
688	87.5	5.6	383	2	Q702Y9_HHV1	Q702y9	human herpe

689	87.5	5.6	442	2	Q7S2Z3_NEUCR	Q7s2z3	neurospora
690	87.5	5.6	462	2	Q8TUE0_METAC	Q8tue0	methanosarc
691	87.5	5.6	463	2	Q5A3K1_CANAL	Q5a3k1	candida alb
692	87.5	5.6	498	2	Q6FVC8_CANGA	Q6fvc8	candida gla
693	87.5	5.6	542	2	Q4V4X7_DROME	Q4v4x7	drosophila
694	87.5	5.6	555	2	Q9U6R7_DERFA	Q9u6r7	dermatophag
695	87.5	5.6	563	2	Q5LKG3_SILPO	Q5lkg3	silicibacte
696	87.5	5.6	571	2	Q4YHW1_PLABE	Q4yhw1	plasmodium
697	87.5	5.6	622	2	Q58SG2_DROSI	Q58sg2	drosophila
698	87.5	5.6	622	2	Q58SH9_DROSI	Q58sh9	drosophila
699	87.5	5.6	622	2	Q5ELQ5_DROSI	Q5elq5	drosophila
700	87.5	5.6	622	2	Q5ELQ9_DROSI	Q5elq9	drosophila
701	87.5	5.6	623	2	Q6T547_LISMO	Q6t547	listeria mo
702	87.5	5.6	625	2	Q5ELP7_DROSI	Q5elp7	drosophila
703	87.5	5.6	626	2	Q9NDD1_LEITR	Q9ndd1	leishmania
704	87.5	5.6	634	2	Q7RWB0_NEUCR	Q7rwb0	neurospora
705	87.5	5.6	639	2	Q6T548_LISMO	Q6t548	listeria mo
706	87.5	5.6	648	2	O44189_CAEEL	O44189	caenorhabdi
707	87.5	5.6	653	2	Q59YC5_CANAL	Q59yc5	candida alb
708	87.5	5.6	653	2	Q8NK55_CANAL	Q8nk55	candida alb
709	87.5	5.6	665	2	Q4IIW3_GIBZE	Q4iiw3	gibberella
710	87.5	5.6	682	2	Q60PP2_CAEBR	Q60pp2	caenorhabdi
711	87.5	5.6	717	2	Q8NAJ6_HUMAN	Q8naj6	homo sapien
712	87.5	5.6	752	2	Q8MNE2_DICDI	Q8mne2	dictyosteli
713	87.5	5.6	785	2	Q7QQI5_GIALA	Q7qqi5	giardia lam
714	87.5	5.6	825	2	Q9LZA6_ARATH	Q9lza6	arabidopsis
715	87.5	5.6	867	2	Q90X49_BRARE	Q90x49	brachydanio
716	87.5	5.6	906	2	Q8UVU1_XENLA	Q8uvu1	xenopus lae
717	87.5	5.6	908	2	Q59PF9_CANAL	Q59pf9	candida alb
718	87.5	5.6	968	2	Q4SSC4_TETNG	Q4ssc4	tetraodon n
719	87.5	5.6	971	2	Q6W3C4_CAEEL	Q6w3c4	caenorhabdi
720	87.5	5.6	989	2	Q19930_CAEEL	Q19930	caenorhabdi
721	87.5	5.6	997	1	VGNM_APMV	P38485	andean pota
722	87.5	5.6	1085	1	CASR_BOVIN	P35384	bos taurus
723	87.5	5.6	1091	1	NCAM1_CHICK	P13590	gallus gall
724	87.5	5.6	1118	2	Q550H5_DICDI	Q550h5	dictyosteli
725	87.5	5.6	1370	2	Q6C3B8_YARLI	Q6c3b8	yarrowia li
726	87.5	5.6	1799	2	Q7KUI0_DROME	Q7kui0	drosophila
727	87.5	5.6	1802	1	HKR1_YEAST	P41809	saccharomyc
728	87.5	5.6	2048	2	Q55GC1_DICDI	Q55gc1	dictyosteli
729	87.5	5.6	2314	2	Q55F23_DICDI	Q55f23	dictyosteli
730	87.5	5.6	2829	1	APC_XENLA	P70039	xenopus lae
731	87	5.5	167	2	O65742_CICAR	O65742	cicer ariet
732	87	5.5	235	2	Q63349_RAT	Q63349	rattus norv
733	87	5.5	259	2	Q70CD5_EIMTE	Q70cd5	eimeria ten
734	87	5.5	363	2	Q91YK8_MOUSE	Q91yk8	mus musculu
735	87	5.5	385	2	Q8T8J9_DROPS	Q8t8j9	drosophila
736	87	5.5	406	2	Q4I3G6_GIBZE	Q4i3g6	gibberella
737	87	5.5	442	2	Q758Q5_ASHGO	Q758q5	ashbya goss
738	87	5.5	456	2	Q5B7G2_EMENI	Q5b7g2	aspergillus
739	87	5.5	478	2	Q55RT1_CRYNE	Q55rt1	cryptococcu
740	87	5.5	484	2	Q4FKQ7_9TRYP	Q4fkq7	trypanosoma
741	87	5.5	532	2	Q4JK69_DERPT	Q4jk69	dermatophag
742	87	5.5	567	2	Q60X66_CAEBR	Q60x66	caenorhabdi
743	87	5.5	585	2	Q58SH0_DROSI	Q58sh0	drosophila
744	87	5.5	627	2	Q7RWT2_NEUCR	Q7rwt2	neurospora
745	87	5.5	639	2	Q6E8S0_LISMO	Q6e8s0	listeria mo
746	87	5.5	661	2	O13444_CLAFU	O13444	cladosporiu
747	87	5.5	686	2	Q61XJ6_CAEBR	Q61xj6	caenorhabdi
748	87	5.5	689	2	Q724Q0_LISMF	Q724q0	listeria mo
749	87	5.5	752	2	Q9YC61_AERPE	Q9yc61	aeropyrum p
750	87	5.5	841	2	Q6AX88_XENLA	Q6ax88	xenopus lae
751	87	5.5	881	2	Q8IMS9_DROME	Q8ims9	drosophila
752	87	5.5	919	2	Q51BH5_ENTHI	Q51bh5	entamoeba h
753	87	5.5	991	2	Q83UW2_CHLTR	Q83uw2	chlamydia t
754	87	5.5	991	2	Q84FV0_CHLTR	Q84fv0	chlamydia t
755	87	5.5	991	2	Q84FV1_CHLTR	Q84fv1	chlamydia t
756	87	5.5	1016	1	PMPH_CHLTR	O84880	chlamydia t
757	87	5.5	1048	2	Q9LAU3_LEGPN	Q9lau3	legionella
758	87	5.5	1055	2	Q55G65_DICDI	Q55g65	dictyosteli
759	87	5.5	1173	2	Q61A60_CAEBR	Q61a60	caenorhabdi
760	87	5.5	1246	2	Q51FG7_ENTHI	Q51fg7	entamoeba h
761	87	5.5	1447	2	Q5B4Q8_EMENI	Q5b4q8	aspergillus
762	87	5.5	1506	2	P79927_XENLA	P79927	xenopus lae
763	87	5.5	1537	1	FLO1_YEAST	P32768	saccharomyc
764	87	5.5	1537	2	Q58HH7_YEAST	Q58hh7	saccharomyc
765	87	5.5	6586	2	Q52FL1_MAGGR	Q52fl1	magnaporthe
766	86.5	5.5	197	2	Q9Z317_MOUSE	Q9z317	mus musculu
767	86.5	5.5	197	2	Q9R0L9_MOUSE	Q9r0l9	mus musculu
768	86.5	5.5	249	2	Q6BVX5_DEBHA	Q6bvx5	debaryomyce
769	86.5	5.5	277	2	Q4KMD4_BRARE	Q4kmd4	brachydanio
770	86.5	5.5	390	2	Q73JV8_TREDE	Q73jv8	treponema d
771	86.5	5.5	400	1	MUA1_XENLA	P10667	xenopus lae
772	86.5	5.5	401	2	Q6BV71_DEBHA	Q6bv71	debaryomyce
773	86.5	5.5	442	2	Q7M8Z3_WOLSU	Q7m8z3	wolinella s
774	86.5	5.5	451	2	Q6DF68_XENTR	Q6df68	xenopus tro
775	86.5	5.5	461	2	Q21004_CAEEL	Q21004	caenorhabdi
776	86.5	5.5	483	2	Q5AT96_EMENI	Q5at96	aspergillus
777	86.5	5.5	484	1	PAPO2_XENLA	P51005	xenopus lae
778	86.5	5.5	493	2	Q23330_CAEEL	Q23330	caenorhabdi
779	86.5	5.5	503	1	WSC2_YEAST	P53832	saccharomyc
780	86.5	5.5	582	2	Q58SG7_DROSI	Q58sg7	drosophila
781	86.5	5.5	582	2	Q58SG8_DROSI	Q58sg8	drosophila
782	86.5	5.5	582	2	Q58SG9_DROSI	Q58sg9	drosophila
783	86.5	5.5	582	2	Q58SH3_DROSI	Q58sh3	drosophila
784	86.5	5.5	598	2	Q5ELV4_DROSI	Q5elv4	drosophila
785	86.5	5.5	598	2	Q5ELV5_DROSI	Q5elv5	drosophila
786	86.5	5.5	598	2	Q5ELW0_DROSI	Q5elw0	drosophila
787	86.5	5.5	601	2	Q6V6S4_DROME	Q6v6s4	drosophila
788	86.5	5.5	604	2	Q6E8Z8_LISMO	Q6e8z8	listeria mo
789	86.5	5.5	604	2	Q6E928_LISMO	Q6e928	listeria mo
790	86.5	5.5	624	2	Q58SF9_DROSI	Q58sf9	drosophila
791	86.5	5.5	629	2	Q4QGJ0_LEIMA	Q4qgj0	leishmania
792	86.5	5.5	639	2	Q8GNR0_LISMO	Q8gnr0	listeria mo
793	86.5	5.5	639	2	Q6E952_LISMO	Q6e952	listeria mo
794	86.5	5.5	639	2	Q6E976_LISMO	Q6e976	listeria mo
795	86.5	5.5	681	1	VGP_MABVP	P35254	marburg vir
796	86.5	5.5	681	2	Q71VM1_9MONO	Q71vm1	lake victor
797	86.5	5.5	687	2	Q6NHU1_CORDI	Q6nhu1	corynebacte
798	86.5	5.5	733	2	Q55E25_DICDI	Q55e25	dictyosteli
799	86.5	5.5	739	1	GAG_SMRVH	P21411	squirrel mo
800	86.5	5.5	768	2	O60279_HUMAN	O60279	homo sapien
801	86.5	5.5	779	2	Q5TRJ3_ANOGA	Q5trj3	anopheles g
802	86.5	5.5	788	2	O18510_TRINI	O18510	trichoplusi
803	86.5	5.5	790	2	Q8TBZ7_HUMAN	Q8tbz7	homo sapien
804	86.5	5.5	807	2	O18511_TRINI	O18511	trichoplusi
805	86.5	5.5	838	2	Q7UNP4_RHOBA	Q7unp4	rhodopirell
806	86.5	5.5	843	2	Q4RQM0_TETNG	Q4rqm0	tetraodon n
807	86.5	5.5	853	2	Q54S28_DICDI	Q54s28	dictyosteli
808	86.5	5.5	941	2	Q9LTH0_ARATH	Q9lth0	arabidopsis
809	86.5	5.5	970	2	Q4W973_ASPFU	Q4w973	aspergillus
810	86.5	5.5	1546	2	Q80SS4_MOUSE	Q80ss4	mus musculu
811	86.5	5.5	1579	2	Q99MP1_MOUSE	Q99mp1	mus musculu
812	86.5	5.5	1683	2	Q810D4_MOUSE	Q810d4	mus musculu
813	86.5	5.5	1684	2	Q9WTQ5_MOUSE	Q9wtq5	mus musculu
814	86.5	5.5	1822	2	Q7R0W4_GIALA	Q7r0w4	giardia lam
815	86.5	5.5	1844	2	Q22579_CAEEL	Q22579	caenorhabdi
816	86.5	5.5	2546	2	Q54ER5_DICDI	Q54er5	dictyosteli
817	86.5	5.5	2781	2	Q9UIG2_HUMAN	Q9uig2	homo sapien
818	86.5	5.5	4509	2	Q54T85_DICDI	Q54t85	dictyosteli
819	86	5.5	337	2	Q5AFI4_CANAL	Q5afi4	candida alb
820	86	5.5	347	2	Q9TZV5_PLAFA	Q9tzv5	plasmodium
821	86	5.5	347	2	Q9TZV6_PLAFA	Q9tzv6	plasmodium
822	86	5.5	385	2	Q8T8K4_DROPE	Q8t8k4	drosophila
823	86	5.5	390	2	Q70LM3_PHLRA	Q70lm3	phlebia rad
824	86	5.5	390	2	Q96TS5_PHLRA	Q96ts5	phlebia rad
825	86	5.5	431	2	Q51WX9_MAGGR	Q51wx9	magnaporthe
826	86	5.5	434	2	Q872V2_NEUCR	Q872v2	neurospora
827	86	5.5	455	2	Q7VNN0_HAEDU	Q7vnn0	haemophilus
828	86	5.5	476	2	Q03996_PLACH	Q03996	plasmodium
829	86	5.5	477	2	Q86YC5_HUMAN	Q86yc5	homo sapien
830	86	5.5	495	2	Q6AK33_DESPS	Q6ak33	desulfotale
831	86	5.5	537	2	Q5AHC9_CANAL	Q5ahc9	candida alb
832	86	5.5	537	2	Q5AHQ5_CANAL	Q5ahq5	candida alb
833	86	5.5	551	1	PODXL_RABIT	Q28645	oryctolagus
834	86	5.5	572	2	Q58SM1_DROME	Q58sm1	drosophila

835	86	5.5	598	2	Q4TVQ7_LISMO	Q4tvq7 listeria mo	908	85.5	5.4	878	2	Q55GH4_DICDI	Q55gh4 dictyosteli		
836	86	5.5	604	2	Q8GNQ9_LISMO	Q8gnq9 listeria mo	909	85.5	5.4	895	2	O80973_ARATH	O80973 arabidopsis		
837	86	5.5	604	2	Q6E9N2_LISMO	Q6e9n2 listeria mo	910	85.5	5.4	935	2	Q6R8J3_BRARE	Q6r8j3 brachydanio		
838	86	5.5	625	2	Q58SG0_DROSI	Q58sg0 drosophila	911	85.5	5.4	954	2	Q55FS4_DICDI	Q55fs4 dictyosteli		
839	86	5.5	629	2	Q5ELS8_DROME	Q5els8 drosophila	912	85.5	5.4	977	2	Q6R8J2_BRARE	Q6r8j2 brachydanio		
840	86	5.5	639	2	Q6E8R4_LISMO	Q6e8r4 listeria mo	913	85.5	5.4	981	2	Q6GQI9_XENLA	Q6gqi9 xenopus lae		
841	86	5.5	697	2	Q7S009_NEUCR	Q7s009 neurospora	914	85.5	5.4	1052	2	Q91G49_IRV6	Q91g49 chilo iride		
842	86	5.5	709	2	Q4P7Y7_USTMA	Q4p7y7 ustilago ma	915	85.5	5.4	1209	2	Q4SFS8_TETNG	Q4sfs8 tetraodon n		
843	86	5.5	714	2	Q59TK9_CANAL	Q59tk9 candida alb	916	85.5	5.4	1868	2	Q5TJ69_9VIRU	Q5tj69 cacao swoll		
844	86	5.5	714	2	Q59TP1_CANAL	Q59tp1 candida alb	917	85.5	5.4	2448	2	Q8WWQ5_HUMAN	Q8wwq5 homo sapien		
845	86	5.5	734	2	Q869R9_DICDI	Q869r9 dictyosteli	918	85.5	5.4	2482	2	Q61GF0_CAEBR	Q61gf0 caenorhabdi		
846	86	5.5	750	2	Q9HFZ4_CANAL	Q9hfz4 candida alb	919	85.5	5.4	3346	2	Q822X0_CHLCV	Q822x0 chlamydophi		
847	86	5.5	780	2	Q9LK78_ARATH	Q9lk78 arabidopsis	920	85.5	5.4	4862	2	Q5RI27_BRARE	Q5ri27 brachydanio		
848	86	5.5	799	2	Q8EXF5_LEPIN	Q8exf5 leptospira	921	85.5	5.4	6995	2	Q96RK2_HUMAN	Q96rk2 homo sapien		
849	86	5.5	799	2	Q75FI7_LEPIC	Q75fi7 leptospira	922	85	5.4	172	2	Q8VC95_MOUSE	Q8vc95 mus musculu		
850	86	5.5	843	2	Q7XJ06_ORYSA	Q7xj06 oryza sativ	923	85	5.4	255	2	Q86HS8_DICDI	Q86hs8 dictyosteli		
851	86	5.5	855	2	Q55C58_DICDI	Q55c58 dictyosteli	924	85	5.4	265	2	Q9GZE5_CAEEL	Q9gze5 caenorhabdi		
852	86	5.5	866	2	Q80XL8_MOUSE	Q80xl8 mus musculu	925	85	5.4	300	2	Q95XH5_CAEEL	Q95xh5 caenorhabdi		
853	86	5.5	955	2	Q55MM6_CRYNE	Q55mm6 cryptococcu	926	85	5.4	317	2	Q8BEK4_COWPX	Q8bek4 cowpox viru		
854	86	5.5	955	2	Q5KB01_CRYNE	Q5kb01 cryptococcu	927	85	5.4	326	2	Q9VW89_DROME	Q9vw89 drosophila		
855	86	5.5	1042	2	Q59X21_CANAL	Q59x21 candida alb	928	85	5.4	343	1	HXDAA_BRARE	Q90469 brachydanio		
856	86	5.5	1080	1	UBP8_MOUSE	Q80u87 mus musculu	929	85	5.4	345	2	Q691Y8_ANOSA	Q691y8 anolis sagr		
857	86	5.5	1266	2	Q6CAR3_YARLI	Q6car3 yarrowia li	930	85	5.4	456	2	Q5R8Q6_PONPY	Q5r8q6 pongo pygma		
858	86	5.5	1266	2	Q626F7_CAEBR	Q626f7 caenorhabdi	931	85	5.4	474	2	Q4I7B2_GIBZE	Q4i7b2 gibberella		
859	86	5.5	1324	2	Q8MMQ2_DICDI	Q8mmq2 dictyosteli	932	85	5.4	477	2	Q7MR34_WOLSU	Q7mr34 wolinella s		
860	86	5.5	1609	2	Q51DL9_ENTHI	Q51dl9 entamoeba h	933	85	5.4	478	2	Q5KG84_CRYNE	Q5kg84 cryptococcu		
861	86	5.5	1674	2	Q80Z18_MOUSE	Q80z18 mus musculu	934	85	5.4	503	2	Q8VCF0_MOUSE	Q8vcf0 mus musculu		
862	86	5.5	1716	2	Q61ZV2_CAEBR	Q61zv2 caenorhabdi	935	85	5.4	510	2	Q8NJT3_KLULA	Q8njt3 kluyveromyc		
863	86	5.5	1785	2	Q25685_PLACH	Q25685 plasmodium	936	85	5.4	516	2	Q5CM29_CRYHO	Q5cm29 cryptospori		
864	86	5.5	2044	2	Q4HZP9_GIBZE	Q4hzp9 gibberella	937	85	5.4	526	2	Q51YT8_MAGGR	Q51yt8 magnaporthe		
865	86	5.5	2247	2	Q55FT4_DICDI	Q55ft4 dictyosteli	938	85	5.4	531	2	Q5TXG4_ANOGA	Q5txg4 anopheles g		
866	85.5	5.4	193	2	Q8LB00_ARATH	Q8lb00 arabidopsis	939	85	5.4	573	2	Q8H7K9_ORYSA	Q8h7k9 oryza sativ		
867	85.5	5.4	206	2	Q6TVK4_9POXV	Q6tvk4 orf virus.	940	85	5.4	576	2	Q06604_YEAST	Q06604 saccharomyc		
868	85.5	5.4	224	2	Q8KKT9_RHIET	Q8kkt9 rhizobium e	941	85	5.4	597	2	Q5AA66_CANAL	Q5aa66 candida alb		
869	85.5	5.4	269	2	Q9U9J2_TOXCA	Q9u9j2 toxocara ca	942	85	5.4	599	2	Q6C2K2_YARLI	Q6c2k2 yarrowia li		
870	85.5	5.4	271	2	Q6DGI9_BRARE	Q6dgi9 brachydanio	943	85	5.4	601	2	Q6V6S1_DROME	Q6v6s1 drosophila		
871	85.5	5.4	346	2	Q5R230_9ZYGO	Q5r230 phycomyces	944	85	5.4	612	2	Q622S9_CAEBR	Q622s9 caenorhabdi		
872	85.5	5.4	370	2	Q7KRX4_DROME	Q7krx4 drosophila	945	85	5.4	625	2	Q58SF8_DROSI	Q58sf8 drosophila		
873	85.5	5.4	378	1	FBSH_MOUSE	Q8r089 mus musculu	946	85	5.4	627	1	PKNB_LACLA	Q9cef5 lactococcus		
874	85.5	5.4	379	2	Q8I050_DROME	Q8i050 drosophila	947	85	5.4	639	2	Q6E9T0_LISMO	Q6e9t0 listeria mo		
875	85.5	5.4	390	2	Q8IGQ0_DROME	Q8igq0 drosophila	948	85	5.4	655	2	Q4SQL5_TETNG	Q4sql5 tetraodon n		
876	85.5	5.4	405	2	Q51PI1_MAGGR	Q51pi1 magnaporthe	949	85	5.4	657	2	Q54E45_DICDI	Q54e45 dictyosteli		
877	85.5	5.4	419	2	Q5TZ27_BRARE	Q5tz27 brachydanio	950	85	5.4	761	2	O22271_ARATH	O22271 arabidopsis		
878	85.5	5.4	427	2	Q4STA8_TETNG	Q4sta8 tetraodon n	951	85	5.4	782	2	Q8GX37_ARATH	Q8gx37 arabidopsis		
879	85.5	5.4	453	2	Q4IGE4_GIBZE	Q4ige4 gibberella	952	85	5.4	852	2	Q6CIA5_YARLI	Q6cia5 yarrowia li		
880	85.5	5.4	459	2	Q5WG39_BACSK	Q5wg39 bacillus cl	953	85	5.4	879	2	Q4IC17_GIBZE	Q4ic17 gibberella		
881	85.5	5.4	575	1	CH62_CUCMA	Q05046 cucurbita m	954	85	5.4	911	2	Q7KWL1_DICDI	Q7kwl1 dictyosteli		
882	85.5	5.4	585	2	Q58SG4_DROSI	Q58sg4 drosophila	955	85	5.4	927	2	Q52F88_MAGGR	Q52f88 magnaporthe		
883	85.5	5.4	595	2	Q7R2J1_GIALA	Q7r2j1 giardia lam	956	85	5.4	989	2	Q9M1E4_ARATH	Q9m1e4 arabidopsis		
884	85.5	5.4	616	2	Q8R0X0_MOUSE	Q8r0x0 mus musculu	957	85	5.4	990	2	Q91803_XENLA	Q91803 xenopus lae		
885	85.5	5.4	622	2	Q6V6D8_DROSI	Q6v6d8 drosophila	958	85	5.4	993	2	Q83TJ6_CHLTR	Q83tj6 chlamydia t		
886	85.5	5.4	622	2	Q6V6E4_DROSI	Q6v6e4 drosophila	959	85	5.4	1002	2	Q60YJ3_CAEBR	Q60yj3 caenorhabdi		
887	85.5	5.4	623	2	Q89QR8_BRAJA	Q89qr8 bradyrhizob	960	85	5.4	1004	2	Q4RRX1_TETNG	Q4rrx1 tetraodon n		
888	85.5	5.4	624	2	Q58SF2_DROSI	Q58sf2 drosophila	961	85	5.4	1013	2	Q6CKC8_KLULA	Q6ckc8 kluyveromyc		
889	85.5	5.4	624	2	Q58SG1_DROSI	Q58sg1 drosophila	962	85	5.4	1025	2	Q626Q9_CAEBR	Q626q9 caenorhabdi		
890	85.5	5.4	624	2	Q5ELN1_DROSI	Q5eln1 drosophila	963	85	5.4	1049	2	Q960E6_DROME	Q960e6 drosophila		
891	85.5	5.4	624	2	Q5ELN5_DROSI	Q5eln5 drosophila	964	85	5.4	1049	2	Q9V6L1_DROME	Q9v6l1 drosophila		
892	85.5	5.4	624	2	Q5ELN9_DROSI	Q5eln9 drosophila	965	85	5.4	1061	2	Q5RA99_PONPY	Q5ra99 pongo pygma		
893	85.5	5.4	625	2	Q9LCJ8_STAAU	Q9lcj8 staphylococ	966	85	5.4	1139	2	Q54Z39_DICDI	Q54z39 dictyosteli		
894	85.5	5.4	643	2	Q5JHI9_PYRKO	Q5jhi9 pyrococcus	967	85	5.4	1170	2	Q95011_CAEEL	Q95011 caenorhabdi		
895	85.5	5.4	649	2	O49445_ARATH	O49445 arabidopsis	968	85	5.4	1286	2	Q9VR49_DROME	Q9vr49 drosophila		
896	85.5	5.4	656	2	Q8BUE7_MOUSE	Q8bue7 mus musculu	969	85	5.4	1354	2	Q9VKA7_DROME	Q9vka7 drosophila		
897	85.5	5.4	693	2	Q54LR1_DICDI	Q54lr1 dictyosteli	970	85	5.4	1429	2	Q61Y04_CAEBR	Q61y04 caenorhabdi		
898	85.5	5.4	716	2	Q54BA1_DICDI	Q54ba1 dictyosteli	971	85	5.4	1693	2	Q51ZG9_MAGGR	Q51zg9 magnaporthe		
899	85.5	5.4	734	2	Q7S939_NEUCR	Q7s939 neurospora	972	85	5.4	1779	2	O52374_9FIRM	O52374 caldicellul		
900	85.5	5.4	746	2	Q54N84_DICDI	Q54n84 dictyosteli	973	85	5.4	17352	2	Q95YM2_PROCL	Q95ym2 procambarus		
901	85.5	5.4	780	1	LMBL3_HUMAN	Q96jm7 homo sapien	974	84.5	5.4	187	2	Q5CYR7_CRYPV	Q5cyr7 cryptospori		
902	85.5	5.4	780	2	Q4VXE1_HUMAN	Q4vxe1 homo sapien	975	84.5	5.4	220	2	Q9EQG0_MOUSE	Q9eqg0 mus musculu		
903	85.5	5.4	786	2	Q21027_CAEEL	Q21027 caenorhabdi	976	84.5	5.4	245	2	Q564Z3_CAEEL	Q564z3 caenorhabdi		
904	85.5	5.4	841	2	Q6R8J4_BRARE	Q6r8j4 brachydanio	977	84.5	5.4	250	2	Q5AP52_CANAL	Q5ap52 candida alb		
905	85.5	5.4	843	2	Q9VYH8_DROME	Q9vyh8 drosophila	978	84.5	5.4	274	2	Q54WW2_DICDI	Q54ww2 dictyosteli		
906	85.5	5.4	863	2	Q851G7_ORYSA	Q851g7 oryza sativ	979	84.5	5.4	278	2	Q51QC1_MAGGR	Q51qc1 magnaporthe		
907	85.5	5.4	866	2	Q4PDE9_USTMA	Q4pde9 ustilago ma	980	84.5	5.4	313	2	Q8BEJ1_9POXV	Q8bej1 skunkpox vi		

981	84.5	5.4	320	2	Q4SCG1_TETNG	Q4scg1	tetraodon n	1054	84	5.3	399	2	Q5MJ02_TETPY	Q5mj02	tetrahymena
982	84.5	5.4	333	2	Q60JT6_CAEBR	Q60jt6	caenorhabdi	1055	84	5.3	420	2	Q8N7W9_HUMAN	Q8n7w9	homo sapien
983	84.5	5.4	378	2	Q6FNP6_CANGA	Q6fnp6	candida gla	1056	84	5.3	420	2	Q8YMH1_ANASP	Q8ymh1	anabaena sp
984	84.5	5.4	396	2	Q51TI2_MAGGR	Q51ti2	magnaporthe	1057	84	5.3	456	1	NRX3B_BOVIN	Q28143	bos taurus
985	84.5	5.4	456	2	Q8R5M8_MOUSE	Q8r5m8	mus musculu	1058	84	5.3	464	2	Q9VX42_DROME	Q9vx42	drosophila
986	84.5	5.4	463	2	Q9JX25_NEIMA	Q9jx25	neisseria m	1059	84	5.3	475	2	Q8FQJ1_COREF	Q8fqj1	corynebacte
987	84.5	5.4	493	1	TNR8_RAT	P97525	rattus norv	1060	84	5.3	487	2	Q8E1P9_STRA5	Q8e1p9	streptococc
988	84.5	5.4	506	2	Q53QT8_HUMAN	Q53qt8	homo sapien	1061	84	5.3	487	2	Q8E764_STRA3	Q8e764	streptococc
989	84.5	5.4	522	2	Q4VAS1_HUMAN	Q4vas1	homo sapien	1062	84	5.3	543	2	Q14879_HUMAN	Q14879	homo sapien
990	84.5	5.4	524	2	Q54B97_DICDI	Q54b97	dictyosteli	1063	84	5.3	598	2	Q5ELV9_DROSI	Q5elv9	drosophila
991	84.5	5.4	532	2	Q6P7V2_MOUSE	Q6p7v2	mus musculu	1064	84	5.3	625	2	Q58SH7_DROSI	Q58sh7	drosophila
992	84.5	5.4	542	2	Q54PF2_DICDI	Q54pf2	dictyosteli	1065	84	5.3	625	2	Q5ELP1_DROSI	Q5elp1	drosophila
993	84.5	5.4	547	2	Q4R5X1_MACFA	Q4r5x1	macaca fasc	1066	84	5.3	636	1	ENV_MCFF	P15073	mink cell f
994	84.5	5.4	560	2	Q4VAS3_HUMAN	Q4vas3	homo sapien	1067	84	5.3	639	2	Q6E934_LISMO	Q6e934	listeria mo
995	84.5	5.4	562	1	NUPL_HUMAN	P52594	homo sapien	1068	84	5.3	640	2	Q55G71_DICDI	Q55g71	dictyosteli
996	84.5	5.4	562	2	Q4VAS0_HUMAN	Q4vas0	homo sapien	1069	84	5.3	641	2	Q6AJU8_DESPS	Q6aju8	desulfotale
997	84.5	5.4	566	2	Q4UKT5_RICFE	Q4ukt5	rickettsia	1070	84	5.3	648	2	Q95QX0_CAEEL	Q95qx0	caenorhabdi
998	84.5	5.4	570	2	Q6GMZ9_XENLA	Q6gmz9	xenopus lae	1071	84	5.3	662	1	MUC1_XENLA	Q05049	xenopus lae
999	84.5	5.4	582	2	Q58SG6_DROSI	Q58sg6	drosophila	1072	84	5.3	668	2	Q5B5D4_EMENI	Q5b5d4	aspergillus
1000	84.5	5.4	622	2	Q6V6E2_DROSI	Q6v6e2	drosophila	1073	84	5.3	668	2	Q4QGK4_LEIMA	Q4qgk4	leishmania
1001	84.5	5.4	624	2	Q58SF4_DROSI	Q58sf4	drosophila	1074	84	5.3	677	2	Q5B9K5_EMENI	Q5b9k5	aspergillus
1002	84.5	5.4	624	2	Q675N0_CORSU	Q675n0	cornus suec	1075	84	5.3	713	2	Q55RT5_CRYNE	Q55rt5	cryptococcu
1003	84.5	5.4	625	2	Q58SF7_DROSI	Q58sf7	drosophila	1076	84	5.3	730	2	Q6CPU9_KLULA	Q6cpu9	kluyveromyc
1004	84.5	5.4	632	2	Q5ELU2_DROME	Q5elu2	drosophila	1077	84	5.3	758	2	Q51JF4_MAGGR	Q51jf4	magnaporthe
1005	84.5	5.4	653	2	Q4P8I9_USTMA	Q4p8i9	ustilago ma	1078	84	5.3	793	2	Q8YAG7_LISMO	Q8yag7	listeria mo
1006	84.5	5.4	657	2	Q86ID0_DICDI	Q86id0	dictyosteli	1079	84	5.3	809	2	Q54J73_DICDI	Q54j73	dictyosteli
1007	84.5	5.4	658	1	SHK1_SCHPO	P50527	schizosacch	1080	84	5.3	812	2	Q5TT09_ANOGA	Q5tt09	anopheles g
1008	84.5	5.4	709	2	O16783_CAEEL	O16783	caenorhabdi	1081	84	5.3	836	2	Q56DP0_PLABE	Q56dp0	plasmodium
1009	84.5	5.4	729	2	Q51WE3_MAGGR	Q51we3	magnaporthe	1082	84	5.3	855	2	Q4P3C5_USTMA	Q4p3c5	ustilago ma
1010	84.5	5.4	773	2	Q8TGH3_9BASI	Q8tgh3	malassezia	1083	84	5.3	864	1	AT7L1_HUMAN	Q9ulk2	homo sapien
1011	84.5	5.4	803	1	IF2_COXBU	Q83bs1	coxiella bu	1084	84	5.3	880	2	Q7YU85_DROME	Q7yu85	drosophila
1012	84.5	5.4	806	2	Q9VCQ7_DROME	Q9vcq7	drosophila	1085	84	5.3	933	2	Q6ZMZ5_HUMAN	Q6zmz5	h cdna flj1
1013	84.5	5.4	814	2	Q6C247_YARLI	Q6c247	yarrowia li	1086	84	5.3	961	1	BNC1_MOUSE	O35914	mus musculu
1014	84.5	5.4	834	2	Q877B7_ASPOR	Q877b7	aspergillus	1087	84	5.3	996	1	LRP8_MOUSE	Q924x6	mus musculu
1015	84.5	5.4	931	2	Q5LHK9_BACFN	Q5lhk9	bacteroides	1088	84	5.3	1021	2	Q6CXY2_KLULA	Q6cxy2	kluyveromyc
1016	84.5	5.4	931	2	Q64YI7_BACFR	Q64yi7	bacteroides	1089	84	5.3	1075	1	FLO5_YEAST	P38894	saccharomyc
1017	84.5	5.4	956	2	Q4P0T6_USTMA	Q4p0t6	ustilago ma	1090	84	5.3	1085	2	Q5BLF7_BRARE	Q5blf7	brachydanio
1018	84.5	5.4	956	2	Q4SFS4_TETNG	Q4sfs4	tetraodon n	1091	84	5.3	1331	1	MANB_CALSA	P22533	caldocellum
1019	84.5	5.4	1047	2	Q874L3_CANAL	Q874l3	candida alb	1092	84	5.3	1343	2	Q960V6_DROME	Q960v6	drosophila
1020	84.5	5.4	1057	2	Q5KE83_CRYNE	Q5ke83	cryptococcu	1093	84	5.3	1343	2	Q9W2G6_DROME	Q9w2g6	drosophila
1021	84.5	5.4	1102	2	Q08964_YEAST	Q08964	saccharomyc	1094	84	5.3	1362	2	Q9V294_PYRAB	Q9v294	pyrococcus
1022	84.5	5.4	1103	2	Q6CA70_YARLI	Q6ca70	yarrowia li	1095	84	5.3	1366	2	Q86AM2_DICDI	Q86am2	dictyosteli
1023	84.5	5.4	1161	1	DAN4_YEAST	P47179	saccharomyc	1096	84	5.3	1601	2	Q54L90_DICDI	Q54l90	dictyosteli
1024	84.5	5.4	1186	2	Q54I94_DICDI	Q54i94	dictyosteli	1097	84	5.3	1645	2	Q9U263_CAEEL	Q9u263	caenorhabdi
1025	84.5	5.4	1189	2	Q54CM2_DICDI	Q54cm2	dictyosteli	1098	84	5.3	1649	2	Q54LW8_DICDI	Q54lw8	dictyosteli
1026	84.5	5.4	1218	2	Q54YZ6_DICDI	Q54yz6	dictyosteli	1099	84	5.3	1832	2	O96503_CRYPV	O96503	cryptospori
1027	84.5	5.4	1355	2	Q86AM1_DICDI	Q86am1	dictyosteli	1100	84	5.3	2044	2	Q55CR5_DICDI	Q55cr5	dictyosteli
1028	84.5	5.4	1380	2	Q556L7_DICDI	Q556l7	dictyosteli	1101	84	5.3	2215	2	Q8IIZ6_PLAF7	Q8iiz6	plasmodium
1029	84.5	5.4	1420	2	Q4FWR7_LEIMA	Q4fwr7	leishmania	1102	84	5.3	2233	2	Q7PRT5_ANOGA	Q7prt5	anopheles g
1030	84.5	5.4	1629	2	Q4IB96_GIBZE	Q4ib96	gibberella	1103	84	5.3	2306	2	Q4WYG2_ASPFU	Q4wyg2	aspergillus
1031	84.5	5.4	1743	2	Q8I1L9_PLAVI	Q8il19	plasmodium	1104	84	5.3	2447	2	Q4RIS7_TETNG	Q4ris7	tetraodon n
1032	84.5	5.4	1827	2	Q4Y6M8_PLACH	Q4y6m8	plasmodium	1105	83.5	5.3	203	2	Q4VHF5_9MONO	Q4vhf5	bovine resp
1033	84.5	5.4	1878	2	Q6CPZ4_KLULA	Q6cpz4	kluyveromyc	1106	83.5	5.3	216	2	Q28501_MACMU	Q28501	macaca mula
1034	84.5	5.4	2163	2	Q61TS1_CAEBR	Q61ts1	caenorhabdi	1107	83.5	5.3	274	2	Q9EX24_STRCO	Q9ex24	streptomyce
1035	84.5	5.4	2180	2	Q9VAS8_DROME	Q9vas8	drosophila	1108	83.5	5.3	279	2	Q14888_HUMAN	Q14888	homo sapien
1036	84.5	5.4	2205	2	Q54C75_DICDI	Q54c75	dictyosteli	1109	83.5	5.3	292	2	O68668_BACME	O68668	bacillus me
1037	84.5	5.4	2206	2	Q4REQ4_TETNG	Q4req4	tetraodon n	1110	83.5	5.3	306	2	Q88V34_LACPL	Q88v34	lactobacill
1038	84.5	5.4	2481	2	Q7A4B1_STAAN	Q7a4b1	staphylococ	1111	83.5	5.3	306	2	Q9QYL4_MOUSE	Q9qyl4	mus musculu
1039	84.5	5.4	2481	2	Q99QR6_STAAM	Q99qr6	staphylococ	1112	83.5	5.3	385	2	Q8T8L3_DROMI	Q8t8l3	drosophila
1040	84.5	5.4	22152	2	Q8WXI7_HUMAN	Q8wxi7	homo sapien	1113	83.5	5.3	385	2	Q83NC5_TROW8	Q83nc5	tropheryma
1041	84	5.3	197	2	Q54GR3_DICDI	Q54gr3	dictyosteli	1114	83.5	5.3	405	2	Q95XV0_CAEEL	Q95xv0	caenorhabdi
1042	84	5.3	259	2	Q9N3B9_CAEEL	Q9n3b9	caenorhabdi	1115	83.5	5.3	446	2	Q9Y849_KLULA	Q9y849	kluyveromyc
1043	84	5.3	262	2	P74577_SYNY3	P74577	synechocyst	1116	83.5	5.3	448	2	Q83FT5_TROWT	Q83ft5	tropheryma
1044	84	5.3	305	2	Q4WUZ7_ASPFU	Q4wuz7	aspergillus	1117	83.5	5.3	455	2	Q4INK6_GIBZE	Q4ink6	gibberella
1045	84	5.3	309	2	Q63549_RAT	Q63549	rattus norv	1118	83.5	5.3	476	2	Q7SEJ2_NEUCR	Q7sej2	neurospora
1046	84	5.3	335	2	Q9C7W2_ARATH	Q9c7w2	arabidopsis	1119	83.5	5.3	476	2	Q6AYP5_RAT	Q6ayp5	rattus norv
1047	84	5.3	359	1	MTDH_MEDSA	O82515	medicago sa	1120	83.5	5.3	498	1	TNR8_MOUSE	Q60846	mus musculu
1048	84	5.3	359	2	Q53X16_MEDSA	Q53x16	medicago sa	1121	83.5	5.3	498	2	Q6C977_YARLI	Q6c977	yarrowia li
1049	84	5.3	376	2	Q54N82_DICDI	Q54n82	dictyosteli	1122	83.5	5.3	575	2	Q58SM2_DROME	Q58sm2	drosophila
1050	84	5.3	385	2	Q8T8I3_DROPB	Q8t8i3	drosophila	1123	83.5	5.3	585	2	Q5SE80_9MONO	Q5se80	avian pneum
1051	84	5.3	385	2	Q8T8I5_DROPB	Q8t8i5	drosophila	1124	83.5	5.3	585	2	Q5SE81_9MONO	Q5se81	avian pneum
1052	84	5.3	385	2	Q8T8K2_DROPE	Q8t8k2	drosophila	1125	83.5	5.3	623	2	Q7XND3_ORYSA	Q7xnd3	oryza sativ
1053	84	5.3	385	2	Q8T8L0_DROPE	Q8t8l0	drosophila	1126	83.5	5.3	624	2	Q58SF5_DROSI	Q58sf5	drosophila

1127	83.5	5.3	624	2	Q5ELP3_DROSI	Q5elp3 drosophila	1200	83	5.3	601	2	Q5VYA1_HUMAN	Q5vya1 homo sapien		
1128	83.5	5.3	624	2	Q5VFJ5_9ASTE	Q5vfj5 cornus cf.	1201	83	5.3	605	1	WSC4_YEAST	P38739 saccharomyc		
1129	83.5	5.3	632	2	Q5ELT8_DROME	Q5elt8 drosophila	1202	83	5.3	632	2	Q5ELU0_DROME	Q5elu0 drosophila		
1130	83.5	5.3	636	2	Q66HZ5_BRARE	Q66hz5 brachydanio	1203	83	5.3	632	2	Q5ELU8_DROME	Q5elu8 drosophila		
1131	83.5	5.3	641	2	Q86SD2_CIOIN	Q86sd2 ciona intes	1204	83	5.3	639	2	Q6E8Z2_LISMO	Q6e8z2 listeria mo		
1132	83.5	5.3	669	2	Q7EZY9_ORYSA	Q7ezy9 oryza sativ	1205	83	5.3	653	1	NUMB_MOUSE	Q9qzs3 mus musculu		
1133	83.5	5.3	674	2	Q6APL0_DESPS	Q6apl0 desulfotale	1206	83	5.3	661	2	Q9V8S2_DROME	Q9v8s2 drosophila		
1134	83.5	5.3	789	2	Q57ZE5_9TRYP	Q57ze5 trypanosoma	1207	83	5.3	679	2	Q59DM1_CAEEL	Q59dm1 caenorhabdi		
1135	83.5	5.3	791	2	Q66VC3_9ALPH	Q66vc3 equid herpe	1208	83	5.3	737	1	KNS1_YEAST	P32350 saccharomyc		
1136	83.5	5.3	800	2	Q8TFG4_SCHPO	Q8tfg4 schizosacch	1209	83	5.3	762	2	Q86AG3_DICDI	Q86ag3 dictyosteli		
1137	83.5	5.3	812	2	Q86AW3_DICDI	Q86aw3 dictyosteli	1210	83	5.3	769	2	Q17921_CAEEL	Q17921 caenorhabdi		
1138	83.5	5.3	822	2	Q54Z52_DICDI	Q54z52 dictyosteli	1211	83	5.3	771	2	Q4WCD2_ASPFU	Q4wcd2 aspergillus		
1139	83.5	5.3	838	2	Q90YM1_BRARE	Q90ym1 brachydanio	1212	83	5.3	786	2	Q9FDM5_STRAG	Q9fdm5 streptococc		
1140	83.5	5.3	899	2	Q58CJ5_DROME	Q58cj5 drosophila	1213	83	5.3	794	2	Q55CQ4_DICDI	Q55cq4 dictyosteli		
1141	83.5	5.3	915	2	Q54BC9_DICDI	Q54bc9 dictyosteli	1214	83	5.3	797	1	VGLX_EHV1B	P28968 equine herp		
1142	83.5	5.3	935	2	Q9VGN4_DROME	Q9vgn4 drosophila	1215	83	5.3	806	2	Q5R6R3_PONPY	Q5r6r3 pongo pygma		
1143	83.5	5.3	984	2	Q4UEB9_THEAN	Q4ueb9 theileria a	1216	83	5.3	814	2	Q55AJ1_DICDI	Q55aj1 dictyosteli		
1144	83.5	5.3	1043	2	Q97E41_CLOAB	Q97e41 clostridium	1217	83	5.3	826	2	Q8V0L5_9ALPH	Q8v0l5 equid herpe		
1145	83.5	5.3	1056	2	Q55P74_CRYNE	Q55p74 cryptococcu	1218	83	5.3	832	2	Q60J61_CAEBR	Q60j61 caenorhabdi		
1146	83.5	5.3	1153	2	Q6A1Q0_DROME	Q6a1q0 drosophila	1219	83	5.3	858	2	Q9H8D9_HUMAN	Q9h8d9 homo sapien		
1147	83.5	5.3	1214	2	Q54LU4_DICDI	Q54lu4 dictyosteli	1220	83	5.3	866	1	VGLX_EHV1V	Q6s6w0 equine herp		
1148	83.5	5.3	1255	2	Q54HF3_DICDI	Q54hf3 dictyosteli	1221	83	5.3	866	2	O39781_9ALPH	O39781 equid herpe		
1149	83.5	5.3	1286	2	Q9TXR6_CAEEL	Q9txr6 caenorhabdi	1222	83	5.3	867	2	O39782_9ALPH	O39782 equid herpe		
1150	83.5	5.3	1570	2	Q61L27_CAEBR	Q61l27 caenorhabdi	1223	83	5.3	904	2	Q5SW65_HUMAN	Q5sw65 homo sapien		
1151	83.5	5.3	1589	2	Q54I34_DICDI	Q54i34 dictyosteli	1224	83	5.3	955	2	Q5SQZ9_HUMAN	Q5sqz9 homo sapien		
1152	83.5	5.3	1607	2	Q6CDM9_YARLI	Q6cdm9 yarrowia li	1225	83	5.3	963	1	LRP8_HUMAN	Q14114 homo sapien		
1153	83.5	5.3	1765	2	Q54WL2_DICDI	Q54wl2 dictyosteli	1226	83	5.3	963	2	Q5SW67_HUMAN	Q5sw67 homo sapien		
1154	83.5	5.3	1820	2	Q54F55_DICDI	Q54f55 dictyosteli	1227	83	5.3	985	2	Q5KL22_CRYNE	Q5kl22 cryptococcu		
1155	83.5	5.3	1855	2	Q4L3P2_STAHJ	Q4l3p2 staphylococ	1228	83	5.3	985	2	Q55V60_CRYNE	Q55v60 cryptococcu		
1156	83.5	5.3	2623	2	Q54SZ1_DICDI	Q54sz1 dictyosteli	1229	83	5.3	1002	2	Q6CBD5_YARLI	Q6cbd5 yarrowia li		
1157	83.5	5.3	2656	2	Q4UEK8_THEAN	Q4uek8 theileria a	1230	83	5.3	1030	2	Q7QV30_GIALA	Q7qv30 giardia lam		
1158	83.5	5.3	2764	2	Q7Z7D6_HUMAN	Q7z7d6 homo sapien	1231	83	5.3	1069	2	Q519R3_ENTHI	Q519r3 entamoeba h		
1159	83.5	5.3	3026	2	Q8ILS9_PLAF7	Q8ils9 plasmodium	1232	83	5.3	1080	2	Q510Y4_ENTHI	Q510y4 entamoeba h		
1160	83.5	5.3	3372	2	Q864S8_FELCA	Q864s8 felis silve	1233	83	5.3	1126	2	Q8E6U1_STRA3	Q8e6u1 streptococc		
1161	83.5	5.3	5179	1	MUC2_HUMAN	Q02817 homo sapien	1234	83	5.3	1183	2	Q8GCD1_CHLAU	Q8gcd1 chloroflexu		
1162	83	5.3	197	2	Q8JL62_GVCF	Q8jl62 choristoneu	1235	83	5.3	1184	2	Q4IHX0_GIBZE	Q4ihx0 gibberella		
1163	83	5.3	198	2	Q7QB72_ANOGA	Q7qb72 anopheles g	1236	83	5.3	1221	2	Q4X1D8_ASPFU	Q4x1d8 aspergillus		
1164	83	5.3	207	2	Q4X0I5_ASPFU	Q4x0i5 aspergillus	1237	83	5.3	1265	2	Q9P2G7_HUMAN	Q9p2g7 homo sapien		
1165	83	5.3	257	2	Q54HH8_DICDI	Q54hh8 dictyosteli	1238	83	5.3	1266	2	Q4X245_ASPFU	Q4x245 aspergillus		
1166	83	5.3	262	2	Q7PRG9_ANOGA	Q7prg9 anopheles g	1239	83	5.3	1377	2	Q54ND2_DICDI	Q54nd2 dictyosteli		
1167	83	5.3	277	2	Q5A5U6_CANAL	Q5a5u6 candida alb	1240	83	5.3	1458	2	Q54PJ4_DICDI	Q54pj4 dictyosteli		
1168	83	5.3	291	2	Q6QPG5_9ADEN	Q6qpg5 simian aden	1241	83	5.3	1646	2	Q5CFZ6_CRYHO	Q5cfz6 cryptospori		
1169	83	5.3	309	2	Q6IEL3_ORYSA	Q6iel3 oryza sativ	1242	83	5.3	1686	2	Q7RZE6_NEUCR	Q7rze6 neurospora		
1170	83	5.3	309	2	Q7XNY3_ORYSA	Q7xny3 oryza sativ	1243	83	5.3	2081	2	Q5SQZ8_HUMAN	Q5sqz8 homo sapien		
1171	83	5.3	314	2	Q9H8R7_HUMAN	Q9h8r7 homo sapien	1244	83	5.3	2162	2	Q8N3U0_HUMAN	Q8n3u0 homo sapien		
1172	83	5.3	316	2	Q8TD14_HUMAN	Q8td14 homo sapien	1245	83	5.3	2210	2	Q7Z3E7_HUMAN	Q7z3e7 homo sapien		
1173	83	5.3	337	2	Q7Z5K8_HUMAN	Q7z5k8 homo sapien	1246	83	5.3	2478	2	Q9LCH2_STAAU	Q9lch2 staphylococ		
1174	83	5.3	342	2	Q54LV1_DICDI	Q54lv1 dictyosteli	1247	83	5.3	2478	2	Q9RL69_STAAU	Q9rl69 staphylococ		
1175	83	5.3	362	2	Q6CGU2_YARLI	Q6cgu2 yarrowia li	1248	83	5.3	2478	2	Q5HE44_STAAC	Q5he44 staphylococ		
1176	83	5.3	378	2	Q8SXS5_DROME	Q8sxs5 drosophila	1249	83	5.3	3300	2	Q4N127_THEPA	Q4n127 theileria p		
1177	83	5.3	382	2	Q9XZZ8_LITSI	Q9xzz8 litomosoide	1250	83	5.3	6011	2	Q4U447_POLCB	Q4u447 polyangium		
1178	83	5.3	385	2	Q8T8K5_DROPE	Q8t8k5 drosophila	1251	82.5	5.2	184	2	Q7PRM2_ANOGA	Q7prm2 anopheles g		
1179	83	5.3	409	1	RD23B_HUMAN	P54727 homo sapien	1252	82.5	5.2	197	2	Q26878_TRYCR	Q26878 trypanosoma		
1180	83	5.3	409	2	Q53F10_HUMAN	Q53f10 homo sapien	1253	82.5	5.2	231	2	Q86LC2_9CNID	Q86lc2 zoanthus sp		
1181	83	5.3	410	2	Q5AYD3_EMENI	Q5ayd3 aspergillus	1254	82.5	5.2	252	2	Q6GZ06_9MONO	Q6gz06 avian pneum		
1182	83	5.3	419	2	Q8TD11_HUMAN	Q8td11 homo sapien	1255	82.5	5.2	258	2	Q7SGP8_NEUCR	Q7sgp8 neurospora		
1183	83	5.3	422	2	Q8TD13_HUMAN	Q8td13 homo sapien	1256	82.5	5.2	286	2	Q7SAZ7_NEUCR	Q7saz7 neurospora		
1184	83	5.3	463	2	O42665_SCHPO	O42665 schizosacch	1257	82.5	5.2	308	2	Q7XA59_LILLO	Q7xa59 lilium long		
1185	83	5.3	485	2	Q9V8B0_DROME	Q9v8b0 drosophila	1258	82.5	5.2	326	2	Q9NFX5_CERCA	Q9nfx5 ceratitis c		
1186	83	5.3	487	2	Q4UHA9_THEAN	Q4uha9 theileria a	1259	82.5	5.2	346	2	Q5CE07_CRYHO	Q5ce07 cryptospori		
1187	83	5.3	512	2	Q4I756_GIBZE	Q4i756 gibberella	1260	82.5	5.2	346	2	Q52J88_9SAUR	Q52j88 heteronotia		
1188	83	5.3	542	2	Q54SA9_DICDI	Q54sa9 dictyosteli	1261	82.5	5.2	346	2	Q52J76_9SAUR	Q52j76 heteronotia		
1189	83	5.3	547	2	Q623V9_CAEBR	Q623v9 caenorhabdi	1262	82.5	5.2	383	1	VE2_HPV57	P22155 human papil		
1190	83	5.3	552	2	Q4N6B9_THEPA	Q4n6b9 theileria p	1263	82.5	5.2	389	2	Q64BB8_9ARCH	Q64bb8 uncultured		
1191	83	5.3	559	2	Q9VN36_DROME	Q9vn36 drosophila	1264	82.5	5.2	389	2	Q6GXX0_9VIRU	Q6gxx0 swine hepat		
1192	83	5.3	564	2	Q5CQC1_CRYPV	Q5cqc1 cryptospori	1265	82.5	5.2	389	2	Q6GXX2_9VIRU	Q6gxx2 swine hepat		
1193	83	5.3	585	2	Q58SG3_DROSI	Q58sg3 drosophila	1266	82.5	5.2	389	2	Q6GXX3_9VIRU	Q6gxx3 swine hepat		
1194	83	5.3	585	2	Q58SG5_DROSI	Q58sg5 drosophila	1267	82.5	5.2	391	2	Q54XF0_DICDI	Q54xf0 dictyosteli		
1195	83	5.3	585	2	Q58SH2_DROSI	Q58sh2 drosophila	1268	82.5	5.2	400	2	Q9SQF7_BRAJU	Q9sqf7 brassica ju		
1196	83	5.3	599	2	Q5ELY7_DROME	Q5ely7 drosophila	1269	82.5	5.2	416	2	Q9K8G4_BACHD	Q9k8g4 bacillus ha		
1197	83	5.3	599	2	Q5ELY8_DROME	Q5ely8 drosophila	1270	82.5	5.2	425	2	Q54VC3_DICDI	Q54vc3 dictyosteli		
1198	83	5.3	600	2	Q59F94_HUMAN	Q59f94 homo sapien	1271	82.5	5.2	452	2	Q6CE56_YARLI	Q6ce56 yarrowia li		
1199	83	5.3	601	1	UBQL4_HUMAN	Q9nrr5 homo sapien	1272	82.5	5.2	456	1	Y883_HAEIN	P44917 haemophilus		

1273	82.5	5.2	456	2	Q4QM25_HAEI8	Q4qm25	haemophilus
1274	82.5	5.2	459	2	Q55SZ8_CRYNE	Q55sz8	cryptococcu
1275	82.5	5.2	464	2	Q9C247_NEUCR	Q9c247	neurospora
1276	82.5	5.2	465	2	Q84DR0_LISMO	Q84dr0	listeria mo
1277	82.5	5.2	508	2	Q6VNX4_DROSA	Q6vnx4	drosophila
1278	82.5	5.2	517	2	Q5AF50_CANAL	Q5af50	candida alb
1279	82.5	5.2	540	1	CH60_STRAP	Q8kj20	streptococc
1280	82.5	5.2	540	2	Q7UPM2_RHOBA	Q7upm2	rhodopirell
1281	82.5	5.2	569	2	Q9SL10_ARATH	Q9sl10	arabidopsis
1282	82.5	5.2	582	2	Q54W91_DICDI	Q54w91	dictyosteli
1283	82.5	5.2	598	2	Q5ELW5_DROSI	Q5elw5	drosophila
1284	82.5	5.2	599	2	Q5ELY0_DROME	Q5ely0	drosophila
1285	82.5	5.2	602	2	Q4V707_DROME	Q4v707	drosophila
1286	82.5	5.2	607	2	Q8GNR4_LISMO	Q8gnr4	listeria mo
1287	82.5	5.2	623	2	Q5LYX7_STRT1	Q5lyx7	streptococc
1288	82.5	5.2	623	2	Q5M3J0_STRT2	Q5m3j0	streptococc
1289	82.5	5.2	624	2	Q5VFJ4_CORSU	Q5vfj4	cornus suec
1290	82.5	5.2	624	2	Q5VFJ6_CORSU	Q5vfj6	cornus suec
1291	82.5	5.2	624	2	Q5VFJ7_CORSU	Q5vfj7	cornus suec
1292	82.5	5.2	624	2	Q5VFJ9_9ASTE	Q5vfj9	cornus unal
1293	82.5	5.2	624	2	Q5VFK1_9ASTE	Q5vfk1	cornus cf.
1294	82.5	5.2	624	2	Q675N1_CORSU	Q675n1	cornus suec
1295	82.5	5.2	635	2	O66065_FIBSU	O66065	fibrobacter
1296	82.5	5.2	639	2	Q6E910_LISMO	Q6e910	listeria mo
1297	82.5	5.2	639	2	Q6E940_LISMO	Q6e940	listeria mo
1298	82.5	5.2	641	2	Q5KHD0_CRYNE	Q5khd0	cryptococcu
1299	82.5	5.2	646	2	Q4J6E4_SULAC	Q4j6e4	sulfolobus
1300	82.5	5.2	686	2	Q8NVE4_STAAW	Q8nve4	staphylococ
1301	82.5	5.2	698	2	Q74LM8_LACJO	Q74lm8	lactobacill
1302	82.5	5.2	711	2	Q7YYX9_CRYPV	Q7yyx9	cryptospori
1303	82.5	5.2	726	1	NFI1_YEAST	Q12216	saccharomyc
1304	82.5	5.2	728	2	Q7NB51_MYCGA	Q7nb51	mycoplasma
1305	82.5	5.2	782	2	Q6CNV3_KLULA	Q6cnv3	kluyveromyc
1306	82.5	5.2	790	1	ADA30_HUMAN	Q9ukf2	homo sapien
1307	82.5	5.2	790	2	Q5T3X6_HUMAN	Q5t3x6	homo sapien
1308	82.5	5.2	808	2	Q8I123_CAEEL	Q8i123	caenorhabdi
1309	82.5	5.2	825	2	Q03088_YEAST	Q03088	saccharomyc
1310	82.5	5.2	833	2	Q602T7_METCA	Q602t7	methylococc
1311	82.5	5.2	848	2	Q6GP20_XENLA	Q6gp20	xenopus lae
1312	82.5	5.2	871	1	POB1_SCHPO	O74653	schizosacch
1313	82.5	5.2	876	2	Q6XLI5_BRARE	Q6xli5	brachydanio
1314	82.5	5.2	896	2	Q52B52_MAGGR	Q52b52	magnaporthe
1315	82.5	5.2	988	2	Q8UVU2_XENLA	Q8uvu2	xenopus lae
1316	82.5	5.2	1042	2	Q54IH7_DICDI	Q54ih7	dictyosteli
1317	82.5	5.2	1091	2	Q7SDT8_NEUCR	Q7sdt8	neurospora
1318	82.5	5.2	1124	2	Q50XX8_ENTHI	Q50xx8	entamoeba h
1319	82.5	5.2	1163	2	Q7PY32_ANOGA	Q7py32	anopheles g
1320	82.5	5.2	1167	2	Q54CK8_DICDI	Q54ck8	dictyosteli
1321	82.5	5.2	1181	2	Q52A92_MAGGR	Q52a92	magnaporthe
1322	82.5	5.2	1206	1	FMN1B_MOUSE	Q05859	mus musculu
1323	82.5	5.2	1258	2	Q4HVR5_GIBZE	Q4hvr5	gibberella
1324	82.5	5.2	1258	2	Q86IA2_DICDI	Q86ia2	dictyosteli
1325	82.5	5.2	1259	2	Q614L3_CAEBR	Q614l3	caenorhabdi
1326	82.5	5.2	1260	2	Q55G51_DICDI	Q55g51	dictyosteli
1327	82.5	5.2	1261	2	Q7R2F4_GIALA	Q7r2f4	giardia lam
1328	82.5	5.2	1267	2	Q54VU8_DICDI	Q54vu8	dictyosteli
1329	82.5	5.2	1343	2	Q61MH3_CAEBR	Q61mh3	caenorhabdi
1330	82.5	5.2	1371	2	Q9VU22_DROME	Q9vu22	drosophila
1331	82.5	5.2	1383	2	Q5B1U5_EMENI	Q5b1u5	aspergillus
1332	82.5	5.2	1460	1	PMPC_CHLMU	Q9pjy1	chlamydia m
1333	82.5	5.2	1468	1	FMN1A_MOUSE	Q05860	mus musculu
1334	82.5	5.2	1472	2	Q6V9R4_STRPU	Q6v9r4	strongyloce
1335	82.5	5.2	1478	1	LPHN2_BOVIN	O97817	bos taurus
1336	82.5	5.2	1809	2	Q4Q8Z9_LEIMA	Q4q8z9	leishmania
1337	82.5	5.2	1851	2	Q9ESP3_RAT	Q9esp3	rattus norv
1338	82.5	5.2	1969	2	Q7SEZ5_NEUCR	Q7sez5	neurospora
1339	82.5	5.2	2311	1	ROS_CHICK	P08941	gallus gall
1340	82.5	5.2	2381	2	Q54QC0_DICDI	Q54qc0	dictyosteli
1341	82.5	5.2	4483	2	Q51QB7_MAGGR	Q51qb7	magnaporthe
1342	82	5.2	166	2	Q5IE00_PINTA	Q5ie00	pinus taeda
1343	82	5.2	166	2	Q5IE20_PINTA	Q5ie20	pinus taeda
1344	82	5.2	166	2	Q56VT9_9STRA	Q56vt9	pythium aph
1345	82	5.2	198	2	Q4WAE1_ASPFU	Q4wae1	aspergillus
1346	82	5.2	208	2	Q8IWS2_HUMAN	Q8iws2	homo sapien
1347	82	5.2	208	2	Q8N131_HUMAN	Q8n131	homo sapien
1348	82	5.2	226	2	Q5A1Y4_CANAL	Q5a1y4	candida alb
1349	82	5.2	235	2	Q5TM43_MACMU	Q5tm43	macaca mula
1350	82	5.2	236	2	Q9LM00_PINTA	Q9lm00	pinus taeda
1351	82	5.2	250	2	Q8FSI6_COREF	Q8fsi6	corynebacte
1352	82	5.2	255	2	Q8I1N1_DROER	Q8i1n1	drosophila
1353	82	5.2	282	2	Q9FSR0_ORYSA	Q9fsr0	oryza sativ
1354	82	5.2	288	2	Q4YH55_PLABE	Q4yh55	plasmodium
1355	82	5.2	301	2	Q4I1K5_GIBZE	Q4i1k5	gibberella
1356	82	5.2	302	2	Q4I5S3_GIBZE	Q4i5s3	gibberella
1357	82	5.2	311	2	Q55LZ4_CRYNE	Q55lz4	cryptococcu
1358	82	5.2	311	2	Q5K8S4_CRYNE	Q5k8s4	cryptococcu
1359	82	5.2	323	2	Q9W1I7_DROME	Q9w1i7	drosophila
1360	82	5.2	338	2	Q8T8J5_DROPS	Q8t8j5	drosophila
1361	82	5.2	339	2	Q9VUX8_DROME	Q9vux8	drosophila
1362	82	5.2	345	2	Q4FKI2_9TRYP	Q4fki2	trypanosoma
1363	82	5.2	345	2	Q690W2_ANOSA	Q690w2	anolis sagr
1364	82	5.2	361	2	Q514P3_ENTHI	Q514p3	entamoeba h
1365	82	5.2	367	2	Q59KD1_CANAL	Q59kd1	candida alb
1366	82	5.2	385	2	Q8T8K9_DROPE	Q8t8k9	drosophila
1367	82	5.2	385	2	Q8T8L2_DROPE	Q8t8l2	drosophila
1368	82	5.2	388	2	Q60KQ3_CAEBR	Q60kq3	caenorhabdi
1369	82	5.2	389	2	O76573_CAEEL	O76573	caenorhabdi
1370	82	5.2	392	2	Q5A484_CANAL	Q5a484	candida alb
1371	82	5.2	397	2	Q55DL3_DICDI	Q55dl3	dictyosteli
1372	82	5.2	410	2	Q4R5B5_MACFA	Q4r5b5	macaca fasc
1373	82	5.2	466	2	Q4PCZ4_USTMA	Q4pcz4	ustilago ma
1374	82	5.2	475	2	Q50ST5_ENTHI	Q50st5	entamoeba h
1375	82	5.2	477	1	MYBPH_HUMAN	Q13203	homo sapien
1376	82	5.2	479	2	Q61AU9_CAEBR	Q61au9	caenorhabdi
1377	82	5.2	483	2	Q9W4M2_DROME	Q9w4m2	drosophila
1378	82	5.2	486	2	Q84DR1_LISMO	Q84dr1	listeria mo
1379	82	5.2	490	2	Q7PV84_ANOGA	Q7pv84	anopheles g
1380	82	5.2	491	2	Q50RL8_ENTHI	Q50rl8	entamoeba h
1381	82	5.2	495	2	Q4RZZ8_TETNG	Q4rzz8	tetraodon n
1382	82	5.2	520	2	Q4XP68_PLACH	Q4xp68	plasmodium
1383	82	5.2	538	2	Q75JS0_DICDI	Q75js0	dictyosteli
1384	82	5.2	544	2	Q8IG67_CAEEL	Q8ig67	caenorhabdi
1385	82	5.2	562	2	Q51ND8_MAGGR	Q51nd8	magnaporthe
1386	82	5.2	584	1	CEJ1_CAEEL	Q17802	caenorhabdi
1387	82	5.2	588	2	Q4S6Y8_TETNG	Q4s6y8	tetraodon n
1388	82	5.2	599	2	Q5ELX9_DROME	Q5elx9	drosophila
1389	82	5.2	599	2	Q9V680_DROME	Q9v680	drosophila
1390	82	5.2	599	2	Q5ELY3_DROME	Q5ely3	drosophila
1391	82	5.2	600	2	Q4PHL9_USTMA	Q4phl9	ustilago ma
1392	82	5.2	601	2	Q6V6S0_DROME	Q6v6s0	drosophila
1393	82	5.2	625	2	Q5VFL0_9ASTE	Q5vfl0	cornus cf.
1394	82	5.2	630	2	Q96YH6_SULTO	Q96yh6	sulfolobus
1395	82	5.2	641	2	Q83363_9GAMR	Q83363	murine leuk
1396	82	5.2	670	2	Q9YWM0_GALV	Q9ywm0	gibbon ape
1397	82	5.2	673	2	Q91VK6_MOUSE	Q91vk6	mus musculu
1398	82	5.2	693	2	Q27394_CAEEL	Q27394	caenorhabdi
1399	82	5.2	713	2	Q5KG88_CRYNE	Q5kg88	cryptococcu
1400	82	5.2	720	1	NUP2_YEAST	P32499	saccharomyc
1401	82	5.2	746	2	Q82GM0_STRAW	Q82gm0	streptomyce
1402	82	5.2	763	2	Q5A8K3_CANAL	Q5a8k3	candida alb
1403	82	5.2	771	2	Q86NN7_DROME	Q86nn7	drosophila
1404	82	5.2	776	2	Q4RHT1_TETNG	Q4rht1	tetraodon n
1405	82	5.2	780	2	Q5CHI0_CRYHO	Q5chi0	cryptospori
1406	82	5.2	789	2	Q9VY98_DROME	Q9vy98	drosophila
1407	82	5.2	824	2	Q6CY28_KLULA	Q6cy28	kluyveromyc
1408	82	5.2	847	2	Q6ZQ82_MOUSE	Q6zq82	mus musculu
1409	82	5.2	894	2	Q7FL10_ARATH	Q7fl10	arabidopsis
1410	82	5.2	894	2	Q9C8I6_ARATH	Q9c8i6	arabidopsis
1411	82	5.2	911	2	Q8GWK9_ARATH	Q8gwk9	arabidopsis
1412	82	5.2	911	2	Q9SA18_ARATH	Q9sa18	arabidopsis
1413	82	5.2	926	1	YIY8_SCHPO	Q9uui5	schizosacch
1414	82	5.2	926	2	Q7LDM3_HUMAN	Q7ldm3	homo sapien
1415	82	5.2	957	2	Q9UKN0_HUMAN	Q9ukn0	homo sapien
1416	82	5.2	963	2	Q99MX4_GLAVO	Q99mx4	glaucomys v
1417	82	5.2	971	2	Q6A036_MOUSE	Q6a036	mus musculu
1418	82	5.2	973	2	Q7CZH1_AGRT5	Q7czh1	agrobacteri

1419	82	5.2	977	2	Q8UFQ8_AGRT5	Q8ufq8 agrobacteri
1420	82	5.2	981	2	Q54SW0_DICDI	Q54sw0 dictyosteli
1421	82	5.2	1019	2	Q9Y6L9_HUMAN	Q9y619 homo sapien
1422	82	5.2	1023	2	Q7M009_SCMVC	Q7m009 simian cyto
1423	82	5.2	1074	2	Q8C0P8_MOUSE	Q8c0p8 mus musculu
1424	82	5.2	1082	1	YK02_SCHPO	Q9hdy9 schizosacch
1425	82	5.2	1083	2	Q06108_YEAST	Q06108 saccharomyc
1426	82	5.2	1099	2	Q7TUJ6_PROMM	Q7tuj6 prochloroco
1427	82	5.2	1100	1	TCRG1_MOUSE	Q8cgf7 mus musculu
1428	82	5.2	1113	2	Q7PMD5_ANOGA	Q7pmd5 anopheles g
1429	82	5.2	1126	2	Q9EQJ9_MOUSE	Q9eqj9 mus musculu
1430	82	5.2	1147	2	Q94248_CAEEL	Q94248 caenorhabdi
1431	82	5.2	1170	2	Q69ZE1_MOUSE	Q69ze1 mus musculu
1432	82	5.2	1215	1	GP158_HUMAN	Q5t848 homo sapien
1433	82	5.2	1234	2	Q4Y8D6_PLACH	Q4y8d6 plasmodium
1434	82	5.2	1256	2	Q54RH9_DICDI	Q54rh9 dictyosteli
1435	82	5.2	1262	2	Q5AI49_CANAL	Q5ai49 candida alb
1436	82	5.2	1275	2	Q5B0V1_EMENI	Q5b0v1 aspergillus
1437	82	5.2	1320	2	Q54QP0_DICDI	Q54qp0 dictyosteli
1438	82	5.2	1339	2	O35788_RAT	O35788 rattus norv
1439	82	5.2	1399	2	Q54GM7_DICDI	Q54gm7 dictyosteli
1440	82	5.2	1423	2	Q6CRU1_KLULA	Q6cru1 kluyveromyc
1441	82	5.2	1526	2	Q5AAL9_CANAL	Q5aal9 candida alb
1442	82	5.2	1564	2	Q95VZ5_DROME	Q95vz5 drosophila
1443	82	5.2	1598	2	Q60RK8_CAEBR	Q60rk8 caenorhabdi
1444	82	5.2	1599	2	Q4QDX1_LEIMA	Q4qdx1 leishmania
1445	82	5.2	1672	1	PMPB_CHLMU	Q9pjy2 chlamydia m
1446	82	5.2	1689	2	Q5EEN9_9VIRU	Q5een9 crimean-con
1447	82	5.2	1854	2	Q7ZA78_CANAL	Q7za78 candida alb
1448	82	5.2	2523	2	Q4IEB9_GIBZE	Q4ieb9 gibberella
1449	82	5.2	2981	2	Q6CEB2_YARLI	Q6ceb2 yarrowia li
1450	82	5.2	3146	2	Q9VUB5_DROME	Q9vub5 drosophila
1451	82	5.2	3529	2	Q9GP30_THEPA	Q9gp30 theileria p
1452	82	5.2	3529	2	Q4N9U4_THEPA	Q4n9u4 theileria p
1453	82	5.2	26926	2	Q4U1Z6_HUMAN	Q4u1z6 homo sapien
1454	81.5	5.2	146	2	Q5W0S5_HUMAN	Q5w0s5 homo sapien
1455	81.5	5.2	171	1	NUOE_BUCBP	Q89au3 buchnera ap
1456	81.5	5.2	234	2	Q6FXA6_CANGA	Q6fxa6 candida gla
1457	81.5	5.2	235	2	Q9M182_ARATH	Q9m182 arabidopsis
1458	81.5	5.2	245	2	Q7SBI6_NEUCR	Q7sbi6 neurospora
1459	81.5	5.2	245	2	Q61F73_CAEBR	Q61f73 caenorhabdi
1460	81.5	5.2	246	2	Q60WW7_CAEBR	Q60ww7 caenorhabdi
1461	81.5	5.2	268	2	Q7Q7W4_ANOGA	Q7q7w4 anopheles g
1462	81.5	5.2	345	2	Q6UJM5_9SAUR	Q6ujm5 diplodactyl
1463	81.5	5.2	364	2	Q521P9_MAGGR	Q521p9 magnaporthe
1464	81.5	5.2	381	2	Q5B2S4_EMENI	Q5b2s4 aspergillus
1465	81.5	5.2	386	2	Q97G38_CLOAB	Q97g38 clostridium
1466	81.5	5.2	390	2	Q6PND6_EMENI	Q6pnd6 emericella
1467	81.5	5.2	412	2	Q9P603_NEUCR	Q9p603 neurospora
1468	81.5	5.2	432	2	Q6NUR0_HUMAN	Q6nur0 homo sapien
1469	81.5	5.2	460	2	O18984_CERAE	O18984 cercopithec
1470	81.5	5.2	463	2	Q5F5W2_NEIG1	Q5f5w2 neisseria g
1471	81.5	5.2	463	2	Q9K1H4_NEIMB	Q9k1h4 neisseria m
1472	81.5	5.2	467	2	Q59PE2_CANAL	Q59pe2 candida alb
1473	81.5	5.2	467	2	Q59PL2_CANAL	Q59pl2 candida alb
1474	81.5	5.2	475	2	Q5CVA2_CRYPV	Q5cva2 cryptospori
1475	81.5	5.2	540	2	Q54T81_DICDI	Q54t81 dictyosteli
1476	81.5	5.2	551	2	Q7S436_NEUCR	Q7s436 neurospora
1477	81.5	5.2	567	2	Q6FR51_CANGA	Q6fr51 candida gla
1478	81.5	5.2	579	2	Q4RLQ7_TETNG	Q4rlq7 tetraodon n
1479	81.5	5.2	599	2	Q5ELX2_DROME	Q5elx2 drosophila
1480	81.5	5.2	599	2	Q5ELY5_DROME	Q5ely5 drosophila
1481	81.5	5.2	599	2	Q9U3W0_DROME	Q9u3w0 drosophila
1482	81.5	5.2	633	2	Q519D6_ENTHI	Q519d6 entamoeba h
1483	81.5	5.2	636	1	YNR6_YEAST	P53882 saccharomyc
1484	81.5	5.2	638	2	Q4ZJ93_9APIC	Q4zj93 theileria l
1485	81.5	5.2	640	2	Q55CW3_DICDI	Q55cw3 dictyosteli
1486	81.5	5.2	687	1	SRB4_YEAST	P32569 saccharomyc
1487	81.5	5.2	687	2	Q6B1B4_YEAST	Q6b1b4 saccharomyc
1488	81.5	5.2	700	2	Q5B6C0_EMENI	Q5b6c0 aspergillus
1489	81.5	5.2	773	2	Q6IDE4_DROME	Q6ide4 drosophila
1490	81.5	5.2	846	2	Q6ZKY0_ORYSA	Q6zky0 oryza sativ
1491	81.5	5.2	860	1	MUTS_LISIN	Q92bv3 listeria in
1492	81.5	5.2	860	1	VG12_BPB03	Q37893 bacteriopha
1493	81.5	5.2	869	2	O01262_CAEEL	O01262 caenorhabdi
1494	81.5	5.2	880	1	PHTF_DROME	Q9v9a8 drosophila
1495	81.5	5.2	884	2	Q4ZJ94_9APIC	Q4zj94 theileria l
1496	81.5	5.2	913	2	Q7NP28_GLOVI	Q7np28 gloeobacter
1497	81.5	5.2	915	2	Q54YM3_DICDI	Q54ym3 dictyosteli
1498	81.5	5.2	917	2	Q7RA65_PLAYO	Q7ra65 plasmodium
1499	81.5	5.2	939	2	Q5SF31_HAEIN	Q5sf31 haemophilus
1500	81.5	5.2	976	2	Q6NTV5_XENLA	Q6ntv5 xenopus lae

ALIGNMENTS

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RESULT 1
Q9UNF4_HUMAN
ID   Q9UNF4_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q9UNF4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hyaluronic acid receptor (XLKD1).
GN   Name=HAR; ORFNames=UNQ230;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AF127670; AAD49220.2; -; mRNA.
DR   EMBL; AY358925; AAQ89284.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSG00000133800; Homo sapiens.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
SQ   SEQUENCE   322 AA;  35213 MW;  8B4D6D623F52D559 CRC64;

 Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
 Best Local Similarity  100.0%;  Pred. No. 1.1e-119;
 Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 2
Q8TC18_HUMAN
ID   Q8TC18_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q8TC18;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Extracellular link domain containing 1.
GN   Name=XLKD1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026231; AAH26231.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   Ensembl; ENSG00000133800; Homo sapiens.
DR   HGNC; HGNC:14687; XLKD1.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35183 MW;  0B1EDBD76CE4610A CRC64;

  Query Match             99.1%;  Score 1561;  DB 2;  Length 322;
  Best Local Similarity   99.7%;  Pred. No. 1.5e-118;
  Matches  305;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIRKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 3
Q9Y5Y7_HUMAN
ID   Q9Y5Y7_HUMAN PRELIMINARY;      PRT;   322 AA.
AC   Q9Y5Y7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA   Jackson D.G.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
DR   EMBL; AF118108; AAD42764.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006928; P:cell motility; TAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
SQ   SEQUENCE   322 AA;  35238 MW;  0EBEA56729CEFFF7 CRC64;

  Query Match             98.8%;  Score 1556;  DB 2;  Length 322;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-118;
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  Matches  303;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVDT 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFGAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSRIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 4
Q6UC88_BOVIN
ID   Q6UC88_BOVIN PRELIMINARY;      PRT;   322 AA.
AC   Q6UC88;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cell surface retention sequence binding protein-1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA   Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA   Huang J.S.;
RT   "Cloning, expression, characterization and role in autocrine cell
RT   growth of cell surface retention sequence binding protein-1.";
RL   J. Biol. Chem. 278:43855-43869(2003).
DR   EMBL; AY372937; AAQ85130.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   322 AA;  35561 MW;  4901DA1BF92648AE CRC64;

  Query Match             71.0%;  Score 1118;  DB 2;  Length 322;
  Best Local Similarity   70.9%;  Pred. No. 1.6e-82;
  Matches  217;  Conservative   33;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||:||:||    |||||:|||:||     ||||||:|||||:||:|| :||||
Db         17 TRLLVQGSLRSEEISILGPCRIMGVTLVTKKTQPLLNFTEAQEACRLVGLTLASQDQVEE 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              | |  ||||||||| : |||| ||  ||||||:||||:||:  :| :  :||:|||| |
Db         77 ARKFGFETCSYGWVKNQFVVIPRIISNPKCGKSGVGVVIWRSSLSSRHRSYCHNSSDIWI 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              |||:|||||| ||:|||:||| ||: :|||||:|  |         ||  |  |||| ||:
Db        137 NSCLPEIITTDDPLFNTETATYTTKLMVSDSTHSELSTDGPDYVTTTVAPPLASTSTPRK 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              :||||:|| ||:|| ::|| |  ::|: |||||| |||||||||||||||| |||||
Db        197 RKLICITEAFMDTSAVATERESDIQNRPAFKNEAVGFGGVPTALLVLALLFFAAAAGLAV 256

Qy        241 CYVKRYVKAFPPTNKNQQKEMIETKVVKEEKADDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||:|||||||||| :| ||| ||| |||||
Db        257 CYVKRYVKAFPPTNKNQQKEMIETKVVKEEKADDSNPNEESKKMNKTPEEPKSPPKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 5
Q8BHC0_MOUSE
ID   Q8BHC0_MOUSE PRELIMINARY;      PRT;   318 AA.
AC   Q8BHC0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE   cDNA, RIKEN full-length enriched library, clone:1200012G08
DE   product:extra cellular link domain-containing 1, full insert
DE   sequence).
GN   Name=Xlkd1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC038653; AAH38653.1; -; mRNA.
DR EMBL; BC038892; AAH38892.1; -; mRNA.
DR EMBL; AK004726; BAC25094.1; -; mRNA.
DR HSSP; P98066; 1O7B.
DR Ensembl; ENSMUSG00000030787; Mus musculus.
DR MGI; MGI:2136348; Xlkd1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS50963; LINK_2; 1.
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

Query Match 67.0%; Score 1055; DB 2; Length 318;
Best Local Similarity 69.0%; Pred. No. 2.1e-77;
Matches 211; Conservative 30; Mismatches 61; Indels 4; Gaps 3;

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Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||  |||:   ::|||  :|||||: || :  | |:||||| |||::|||:|| :||||:
Db         17 TRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLGLTLASRDQVES 75

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              | |: |||||||||: | || ||  ||:||||| |||||  | |::| |||:||||||
Db         76 AQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFKAYCHNSSDTWV 135

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              |||||||:||  |: :||  |  ||| || | |  :|| || |   ||  ||  ||: |:
Db        136 NSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT-RAPPLTSMARK 192

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              | ||:|||: |  ||:|||| || : ||||||||||||||||||||||||||||| |
Db        193 TKKICITEVYTEPITMATETEAFVASGAAFKNEAAGFGGVPTALLVLALLFFGAAAVLAV 252

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              |||||||||||| ||||||||||||||||:| | ||||||| |||||:||| |||||
Db        253 CYVKRYVKAFPFTTKNQQKEMIETKVVKEEKADDVNANEESKKTIKNPEEAKSPPKTTVR 312

Qy        301 CLEAEV 306
              ||||||
Db        313 CLEAEV 318
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RESULT 6
Q99NE4_MOUSE
ID Q99NE4_MOUSE PRELIMINARY; PRT; 318 AA.
AC Q99NE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

```
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hyaluronan receptor precursor.
GN   Name=Xlkd1; Synonyms=LYVE-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA   Banerji S.;
RT   "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT   receptor for hyaluronan.";
RL   J. Cell Biol. 144:789-801(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c; TISSUE=Digestive tract;
RX   MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;
RA   Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT   "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT   endothelium.";
RL   J. Biol. Chem. 276:19420-19430(2001).
DR   EMBL; AJ311501; CAC33082.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   MGI; MGI:2136348; Xlkd1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR   GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor; Signal.
FT   SIGNAL       1     23       Potential.
FT   CHAIN        24    318      LYVE-1.
SQ   SEQUENCE   318 AA;  34641 MW;  1248974A16113330 CRC64;

  Query Match             67.0%;  Score 1055;  DB 2;  Length 318;
  Best Local Similarity   69.0%;  Pred. No. 2.1e-77;
  Matches  211;  Conservative   30;  Mismatches   61;  Indels    4;  Gaps    3;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||  |||:   ::|||  :|||||: || :  | |:||||| |||::|||:|| :||||:
Db         17 TRHPVQGADLVQDLSIS-TCRIMGVALVGRNKNPQMNFTEANEACKMLGLTLASRDQVES 75

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              | |: |||||||||||: | || ||  ||:||||| |||||  | |::| |||:||||||
Db         76 AQKSGFETCSYGWVGEQFSVIPRIFSNPRCGKNGKGVLIWNAPSSQKFKAYCHNSSDTWV 135

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              |||||||:||  |: :||  |  ||| || | |  :|| || |   ||  ||  ||: |:
Db        136 NSCIPEIVTTFYPVLDTQ--TPATEFSVSSSAYLASSPDSTTPVSATT-RAPPLTSMARK 192

Qy        181 KKLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              | ||:|||: |  ||:|||| || : ||||||||||||||||||||||||||||| |
Db        193 TKKICITEVYTEPITMATETEAPVASGAAFKNEAAGFGGVPTALLVLALLFFGAAAVLAV 252

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              |||||||||||| ||||||||||||||:| | ||||||| |||||:||| |||||
Db        253 CYVKRYVKAFPFTTKNQQKEMIETKVVKEEKADDVNANEESKKTIKNPEEAKSPPKTTVR 312

Qy        301 CLEAEV 306
              ||||||
Db        313 CLEAEV 318
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RESULT 7
Q7YS22_PIG
ID   Q7YS22_PIG  PRELIMINARY;      PRT;   201 AA.
AC   Q7YS22;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA   Sellke F.W., Bianchi C.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY304537; AAP69946.1; -; mRNA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     201    201
SQ   SEQUENCE   201 AA;  22219 MW;  BAAF34E7EACBBAE3 CRC64;

  Query Match             46.1%;  Score 726.5;  DB 2;  Length 201;
  Best Local Similarity   70.1%;  Pred. No. 6.4e-51;
  Matches  141;  Conservative   21;  Mismatches   36;  Indels    3;  Gaps    2;

Qy         65 SFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCI 124
              |||||||||| | |:|| || ||||||||| |||:|:  :|::| |||:||||| |||||
Db          1 SFETCSYGWVKDQFLVIPRIYPNPKCGKNGKGVLVWRHSLSQKFEAYCHNSSDTRTNSCI 60

Qy        125 PEIITTKDPIFNTQTATQTTEFIVSDSTYSVAS--PYSTI-PAPTTTPPAPASTSIPRRK 181
              |||| | || ||| ||  |||  |:| | | ::  | |:: |   ||    |:|| ||::
Db         61 PEIIPTNDPTFNTNTAPYTTEMTVNDRTSSSSTNGPSSSVMPTVVTTSLPLATTSTPRKR 120

Qy        182 KLICVTEVFMETSTMSTETEPPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFC 241
              ||||:|| ||||||:||||| ::||: |||||| ||||:|||||||||||| ||||| |
Db        121 KLICITEAFMETSTISTETELYIENRTAFKNEAIGFGGIPTALLVLALLFFAAAAGLAVC 180

Qy        242 YVKRYVKAFPFTNKNQQKEMI 262
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Db        181 YVKRYVKAFPFTNKNQQKEMI 201
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RESULT 8
Q58E15_XENLA
ID   Q58E15_XENLA PRELIMINARY;      PRT;   392 AA.
AC   Q58E15;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092113; AAH92113.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER     392    392
SQ   SEQUENCE   392 AA;  43658 MW;  AF47C05AC550C6A1 CRC64;

  Query Match             15.6%;  Score 245;  DB 2;  Length 392;
  Best Local Similarity   34.9%;  Pred. No. 2.1e-11;
  Matches   58;  Conservative   18;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         18 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 77
              :|||  |:  | |     ||  :| : | :|  |:|   |:| ||   |||| |||: |
Db         33 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTSIANYTQLEIALDFGFETCRYGWIEDR 92

Qy         78 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 127
               |:| || ||| |  |  |:       | ::  ||||:|:|   ||:| :
Db         93 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 151

Qy        128 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 172
               | : ||  :||           ||         | |||    | |
Db        152 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 189


RESULT 9
Q6GM56_XENLA
ID   Q6GM56_XENLA PRELIMINARY;      PRT;   441 AA.
AC   Q6GM56;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC443701 protein (Fragment).
GN   Name=LOC443701;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC074228; AAH74228.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   441 AA;  49207 MW;  DF9AA596D506D1A1 CRC64;

  Query Match             15.3%;  Score 241;  DB 2;  Length 441;
  Best Local Similarity   34.3%;  Pred. No. 5.1e-11;
  Matches   57;  Conservative   19;  Mismatches   70;  Indels   20;  Gaps    3;

Qy         18 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 77
              :|||  |:  | |     ||  :| : | :|  ::|   |:| ||   |||| |||: |
Db         32 ISCRFKGVFHVEKNDRYSLNQEDAVKLCGMLNTTIASYAQLEIALDFGFETCRYGWIEDR 91

Qy         78 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI---------- 127
               |:| || ||| |  |  |:       | ::  ||||:|:|   ||:| :
Db         92 -VLIPRIKPNPICAANYTGIYTLGNNESLRYDVYCYNASETEDKSCLPVLLLNETDFSHN 150

Qy        128 -ITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAP 172
               | : ||  :||           ||         | |||    | |
Db        151 TIDSYDPTLDTQIQNSDKSGYQGDSV--------TDPAPAMITPDP 188


RESULT 10
CD44_CRIGR
ID   CD44_CRIGR     STANDARD;      PRT;   362 AA.
AC   P20944;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
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```
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN   Name=CD44;
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90304889; PubMed=1694723; DOI=10.1016/0092-8674(90)90694-A;
RA   Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
RT   "CD44 is the principal cell surface receptor for hyaluronate.";
RL   Cell 61:1303-1313(1990).
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- INDUCTION: By EBV.
CC   -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC       addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC       of phosphate to cytoplasmic domain serine residues.
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M33827; AAA36967.1; -; mRNA.
DR   PIR; A35616; A35616.
DR   HSSP; P98066; 1TSG.
DR   SMR; P20944; 23-170.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW   Transmembrane.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    362       CD44 antigen.
FT   TOPO_DOM    23    269       Extracellular (Potential).
FT   TRANSMEM   270    290       Potential.
FT   TOPO_DOM   291    362       Cytoplasmic (Potential).
FT   DOMAIN      34    122       Link.
FT   REGION     226    269       Stem.
FT   COMPBIAS   152    160       Arg/Lys-rich (basic).
FT   MOD_RES     23     23       Pyrrolidone carboxylic acid (By
FT                               similarity).
FT   MOD_RES    292    292       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES    326    326       Phosphoserine (By similarity).
FT   CARBOHYD    27     27       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    59     59       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   112    112       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   122    122       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   174    174       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   256    256       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    55    120       By similarity.
FT   DISULFID    79     99       By similarity.
SQ   SEQUENCE   362 AA;  39775 MW;  E89EB434E9EEC948 CRC64;

  Query Match           14.8%;  Score 233.5;  DB 1;  Length 362;
  Best Local Similarity 26.3%;  Pred. No. 1.6e-10;
  Matches   91;  Conservative   45;  Mismatches  147;  Indels   63;  Gaps   12;

Qy          8 SLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFE 67
              ||  |:: : ::||  |:  | |     :: |||: |:   :|   ||:  ||   ||
Db         18 SLAHEQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVMALSKGFE 77

Qy         68 TCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIPEI 127
              || ||:: :| ||| || ||  |  |  || |     |  :  ||:|:|      |
Db         78 TCRYGFI-EGHVVIPRIQPNAICAANHTGVYILTSNTS-HYDTYCFNASAPLEEDC---- 131

Qy        128 ITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPTTTPPAPAS-------- 174
               |:   : |:     |  :  | | ||    | |    | |  ||    :|
Db        132 -TSVTDLPNSFEGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNTTDDDVSSGSSSEKST 190

Qy        175 -------TSIPRRKKLICVTEVFMETSTMSTE--------------------TEPFVEN 206
                    | :|          : :   |||:|                      ||    |
Db        191 SGGYVFHTYLPTIHSTADQDDPYFIGSTMATRDQDSSMDPRGNSLTVTDGSKLTEHSSGN 250

Qy        207 KAAFKNEAAGFGG---VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIE 263
              : :  |  :  ||   ||  |:||| |    |  |  |    :          |:|:::
Db        251 QDSGLNSTSRPGGKPRVPEWLIVLASL-LALALILAVC-----IAVNSRRRCGQKKKLVI 304

Qy        264 TKVVKEEKANDSNPNEESKKTDKNPE----ESKSPSKTTVRCLEAE 305
                |  |  |:| : :  |: |     :| ||:|  : : |:
Db        305 NS--GNGKVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQFMTAD 348


RESULT 11
Q6P8A2_XENTR
ID   Q6P8A2_XENTR PRELIMINARY;      PRT;   437 AA.
AC   Q6P8A2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75816.
GN   Name=MGC75816;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061327; AAH61327.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
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DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   437 AA;  49108 MW;  7088441D0E138C10 CRC64;

  Query Match             14.6%;  Score 229.5;  DB 2;  Length 437;
  Best Local Similarity   26.3%;  Pred. No. 4.4e-10;
  Matches   82;  Conservative   34;  Mismatches  111;  Indels   85;  Gaps   10;

Qy         18 VSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALKASFETCSYGWVGDG 77
              :|||  |:  | |    ||  :| : |  |  ::|    :| |    |||| |||: |
Db         24 ISCRFKGVFHVEKYDRYALNREDAIKLCHELNTTIANLTLMEIAQDIGFETCRYGWIEDR 83

Qy         78 FVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSCIP----------E 126
               ||| || ||| |  |  |:       | :: |||||:|:|   || |          :
Db         84 -VVIPRIKPNPICAANYTGIFTLGNNDSLRYDAYCYNASETEDKSCEPVLLLNETDLSHK 142

Qy        127 IITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAP---------TTTPPA-PASTS 176
              | : ||  :||   :|     | | :   |    | |          || |   | ||
Db        143 TIDSYDPTLDTQNPFRTQNSDKSGDTVTDPGPAMITPDPGQDWDDIQGTTDPHGDPFSTK 202

Qy        177 IPRRKKLICVTEVFMETSTMSTE--TEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGA 234
                          : |||   || :::      :|:  ||
Db        203 --------------GDGSDSTEQTNEPGIDH--------SGYQEVPG------------ 227

Qy        235 AAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKK---------- 283
                           ||    ::  |  :|:    | ::||: : |  :
Db        228 -------------HHFPEGTDHEVNE-FDTEHTTTENSHDSDGHYEHPRHHDHQDNTGRD 273

Qy        284 -TDKNPEESKSP 294
               |  : | || |
Db        274 YTRPDDESSKEP 285


RESULT 12
CD44_PAPHA
ID   CD44_PAPHA     STANDARD;      PRT;   362 AA.
AC   P14745;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN   Name=CD44;
OS   Papio hamadryas (Hamadryas baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9557;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 66-74.
RX   MEDLINE=89282830; PubMed=2471974;
RA   Idzerda R.L., Carter W.G., Nottenburg C., Wayner E.A., Gallatin W.M.,
RA   St John T.;
RT   "Isolation and DNA sequence of a cDNA clone encoding a lymphocyte
RT   adhesion receptor for high endothelium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663(1989).
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC       addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC       of phosphate to cytoplasmic domain serine residues.
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M22452; AAA35385.1; -; mRNA.
DR   HSSP; P98066; 1TSG.
DR   SMR; P14745; 20-168.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Direct protein sequencing;
KW   Glycoprotein; Phosphorylation; Proteoglycan;
KW   Pyrrolidone carboxylic acid; Receptor; Signal; Transmembrane.
FT   SIGNAL       1    20       By similarity.
FT   CHAIN       21   362       CD44 antigen.
FT   TOPO_DOM    21   269       Extracellular (Potential).
FT   TRANSMEM   270   290       Potential.
FT   TOPO_DOM   291   362       Cytoplasmic (Potential).
FT   DOMAIN      32   120       Link.
FT   REGION     225   269       Stem.
FT   COMPBIAS   150   158       Arg/Lys-rich (basic).
FT   MOD_RES     21    21       Pyrrolidone carboxylic acid (Probable).
FT   MOD_RES    292   292       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES    326   326       Phosphoserine (By similarity).
FT   CARBOHYD    25    25       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    57    57       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   100   100       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   110   110       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   120   120       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   256   256       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    53   118       By similarity.
FT   DISULFID    77    97       By similarity.
FT   CONFLICT    67    67       E -> V (in Ref. 1; AA sequence).
SQ   SEQUENCE   362 AA;  39379 MW;  578BFCE7C3D52FFF CRC64;

  Query Match             14.1%;  Score 222.5;  DB 1;  Length 362;
  Best Local Similarity   25.5%;  Pred. No. 1.3e-09;
  Matches   92;  Conservative   43;  Mismatches  127;  Indels   99;  Gaps   16;

Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              ||| ||   :: : ::||  ||  | |     :: ||| : |:    :|    |:| ||
Db         14 LVQLSL--AQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS 71

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
                |||| ||:: :| ||| || ||  |  | || |     | |:  ||:|:|     |
Db         72 IGFETCRYGFI-EGHVVIPRIHPNSICAANNTGVYILTSNTS-QYDTYCFNASAPPGEDC 129

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYSTIP------APT---------- 166
                  |:   : |       |   :  | | |     | | |       :||
Db        130 -----TSVTDLPNAFDGPITITIVNRDGTRYVKKGEYRTNPEDINPSSPTDDDVSSGSSS 184

Qy        167 ----------------TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAF 210
                             |:|| |                         | ||:  |   :: ||
Db        185 ERSSTLGGYIFYNHFSTSPPIPDEDG--------------PWITDSTDRTPATRDQGAF 229

Qy        211 K----------NEAAGF------GG------------VPTALLVLALLFFGAAAGLGFCY 242
                       :|:||       ||            :|  |::|| |    |  | | |
Db        230 DPSGGSHTTHGSESAGHSHGSREGGANTTSGPLRTPQIPEWLIILASL-LALALILAVC- 287

Qy        243 VKRYVKAFPFTNKNQQKEMIETK---VVKEEKANDSNPNEESKKTDK----NPEESKSPS 295
                  :         |:|:::       |:: |::  |  | ||  :     | | |::|
Db        288 ----IAVNSRRRCGQKKKLVINNGNGAVEDRKSSGLN-GEASKSQEMVHLVNKESSETPD 342
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Qy        296 K 296
              :
Db        343 Q 343


RESULT 13
O70509_RAT
ID   O70509_RAT  PRELIMINARY;      PRT;   364 AA.
AC   O70509;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Glycoprotein CD44s (Cd44 protein).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA   Stevens J.W.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney, and Pituitary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065147; AAC17117.1; -; mRNA.
DR   EMBL; BC061531; AAH61531.1; -; mRNA.
DR   EMBL; BC085703; AAH85703.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O70509; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   364 AA;  39725 MW;  BA249776C4419AA7 CRC64;

  Query Match             14.1%;  Score 222;  DB 2;  Length 364;
  Best Local Similarity   24.4%;  Pred. No. 1.4e-09;
  Matches   85;  Conservative   55;  Mismatches  149;  Indels   60;  Gaps   13;

Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALS 74

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
                |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT----------- 166
                  |:   : |:      |   :  | | ||    | |    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVSSGSTI 188

Qy        167 --TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAFK-----NEAAGF 217
                :||       | :|  :       :  |   ||::| : :  :: :  |       :| ||
Db        189 EKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATSDGDSSMDPRGGFDTVTHGSELAGH 248

Qy        218 GG-----------------VPTALLVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQK 259
                                  :|  |::|| |    |  |  |    :         |:|
Db        249 SSGNQDSGVTTTSGPARRPQIPEWLIILASL-LALALILAVC-----IAVNSRRRCGQKK 302

Qy        260 EMIETK---VVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAE 305
                :::       |:: | :: |  | ||  :     :| |::|  : : |:
Db        303 KLVINSGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPTETPDQFMTAD 350


RESULT 14
CD44_RAT
ID   CD44_RAT       STANDARD;      PRT;   503 AA.
AC   P26051; Q99021;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE   (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE   homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE   24).
GN   Name=Cd44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC   STRAIN=BDIX; TISSUE=Pancreas;
RX   MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA   Guenthert U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA   Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT   "A new variant of glycoprotein CD44 confers metastatic potential to
RT   rat carcinoma cells.";
RL   Cell 65:13-24(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RA   Stevens J.W., Midura R.J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SULFATION OF TYR-288.
RX   PubMed=9692903;
RA   Sleeman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT   "CD44 variant exon v5 encodes a tyrosine that is sulphated.";
RL   Eur. J. Biochem. 255:74-80(1998).
```

```
CC   -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC       mucosal high endothelial venule and to types I and VI collagen.
CC       Probably involved in matrix adhesion, lymphocyte activation and
CC       lymph node homing.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=2; Synonyms=Long, Meta-1;
CC         IsoId=P26051-1; Sequence=Displayed;
CC       Name=1; Synonyms=Short;
CC         IsoId=P26051-2; Sequence=VSP_005330;
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC       can be more or less sulfated (By similarity).
CC   -!- PTM: Phosphorylated; activation of PKC results in the
CC       dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC       and the phosphorylation of Ser-433 (By similarity).
CC   -!- SIMILARITY: Contains 1 Link domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M61875; AAA53532.1; -; mRNA.
DR   EMBL; M61874; AAA53534.1; -; mRNA.
DR   EMBL; U52179; AAA97915.1; -; mRNA.
DR   EMBL; U46957; AAA92920.1; -; mRNA.
DR   PIR; B38745; B38745.
DR   HSSP; P98066; 1TSG.
DR   SMR; P26051; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0007155; P:cell adhesion; NAS.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
KW   Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW   Sulfation; Transmembrane.
FT   SIGNAL       1     21
FT   CHAIN       22    503       CD44 antigen.
FT   TOPO_DOM    22    410       Extracellular (Potential).
FT   TRANSMEM   411    431       Potential.
FT   TOPO_DOM   432    503       Cytoplasmic (Potential).
FT   DOMAIN      35    124       Link.
FT   REGION     228    410       Stem.
FT   COMPBIAS   154    162       Arg/Lys-rich (basic).
FT   MOD_RES     22     22       Pyrrolidone carboxylic acid (Probable).
FT   MOD_RES    288    288       Sulfotyrosine (in isoform 2).
FT   MOD_RES    433    433       Phosphoserine (by PKC) (By similarity).
FT   MOD_RES    467    467       Phosphoserine (By similarity).
FT   CARBOHYD    28     28       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    60     60       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   114    114       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   124    124       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   266    266       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   306    306       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    56    122       By similarity.
FT   DISULFID    80    100       By similarity.
FT   VARSPLIC   224    385       IATTPWVSAHTKQNQERTQWNPIHSNPEVLLQTTTRMTDID
FT                               RNSTSAHGENWTQEPQPPFNNHEYQDEEETPHATSTTWADP
FT                               NSTTEEAATQKEKWFENEWQGKNPPTPSEDSHVTEGTTASA
FT                               HNNHPSQRMTTQSQEDVSWTDFFDPISHPMGQGHQTESK
FT                               -> SDGDSSMDPRGGFDTVTHGSELA (in isoform
FT                                  1).
FT                               /FTId=VSP_005330.
FT   CONFLICT    74     74       R -> S (in Ref. 2).
SQ   SEQUENCE   503 AA;  55946 MW;  FB489D009BD4EE22 CRC64;

  Query Match             13.8%;  Score 217;  DB 1;  Length 503;
  Best Local Similarity   25.8%;  Pred. No. 5.4e-09;
  Matches   83;  Conservative   40;  Mismatches  161;  Indels   38;  Gaps   11;

Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              |:| ||  ::: : ::||  |:  | |     :: ||| : |    :|   |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
              |||| ||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------------ 166
                 |:   : |:     |   :  | | ||    | |    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVSSGSTI 188

Qy        167 --TTPPA-PASTSIPRRKKLICVTEVPMETSTMST-ETEPFVENKAAFKNEAAGFGGV-- 220
                :||     | :|  :     : |   ||::|  | |:|        |  :  :
Db        189 EKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLATIATTPWVSAHTKQNQERTQWNPIHS 248

Qy        221 -PTALLVLALLFFGAAAGLGFCYVKRYVK--AFPFTNKNQQKEMIETKVVKEEKANDSNP 277
               | ||                  : : : :    || |   | |  ||         | |
Db        249 NPEVLLQTTTRMTDIDRNSTSAHGENWTQEPQPPFNNHEYQDEE-ETPHATSTTWADPNS 307

Qy        278 NEESKKTDK-----NPEESKSP 294
               |   | |     |  : |:|
Db        308 TTEEAATQKEKWFENEWQGKNP 329


RESULT 15
O08779_RAT
ID   O08779_RAT  PRELIMINARY;      PRT;   780 AA.
AC   O08779;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD44 protein.
GN   Name=CD44;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BDX; TISSUE=Pancreas;
RA   Hofmann M.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U96138; AAB54002.1; -; mRNA.
DR   HSSP; P98066; 1O7B.
DR   SMR; O08779; 24-172.
DR   Ensembl; ENSRNOG00000006094; Rattus norvegicus.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR001231; CD44_antigen.
DR   InterPro; IPR000538; Link.
DR   Pfam; PF00193; Xlink; 1.
DR   PRINTS; PR00658; CD44.
DR   PRINTS; PR01265; LINKMODULE.
DR   ProDom; PD000918; Link; 1.
DR   SMART; SM00445; LINK; 1.
DR   PROSITE; PS01241; LINK_1; 1.
DR   PROSITE; PS50963; LINK_2; 1.
SQ   SEQUENCE   780 AA;  85917 MW;  CC4D35AB1EA7377C CRC64;
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Query Match 13.6%; Score 214.5; DB 2; Length 780;
Best Local Similarity 24.9%; Pred. No. 1.5e-08;
Matches 85; Conservative 45; Mismatches 140; Indels 71; Gaps 13;

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Qy          4 LVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVETALK 63
              |:| ||  ::: : ::||  |:  | |     :: ||| : |     :|    |:| ||:
Db         15 LLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQMELALR 74

Qy         64 ASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWTNSC 123
                |||| .||:: :| ||| || ||  |  |  || |     :  :  ||:|:|      |
Db         75 KGFETCRYGFI-EGHVVIPRIHPNAICAANNTGVYILLASNTSHYDTYCFNASAPLEEDC 133

Qy        124 IPEIITTKDPIFNTQTATQTTEFIVSDST-YSVASPYST----IPAPT------------ 166
                   |:   : |:     |   :  | | ||    | |    | |
Db        134 -----TSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDEDVSSGSTI 188

Qy        167 --TTPPA-PASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAG------- 216
               :||      | :|  :      : |   ||::|     : :    |: |
Db        189 EKSTPEGYILHTDLPTSQPTGDRDDAFFIGSTLAT-----IASTVYSKSHATAQKQNNWI 243

Qy        217 ---FGG---------VPTALLVLALLFFGAA------AGLGFCYVKRYVKAFPFTNKNQQ 258
                 ||           ||     ||:           |   | :         |   ::
Db        244 WSWFGNSQSTTQTQDSPTTTATTALMTTPETPPKRQEAQNWFSW---------FFQPSES 294

Qy        259 KEMIETKVVKEEKANDSN-----PNEESK-KTDKNPEESKS 293
              |  : |        :::|     ||||:: :||| |  | |
Db        295 KSHLHTTTKMPGTESNTNPTGWKPNEENEDETDKYPNFSGS 335
```

Search completed: March 20, 2006, 14:13:22
Job time : 69.0354 secs

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OM protein - protein search, using sw model
Run on: March 20, 2006, 14:17:31 ; Search time 61.3443 Seconds
(without alignments)
2191.725 Million cell updates/sec
Title: US-10-063-510-6_COPY_17_322
Perfect score: 1575
Sequence: 1 TRLLVQGSLRAEELSIQVSC.....NPEESKSPSKTTVRCLEAEV 306
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description

RESULT 1
ID AAY13379 standard; protein; 322 AA.
DE Amino acid sequence of protein PRO263.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 2
ID AAY87287 standard; protein; 322 AA.
DE Human signal peptide containing protein HSPP-64 SEQ ID NO:64.
PN WO200000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 100.0%; Score 1575; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 3
ID ADC78521 standard; protein; 322 AA.
DE Human PRO263 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 4
ID AAB80247 standard; protein; 322 AA.
DE Human PRO263 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 5
ID AAB87528 standard; protein; 322 AA.
DE Human PRO263.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 6
ID AAB88391 standard; protein; 322 AA.
DE Human membrane or secretory protein clone PSEC0135.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 100.0%; Score 1575; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 7
ID ABG95853 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 8
ID ABB84832 standard; protein; 322 AA.
DE Human PRO263 protein sequence SEQ ID NO:32.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 9
ID ABB95438 standard; protein; 322 AA.
DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 10
ID ABU71625 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 11
ID ABU71480 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 12
ID ABU71926 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 13
ID ABO01809 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002197671-A1.
PD 26-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 14
ID ABU90878 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 15
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 16
ID ABU71954 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 17
ID ABU54382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 18
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 19
ID ABU71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 20
ID ABU72289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 21
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 22
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 23
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 24
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 25
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 26
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 27
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 28
ID ABO53263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 29
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 30
ID ABU89270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 31
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;

Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 32
ID ABU69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 33
ID ABU96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 34
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 35
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 36
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 37
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 38
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 39
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 40
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 41
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 42
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 43
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 44
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 45
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 46
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 47
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 48
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 49
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 50

ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 51
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 52
ID ADA41958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 53
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 54
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 55
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 56
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 57
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 58
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 59
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 60
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 61
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 62
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 63
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 64
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 65
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 66
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 67
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 68
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 69
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 70
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 71
ID ADC06962 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 72
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 73
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 74
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 75
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 76
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 77
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 78
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 79
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 80
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 81
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 82
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 83
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 84
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 85
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 86
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 87
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 88
ID ADF95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 89
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 90
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 91
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 92
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 93
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 94
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 95
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 96
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 97
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 98
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 99
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 100
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 101
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 102
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 103
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 104
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;

Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 105
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 106
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 107
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 108
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 109
ID ADH53653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 110
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 111
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 112
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 113
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 114
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 115
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 116
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 117
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 118
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 119
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 120
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 121
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 122
ID ADI11563 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 123

ID ADH98208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 124
ID ADH98548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 125
ID ADH98038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 126
ID ADI05026 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 127
ID ADI03376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 128
ID ADI04771 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 129
ID ADH78225 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 130
ID ADI19569 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 131
ID ADH90317 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 132
ID ADI03036 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 133
ID ADH77885 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 134
ID ADH97868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 135
ID ADI01253 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 136
ID ADI01948 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 137
ID ADI03206 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 138
ID ADI11393 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 139
ID ADI02295 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 140
ID ADI11733 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 141
ID ADI05370 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 142
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 143
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 144
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 145
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 146
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 147
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 148
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 149
ID ADH79782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 150
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 151
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 152
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 153
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 154
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 155
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 156
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 157
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 158
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 159
ID ADL93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 160
ID ADC52144 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 161
ID ADE79279 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 162
ID ADE79703 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 163
ID ADE73379 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 164
ID ADE41282 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 165
ID ADE71444 standard; protein; 322 AA.
DE Human PDEBC Incyte 3044710CD1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 166
ID ADE73914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 167
ID ADE99468 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 168
ID ADE98587 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 169
ID ADE99014 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 170
ID ADG40484 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 171
ID ADF73878 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 172
ID ADF73454 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 173
ID ADH06576 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 174
ID ADH06406 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 175
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 176
ID ADH27717 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 177
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 178
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 179
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 180
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 181
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 182
ID ADG69337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 183
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 184
ID ADG92724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 185
ID ADG83898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 186
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 187
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 188
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 189
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 190
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 191
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 192
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 193
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 194
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 195
ID ADH33860 standard; protein; 322 AA.

DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 196
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 197
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 198
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 199
ID ADG69167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 200
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 201
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 202
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 203
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 204
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 205
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 206
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 207
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 208
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 209
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 210
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 211
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 212
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 213
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.

PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 214
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 215
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 216
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 217
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 218
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 219
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 220
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 221
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 222
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 223
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 224
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 225
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 226
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 227
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 228
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 229
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 230
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 231
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 232
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 233
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 234
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 235
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 236
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 237
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 238
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 239
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 240
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 241
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 242
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 243
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 244
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 245
ID ADR11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 246
ID ADR17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 247
ID ADS74636 standard; protein; 322 AA.
DE Human secreted/transmembrane protein #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 248
ID ADT03673 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 249
ID ADY77701 standard; protein; 322 AA.
DE Neoplastic disease detection protein PRO263.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1575; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 250
ID ADY63147 standard; protein; 322 AA.
DE Human clone PSEC0135 protein, SEQ ID 150.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1575; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 251
ID AEA37911 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1575; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 252
ID ADR41495 standard; protein; 344 AA.
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1575; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
RESULT 253
ID ABB11979 standard; peptide; 344 AA.
DE Human PRO263 homologue, SEQ ID NO:2349.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 1572; DB 4; Length 344;
Best Local Similarity 99.7%; Pred. No. 2.2e-140;
RESULT 254
ID AAW56249 standard; protein; 322 AA.
DE Amino acid sequence of a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.6%; Score 1569; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 3.8e-140;
RESULT 255
ID ABB90289 standard; protein; 322 AA.
DE Human polypeptide SEQ ID NO 2665.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.6%; Score 1569; DB 5; Length 322;
Best Local Similarity 99.7%; Pred. No. 3.8e-140;
RESULT 256
ID ADN05866 standard; protein; 322 AA.
DE Antipsoriatic protein sequence #1096.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.8%; Score 1556; DB 8; Length 322;
Best Local Similarity 99.0%; Pred. No. 6.6e-139;
RESULT 257
ID ADQ21089 standard; protein; 322 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 98.8%; Score 1556; DB 8; Length 322;
Best Local Similarity 99.0%; Pred. No. 6.6e-139;
RESULT 258
ID ABU69126 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 90.8%; Score 1429.5; DB 6; Length 297;
Best Local Similarity 91.8%; Pred. No. 6.1e-127;
RESULT 259
ID ADO08255 standard; protein; 297 AA.

DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 90.1%; Score 1418.5; DB 8; Length 297;
Best Local Similarity 91.5%; Pred. No. 6.8e-126;
RESULT 260
ID AAB34702 standard; protein; 250 AA.
DE Human secreted protein encoded by DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 72.2%; Score 1136.5; DB 3; Length 250;
Best Local Similarity 91.5%; Pred. No. 3.3e-99;
RESULT 261
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 67.0%; Score 1055; DB 4; Length 318;
Best Local Similarity 69.0%; Pred. No. 2.6e-91;
RESULT 262
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 49.1%; Score 773; DB 5; Length 255;
Best Local Similarity 63.8%; Pred. No. 1.2e-64;
RESULT 263
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 32.4%; Score 510; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.9e-40;
RESULT 264
ID ADW24431 standard; protein; 364 AA.
DE Rat CD44.
PN WO200024869-A2.
PD 04-MAY-2000.
PA (UYYA) UNIV YALE.
PA (VIGN/) VIGNERY A.
Query Match 14.2%; Score 224; DB 3; Length 364;
Best Local Similarity 24.4%; Pred. No. 2.8e-12;
RESULT 265
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 14.2%; Score 224; DB 5; Length 364;
Best Local Similarity 24.4%; Pred. No. 2.8e-12;
RESULT 266
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 14.1%; Score 222.5; DB 2; Length 362;
Best Local Similarity 25.5%; Pred. No. 3.8e-12;
RESULT 267
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 14.1%; Score 222; DB 6; Length 365;
Best Local Similarity 24.0%; Pred. No. 4.3e-12;
RESULT 268
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 14.1%; Score 222; DB 7; Length 365;
Best Local Similarity 24.0%; Pred. No. 4.3e-12;
RESULT 269
ID AEA03024 standard; protein; 365 AA.
DE CD14 receptor amino acid sequence SEQ ID NO:50.
PN US2005112141-A1.
PD 26-MAY-2005.
PA (TERM/) TERMAN D S.
Query Match 14.1%; Score 222; DB 9; Length 365;
Best Local Similarity 24.0%; Pred. No. 4.3e-12;
RESULT 270
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 13.8%; Score 217; DB 2; Length 503;
Best Local Similarity 25.8%; Pred. No. 2e-11;
RESULT 271
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.8%; Score 217; DB 7; Length 503;
Best Local Similarity 25.8%; Pred. No. 2e-11;
RESULT 272
ID ADZ51063 standard; protein; 778 AA.
DE Amino acid sequence of murine CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 13.3%; Score 209.5; DB 9; Length 778;
Best Local Similarity 32.7%; Pred. No. 1.9e-10;
RESULT 273
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.

PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.2%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 1.9e-10;
RESULT 274
ID ADQ39384 standard; protein; 668 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 13.2%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 1.9e-10;
RESULT 275
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 276
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 277
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 278
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 279
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 280
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.1%; Score 207; DB 4; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 281
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 282
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 283
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 284
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 285
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 286
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 287
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.1%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 288
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 13.1%; Score 207; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.1e-10;
RESULT 289
ID AAY99851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 13.0%; Score 205; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 290
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.

PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.0%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 291
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.0%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 292
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.0%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 293
ID ADV70207 standard; protein; 361 AA.
DE Tumor-associated antigenic target polypeptide TAT449.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 294
ID ADY19504 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 5310.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 295
ID AEA63870 standard; protein; 361 AA.
DE Protein of human anti-CD44 antibody.
PN JP2005154389-A.
PD 16-JUN-2005.
PA (UYTY) UNIV TOKYO.
PA (FUJY) FUJI PHARM IND CO LTD.
Query Match 13.0%; Score 205; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;
RESULT 296
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 13.0%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 297
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 13.0%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 298
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 13.0%; Score 204; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 299
ID ADY16699 standard; protein; 361 AA.
DE PRO polypeptide SEQ ID NO 2505.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 204; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.2e-10;
RESULT 300
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.9%; Score 203.5; DB 6; Length 608;
Best Local Similarity 21.8%; Pred. No. 5e-10;
RESULT 301
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 12.9%; Score 203.5; DB 4; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.1e-10;
RESULT 302
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.9%; Score 203.5; DB 6; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.1e-10;
RESULT 303
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.9%; Score 203.5; DB 7; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.1e-10;
RESULT 304
ID ADW43568 standard; protein; 700 AA.
DE CD44vRA.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.9%; Score 203.5; DB 9; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.1e-10;
RESULT 305
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.9%; Score 203; DB 7; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.7e-10;
RESULT 306
ID ADW43572 standard; protein; 361 AA.
DE CD44s.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.9%; Score 203; DB 9; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.7e-10;
RESULT 307
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/tmFAScyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.9%; Score 203; DB 4; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.5e-10;
RESULT 308
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.

PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.9%; Score 203; DB 6; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.5e-10;
RESULT 309
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.9%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 310
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.9%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 311
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.9%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 312
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 313
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 314
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 315
ID ADU06304 standard; protein; 742 AA.
DE Novel bronchial cancer-associated human protein SeqID528.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 12.9%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 316
ID ADY15336 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1142.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.9%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 317
ID ADY15338 standard; protein; 742 AA.
DE PRO polypeptide SEQ ID NO 1144.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.9%; Score 203; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 7.3e-10;
RESULT 318
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.9%; Score 202.5; DB 8; Length 330;
Best Local Similarity 25.1%; Pred. No. 2.7e-10;
RESULT 319
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFAStm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.9%; Score 202.5; DB 4; Length 431;
Best Local Similarity 24.7%; Pred. No. 3.9e-10;
RESULT 320
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.9%; Score 202.5; DB 6; Length 431;
Best Local Similarity 24.7%; Pred. No. 3.9e-10;
RESULT 321
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.8%; Score 202; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 3.4e-10;
RESULT 322
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.8%; Score 202; DB 8; Length 361;
Best Local Similarity 24.1%; Pred. No. 3.4e-10;
RESULT 323
ID ADS75483 standard; protein; 361 AA.
DE Human cell surface glycoprotein CD44 amino acid sequence.
PN JP2004275060-A.
PD 07-OCT-2004.
PA (SANY) SANKYO CO LTD.
Query Match 12.8%; Score 202; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 3.4e-10;
RESULT 324
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.8%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 325
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 12.8%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 8.3e-10;
RESULT 326
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.8%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 8.3e-10;
RESULT 327
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.8%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 328
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.8%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 329
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 12.8%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 330
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 331
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 12.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 332
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 333
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.8%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 334
ID ADW72142 standard; protein; 742 AA.
DE Human CD44 protein as biomarker for colorectal cancer.
PN US2005014165-A1.
PD 20-JAN-2005.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 12.8%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 335
ID ADZ51062 standard; protein; 742 AA.
DE Amino acid sequence of human CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
Query Match 12.8%; Score 202; DB 9; Length 742;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 336
ID ABU04617 standard; protein; 425 AA.
DE Human expressed protein tag (EPT) #1283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.8%; Score 201; DB 6; Length 425;
Best Local Similarity 22.0%; Pred. No. 5.3e-10;
RESULT 337
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.7%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.2e-09;
RESULT 338
ID ADW43570 standard; protein; 699 AA.
DE CD44v3-v10.
PN WO2005007700-A1.
PD 27-JAN-2005.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.7%; Score 200.5; DB 9; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.2e-09;
RESULT 339
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 340
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 341
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 342
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 343
ID AAY96140 standard; protein; 493 AA.
DE Human epithelial CD44.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.

Query Match 12.7%; Score 199.5; DB 3; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 344
ID AAU02449 standard; protein; 493 AA.
DE Human epithelial antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.7%; Score 199.5; DB 4; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 345
ID AAU99123 standard; protein; 493 AA.
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN WO200244342-A2.
PD 06-JUN-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 12.7%; Score 199.5; DB 5; Length 493;
Best Local Similarity 22.2%; Pred. No. 9e-10;
RESULT 346
ID ABU04637 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1303.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 347
ID ABU04627 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1293.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 348
ID ABU04639 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1305.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 349
ID ABU04623 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1289.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9e-10;
RESULT 350
ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 351
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 352
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9e-10;
RESULT 353
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 354
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.7%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 355
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.7%; Score 199.5; DB 8; Length 493;
Best Local Similarity 22.2%; Pred. No. 9e-10;
RESULT 356
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.7%; Score 199.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 357
ID AEB87764 standard; protein; 493 AA.
DE Human CD44, breast tumor marker.
PN WO2005071419-A2.
PD 04-AUG-2005.
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES.
Query Match 12.7%; Score 199.5; DB 9; Length 493;
Best Local Similarity 23.6%; Pred. No. 9e-10;
RESULT 358
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.6%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6e-10;
RESULT 359
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.6%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6e-10;
RESULT 360
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.
Query Match 12.6%; Score 198; DB 6; Length 395;
Best Local Similarity 23.0%; Pred. No. 9.2e-10;
RESULT 361
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.6e-09;
RESULT 362
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.6e-09;
RESULT 363
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 1.9e-09;
RESULT 364
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 1.9e-09;
RESULT 365
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 366
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 367
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 368
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 369
ID ADV73230 standard; protein; 699 AA.
DE Human colon tumor cell upregulated protein SEQ ID NO 71.
PN WO2004110345-A2.
PD 23-DEC-2004.
PA (PHAA) PHARMACIA CORP.
Query Match 12.5%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 370
ID ADY16689 standard; protein; 699 AA.
DE PRO polypeptide SEQ ID NO 2495.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 196.5; DB 9; Length 699;
Best Local Similarity 25.4%; Pred. No. 2.8e-09;
RESULT 371
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 8.1e-10;
RESULT 372
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 9.5e-10;
RESULT 373
ID ABU04624 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 9.5e-10;
RESULT 374
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 9.5e-10;
RESULT 375
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.4%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.4e-09;
RESULT 376
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.4%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 1.6e-09;
RESULT 377
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.4%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 1.9e-09;
RESULT 378
ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 12.4%; Score 195; DB 2; Length 58;

Best Local Similarity 97.6%; Pred. No. 1.3e-10;
RESULT 379
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 4.7e-09;
RESULT 380
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 12.3%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 8.4e-10;
RESULT 381
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 12.3%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 8.7e-10;
RESULT 382
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 12.3%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 1.3e-09;
RESULT 383
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 8e-09;
RESULT 384
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 8e-09;
RESULT 385
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 2.5e-09;
RESULT 386
ID ABU04606 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 2.5e-09;
RESULT 387
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 5.4e-09;
RESULT 388
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 5.4e-09;
RESULT 389
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.9%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 2.6e-09;
RESULT 390
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.9%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 1.8e-09;
RESULT 391
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.8%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.3%; Pred. No. 2.1e-09;
RESULT 392
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.7%; Score 185; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 2.8e-09;
RESULT 393
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.6%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 4.4e-09;
RESULT 394
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.6%; Score 182; DB 6; Length 112;
Best Local Similarity 34.2%; Pred. No. 5.4e-09;
RESULT 395
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.

PA (PAEL/) PAELL T.
Query Match 11.5%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 6.8e-09;
RESULT 396
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 11.4%; Score 179; DB 2; Length 69;
Best Local Similarity 95.0%; Pred. No. 5.4e-09;
RESULT 397
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.1%; Score 175.5; DB 4; Length 920;
Best Local Similarity 25.9%; Pred. No. 4e-07;
RESULT 398
ID ADI60410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.1%; Score 175.5; DB 7; Length 920;
Best Local Similarity 25.9%; Pred. No. 4e-07;
RESULT 399
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.8%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
RESULT 400
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.8%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
RESULT 401
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.5%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 4.8e-05;
RESULT 402
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 9.4%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 5.2e-06;
RESULT 403
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.2%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 3e-05;
RESULT 404
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.2%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 5e-05;
RESULT 405
ID AAR26044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 9.2%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 406
ID AAW13654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 9.2%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 407
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 9.2%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 408
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 9.2%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 409
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 9.2%; Score 145; DB 5; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 410
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.2%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 411
ID ABU56653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.2%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 412
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.2%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 413
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.

PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.2%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 414
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.2%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 415
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.2%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 416
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 9.2%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 417
ID ADW38508 standard; protein; 277 AA.
DE Immunomodulatory gene TNFa induced protein 6.
PN WO2005000099-A2.
PD 06-JAN-2005.
PA (GENZ) GENZYME CORP.
Query Match 9.2%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 418
ID AEA23596 standard; protein; 277 AA.
DE Human PRO polypeptide SEQ ID NO 138.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 9.2%; Score 145; DB 9; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.2e-05;
RESULT 419
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 9.2%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.0013;
RESULT 420
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 9.1%; Score 144; DB 8; Length 275;
Best Local Similarity 33.0%; Pred. No. 7.6e-05;
RESULT 421
ID ADO09968 standard; protein; 897 AA.
DE Human NOV1c cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.6%; Score 136; DB 8; Length 897;
Best Local Similarity 21.2%; Pred. No. 0.0022;
RESULT 422
ID ABJ10588 standard; protein; 897 AA.
DE Human novel protein NOV1c SEQ ID NO: 211.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.5%; Score 134; DB 5; Length 897;
Best Local Similarity 20.7%; Pred. No. 0.0034;
RESULT 423
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.5%; Score 134; DB 8; Length 897;
Best Local Similarity 20.7%; Pred. No. 0.0034;
RESULT 424
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.5%; Score 134; DB 8; Length 1502;
Best Local Similarity 20.7%; Pred. No. 0.0069;
RESULT 425
ID ABJ10586 standard; protein; 2675 AA.
DE Human novel protein NOV1a SEQ ID NO: 2.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.5%; Score 134; DB 5; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.015;
RESULT 426
ID ADO09971 standard; protein; 2675 AA.
DE Human NOV1a variant.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.

PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.5%; Score 134; DB 8; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.015;
RESULT 427
ID ADO09836 standard; protein; 2675 AA.
DE Human NOV1a.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 8.5%; Score 134; DB 8; Length 2675;
Best Local Similarity 17.8%; Pred. No. 0.015;
RESULT 428
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 8.4%; Score 133; DB 5; Length 1394;
Best Local Similarity 20.7%; Pred. No. 0.0078;
RESULT 429
ID ABG72499 standard; protein; 1416 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.4%; Score 133; DB 6; Length 1416;
Best Local Similarity 20.7%; Pred. No. 0.0079;
RESULT 430
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 8.4%; Score 133; DB 5; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0081;
RESULT 431
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.4%; Score 133; DB 6; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0081;
RESULT 432
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 133; DB 8; Length 1510;
Best Local Similarity 20.7%; Pred. No. 0.0087;
RESULT 433
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 8.4%; Score 133; DB 6; Length 1653;
Best Local Similarity 20.7%; Pred. No. 0.0098;
RESULT 434
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 8.4%; Score 133; DB 8; Length 1895;
Best Local Similarity 20.7%; Pred. No. 0.012;
RESULT 435
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 133; DB 8; Length 2551;
Best Local Similarity 20.7%; Pred. No. 0.018;
RESULT 436
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.4%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.017;
RESULT 437
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.4%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.018;
RESULT 438
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 8.3%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0058;
RESULT 439
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 8.3%; Score 131.5; DB 8; Length 883;

Best Local Similarity 24.3%; Pred. No. 0.0058;
RESULT 440
ID AEB34752 standard; protein; 883 AA.
DE Mammalian mutant BEHAB protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 8.3%; Score 131.5; DB 9; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0058;
RESULT 441
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 4; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0042;
RESULT 442
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 8.3%; Score 131; DB 6; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0042;
RESULT 443
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0042;
RESULT 444
ID ADF71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0042;
RESULT 445
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 8; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0042;
RESULT 446
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 4; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0044;
RESULT 447
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 8.3%; Score 131; DB 6; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0044;
RESULT 448
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0044;
RESULT 449
ID ADF71511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0044;
RESULT 450
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 131; DB 8; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0044;
RESULT 451
ID ADH18892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 8.3%; Score 131; DB 8; Length 806;
Best Local Similarity 20.4%; Pred. No. 0.0057;
RESULT 452
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 4; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 453
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 454
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.3%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 455
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 456
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 457
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 458
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 459
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 460
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 461
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 462
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 463
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 464
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 465
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 466
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 467
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 468
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 469
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 470
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 471
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 472
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 473
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 474
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 475
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 476
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 477
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 478
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 479
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 480
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 481
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 482
ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 483
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 484
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 485
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 486
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 487
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 488
ID ADD95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 489
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 490
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 491
ID ADE39444 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;

RESULT 492
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 493
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 494
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 495
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 496
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 497
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 498
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 499
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 500
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 501
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 502
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 503
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 504
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 505
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 506
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 507
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 508
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 509
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 510
ID ADD88932 standard; protein; 911 AA.

DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 511
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 512
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 513
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 514
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 515
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 516
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 517
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 518
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 519
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 520
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 521
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 522
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 523
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 524
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 525
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 526
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 527
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 528
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 529
ID ADH40040 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 530
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 531
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 532
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 533
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 534
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 535
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 536
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 537
ID ADH58488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 538
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 539
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 540
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 541
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 542
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 543
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 544
ID AEA00137 standard; protein; 911 AA.
DE Human TAT145 protein SEQ ID NO:89.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 9; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 545
ID AEA00657 standard; protein; 911 AA.
DE Human TAT145 protein sequence SeqID89.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 131; DB 9; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 546
ID AAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 8.3%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0072;
RESULT 547
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 8.3%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0072;
RESULT 548
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 8.3%; Score 130.5; DB 6; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0072;
RESULT 549
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevican protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0072;
RESULT 550
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 130.5; DB 7; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0072;
RESULT 551
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0072;
RESULT 552
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 8.3%; Score 130.5; DB 8; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0072;
RESULT 553
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0072;
RESULT 554
ID AEB34755 standard; protein; 883 AA.
DE Rat poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 8.3%; Score 130.5; DB 9; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0072;
RESULT 555
ID ABB90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 130.5; DB 5; Length 1082;
Best Local Similarity 20.6%; Pred. No. 0.0095;
RESULT 556
ID ADX15811 standard; protein; 2316 AA.
DE Human aggrecan.
PN WO2005012512-A1.
PD 10-FEB-2005.
PA (NAKA/) NAKAMURA N.
Query Match 8.3%; Score 130.5; DB 9; Length 2316;
Best Local Similarity 27.4%; Pred. No. 0.027;
RESULT 557
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 130.5; DB 8; Length 2570;
Best Local Similarity 20.6%; Pred. No. 0.031;
RESULT 558
ID AAY93911 standard; protein; 457 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 8.2%; Score 129.5; DB 3; Length 457;
Best Local Similarity 20.9%; Pred. No. 0.0036;
RESULT 559
ID ABM83434 standard; protein; 761 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.2%; Score 129.5; DB 8; Length 761;
Best Local Similarity 22.8%; Pred. No. 0.0073;
RESULT 560
ID AAY93910 standard; protein; 2157 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 8.2%; Score 129.5; DB 3; Length 2157;
Best Local Similarity 20.9%; Pred. No. 0.03;
RESULT 561
ID ABR82200 standard; protein; 2570 AA.
DE Human CLEVER-1 protein SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Query Match 8.2%; Score 129.5; DB 6; Length 2570;
Best Local Similarity 20.9%; Pred. No. 0.039;
RESULT 562
ID AAB08023 standard; protein; 95 AA.
DE The domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 8.2%; Score 128.5; DB 3; Length 95;

Best Local Similarity 28.7%; Pred. No. 0.00053;
RESULT 563
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 8.2%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00053;
RESULT 564
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 8.2%; Score 128.5; DB 2; Length 912;
Best Local Similarity 22.0%; Pred. No. 0.012;
RESULT 565
ID ADV70173 standard; protein; 671 AA.
DE Tumor-associated antigenic target polypeptide TAT152.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 566
ID AEA00138 standard; protein; 671 AA.
DE Human TAT152 protein SEQ ID NO:90.
PN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 567
ID AEA00658 standard; protein; 671 AA.
DE Human TAT152 protein sequence SeqID90.
PN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 568
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.1%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.013;
RESULT 569
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.1%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.013;
RESULT 570
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 8.1%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 571
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 572
ID ADK67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Query Match 8.1%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 573
ID AEB34757 standard; protein; 911 AA.
DE Human poly-sialyated brain-enriched hyaluronan binding protein.
PN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYYA) UNIV YALE.
Query Match 8.1%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 574
ID ABR58557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 575
ID ABU56654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 576
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 577
ID ADO24439 standard; protein; 277 AA.
DE Human PRO87335 protein SEQ ID NO:78.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 578
ID ADR14117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.1%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 579
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.

PA (BIRS/) BIRSE C E.
Query Match 8.0%; Score 126.5; DB 7; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.007;
RESULT 580
ID ADJ55382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.0%; Score 126.5; DB 8; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.007;
RESULT 581
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.0%; Score 126; DB 8; Length 277;
Best Local Similarity 34.1%; Pred. No. 0.0039;
RESULT 582
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.9%; Score 124.5; DB 7; Length 482;
Best Local Similarity 22.1%; Pred. No. 0.012;
RESULT 583
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.7%; Score 121.5; DB 8; Length 259;
Best Local Similarity 34.9%; Pred. No. 0.0096;
RESULT 584
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 2; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 585
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 3; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 586
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 587
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 588
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 589
ID ABU58413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 590
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 591
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 592
ID ABU84276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 593
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 594
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 595
ID ABU99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 596
ID ABU82719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 597
ID ABU89840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 598
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 599
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 600
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 601
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 602
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 603
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 604
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 605
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 606
ID ABU85591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 607
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 608
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 609
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 610
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 611
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 612
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 613
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 614
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 615
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 616
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 617
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 618
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.

Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 619
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 620
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 621
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 622
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 623
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 624
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 625
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 626
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 627
ID ABU88666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 628
ID ABU83361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 629
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 630
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 631
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 632
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 633
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 634
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 635
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 636
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 637
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 638
ID ABU65582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 639
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 640
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 641
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 642
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 643
ID ABU55949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 644
ID ABU65277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 645
ID ABU95222 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 646
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 647
ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 648
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 649
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 650
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 651
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 652
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 653
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 654
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 655
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 656
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 657
ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 658
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 659
ID ABU83056 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 660
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 661
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 662
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 663
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 664
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 665
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 666
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 667
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 668
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 669
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 670
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 671
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 672
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 673
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 674
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 675
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 676
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 677
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 678
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 679
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.

PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 680
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 681
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 682
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 683
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 684
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 685
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 686
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 687
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 688
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 689
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 690
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 691
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 692
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 693
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 694
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 695
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 696
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 697
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 698
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 699
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 700

ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 701
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 702
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 703
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 704
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 705
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 706
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 707
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 708
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 709
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 710
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 711
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 712
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 713
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 714
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 715
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 716
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 717
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 718
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 719
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 720
ID ABR95533 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 721
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 722
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 723
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 724
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 725
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 726
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 727
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 728
ID ABM07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 729
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 730
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 731
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 732
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 733
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 734
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 735
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 736
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 737
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 738
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 739
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 740
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 741
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 742
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 743
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 744
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 745
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 746
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 747
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 748
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 749
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 750
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 751
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 752
ID ABM11560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 753
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 754
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 755
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 756
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 757
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 758
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 759
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 760
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 761
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 762
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 763
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 764
ID ABM76035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 765
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 766
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 767
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 768
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 769
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 770
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 771
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 772
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 773
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 774
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 775
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 776
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 777
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 778
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 779
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 780
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 781
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 782
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 783
ID ABM04855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 784
ID ABM08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 785
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 786
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 787
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 788
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 789
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 790
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 791
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 792
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 793
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 794
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 795
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 796
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 797
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 798
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 799
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 800
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 801
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 802
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 803
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 804
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 805
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 806
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 807
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 808
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 809
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 810
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 811
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 812
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 813
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 814
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 815
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 816
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 817
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 818
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 819
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 820
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 821
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 822
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 823
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 824
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 825
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 826
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 827
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 828
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 829
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 830
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 831
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 832
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 833
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 834
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 835
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 836
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 837
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 838
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 839
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 840
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 841
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 842
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 843
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 844
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 845
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 846
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 847
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 848
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 849
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 850
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 851
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 852
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 853
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 854
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 855
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 856
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 857
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 858
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 859
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 860
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 861
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 862
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 863
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 864
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 865
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 866
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 867
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 868
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 869
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 870
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 871
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 872
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 873
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 874
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 875
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 876
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 877
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 878
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 879
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 880
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 881
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 882
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 883
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 884
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 885
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 886
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 887
ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 888
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 889

ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 890
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 891
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 892
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 893
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 894
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 895
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 896
ID ABM06680 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 897
ID ABM09120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 898
ID ABO39160 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 899
ID ABM75425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 900
ID ABM25349 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 901
ID ABM19859 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 902
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 903
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 904
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 905
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 906
ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 907
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 908
ID ABO06820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 909
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 910
ID ABR73331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 911
ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 912
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 913
ID ABM18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 914
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 915
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 916
ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 917
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 918
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 919
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 920
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 921
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 922
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 923
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 924
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 925
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 926
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 927
ID ABM08510 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 928
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 929
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 930
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 931
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 932
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 933
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 934
ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 935
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 936
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 937
ID ABR88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 938
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 939
ID ABM03271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 940
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 941
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 942
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 943
ID ABO05247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 944
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 945
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 946
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 947
ID ABM17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 948
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 949
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 950
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 951
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 952
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 953
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 954
ID ABM10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 955
ID ABM76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 956
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 957
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 958
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 959
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 960
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 961
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 962
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 963
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 964
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 965
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 966
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 967
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 968
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 969
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 970
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 971
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 972
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 973
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 974
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 975
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 976
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 977
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 978
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 979
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 980
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 981
ID ABM14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 982
ID ABM09730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 983
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 984
ID ABM34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 985
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 986
ID ADA42820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 987
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 988
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 989
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 990
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 991
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 992
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 993
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 994
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 995
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 996
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 997
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 998
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 999
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1000
ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1001
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1002
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1003
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1004
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1005
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1006
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1007
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1008
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1009
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1010
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1011
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1012
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1013
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1014
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1015
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1016
ID ABM22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1017
ID ABM30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1018
ID ABM21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1019
ID ABM21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1020
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1021
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1022
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1023
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1024
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1025
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1026
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1027
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1028
ID ABM31754 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1029
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1030
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1031
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1032
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1033
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1034
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1035
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1036
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1037
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1038
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1039
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1040
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1041
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1042
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1043
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1044
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1045
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1046
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1047
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1048
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1049
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1050
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1051
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1052
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1053
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1054
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1055
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1056
ID ADF95378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1057
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1058
ID ADH08853 standard; protein; 360 AA.

DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1059
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1060
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1061
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1062
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1063
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1064
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1065
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1066
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1067
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1068
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1069
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1070
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1071
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1072
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1073
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1074
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1075
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1076

ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1077
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1078
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1079
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1080
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1081
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1082
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1083
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1084
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1085
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1086
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1087
ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1088
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1089
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1090
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1091
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1092
ID ADI65842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1093
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1094
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1095
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1096
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1097
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1098
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1099
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1100
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1101
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1102
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1103
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1104
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1105
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1106
ID ADR11100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1107
ID ADR18009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1108
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1109
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1110
ID AEA37923 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 9; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1111
ID AEA20028 standard; protein; 422 AA.
DE Novel human polypeptide SEQ ID NO 722.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.7%; Score 121.5; DB 9; Length 422;
Best Local Similarity 34.9%; Pred. No. 0.019;
RESULT 1112
ID AAW59882 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 7.7%; Score 121; DB 2; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1113
ID AAB61241 standard; protein; 528 AA.
DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 121; DB 4; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1114
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.7%; Score 121; DB 6; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1115
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1116
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1117
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 121; DB 8; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.028;
RESULT 1118
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 7.7%; Score 120.5; DB 2; Length 1257;
Best Local Similarity 23.6%; Pred. No. 0.1;
RESULT 1119
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.23;
RESULT 1120
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.23;
RESULT 1121
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.

PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.3;
RESULT 1122
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.3;
RESULT 1123
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1124
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1125
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1126
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1127
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1128
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1129
ID ADZ09841 standard; protein; 3396 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.5%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1130
ID ADZ70548 standard; protein; 3396 AA.
DE Human protein from lung cancer marker gene CSPG2.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 7.5%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1131
ID AEA04473 standard; protein; 3396 AA.
DE Human protein from gene overexpressed in cancer, CSPG2.
PN WO2005044990-A2.
PD 19-MAY-2005.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.5%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1132
ID AEB17604 standard; protein; 3396 AA.
DE Human CSPG2 protein SeqID18.
PN JP2005110602-A.
PD 28-APR-2005.
PA (SUMU) SUMITOMO SEIYAKU KK.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 7.5%; Score 118.5; DB 9; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1133
ID ADZ09886 standard; protein; 6792 AA.
DE Human breast cancer marker CSPG2 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.5%; Score 118.5; DB 9; Length 6792;
Best Local Similarity 25.5%; Pred. No. 1.6;
RESULT 1134
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.4%; Score 116; DB 8; Length 2397;
Best Local Similarity 28.4%; Pred. No. 0.67;
RESULT 1135
ID AAR85443 standard; protein; 908 AA.
DE Rat brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 7.3%; Score 115; DB 2; Length 908;
Best Local Similarity 22.2%; Pred. No. 0.22;
RESULT 1136
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 7.3%; Score 114.5; DB 8; Length 1257;
Best Local Similarity 23.1%; Pred. No. 0.39;
RESULT 1137
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 114; DB 7; Length 656;
Best Local Similarity 28.4%; Pred. No. 0.18;
RESULT 1138
ID ADP71273 standard; protein; 191 AA.
DE Human LP2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 7.1%; Score 112.5; DB 8; Length 191;
Best Local Similarity 26.6%; Pred. No. 0.045;
RESULT 1139

ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 112.5; DB 4; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1140
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 7.1%; Score 112.5; DB 5; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1141
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 112.5; DB 8; Length 340;
Best Local Similarity 26.6%; Pred. No. 0.1;
RESULT 1142
ID ABU11635 standard; protein; 343 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 112.5; DB 6; Length 343;
Best Local Similarity 26.6%; Pred. No. 0.1;
RESULT 1143
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 111.5; DB 6; Length 402;
Best Local Similarity 22.5%; Pred. No. 0.16;
RESULT 1144
ID ADP71271 standard; protein; 200 AA.
DE Human aggrecan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 7.0%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.067;
RESULT 1145
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match 7.0%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1146
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.0%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1147
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 7.0%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1148
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 7.0%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1149
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.0%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1150
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.0%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1151
ID ADV70260 standard; protein; 2409 AA.
DE Tumor-associated antigenic target polypeptide TAT498.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 111; DB 9; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1152
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 6.9%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.23;
RESULT 1153
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1154
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.9%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1155
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.9%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1156
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.

PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.9%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1157
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1158
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1159
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1160
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.9%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1161
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.9%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1162
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1163
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1164
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1165
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1166
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1167
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1168
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1169
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1170
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1171
ID ABJ56899 standard; protein; 354 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1172
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1173
ID ABJ56893 standard; protein; 354 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1174
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;

Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1175
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1176
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1177
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant 121P1F1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1178
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1179
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 108; DB 8; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1180
ID AAR77034 standard; protein; 355 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 6.9%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.28;
RESULT 1181
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.52;
RESULT 1182
ID ABJ56890 standard; protein; 721 AA.
DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.75;
RESULT 1183
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.75;
RESULT 1184
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.75;
RESULT 1185
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 6.8%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.056;
RESULT 1186
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1187
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1188
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.8%; Score 107; DB 3; Length 339;
Best Local Similarity 28.6%; Pred. No. 0.33;
RESULT 1189
ID ABJ56915 standard; protein; 354 AA.
DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1190
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.8%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.35;
RESULT 1191
ID ABJ56907 standard; protein; 355 AA.
DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1192
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.62;

RESULT 1193
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.62;
RESULT 1194
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1195
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1196
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1197
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1198
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1199
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1200
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.65;
RESULT 1201
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.8%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 1;
RESULT 1202
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.8%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 1.1;
RESULT 1203
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.8%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 2;
RESULT 1204
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 107; DB 4; Length 1795;
Best Local Similarity 24.1%; Pred. No. 3.2;
RESULT 1205
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1206
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.8%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1207
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 6.8%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1208
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.7%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.8;
RESULT 1209
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 105.5; DB 3; Length 341;
Best Local Similarity 28.9%; Pred. No. 0.46;
RESULT 1210
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.7%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1211
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1212
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.6%; Score 104.5; DB 3; Length 330;
Best Local Similarity 18.7%; Pred. No. 0.55;
RESULT 1213
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.6%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.19;
RESULT 1214
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.6%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.19;
RESULT 1215
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.6%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.19;
RESULT 1216
ID ADY16502 standard; protein; 139 AA.
DE PRO polypeptide SEQ ID NO 2308.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.19;
RESULT 1217
ID AEB29759 standard; protein; 139 AA.
DE Human CD44 isoform RC.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.6%; Score 104; DB 9; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.19;
RESULT 1218
ID ADP71269 standard; protein; 195 AA.
DE Human LP1 protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.6%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.3;
RESULT 1219
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.6%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.31;
RESULT 1220
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.6%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 1.2;
RESULT 1221
ID ABB60536 standard; protein; 1712 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.6%; Score 104; DB 4; Length 1712;
Best Local Similarity 22.7%; Pred. No. 5.9;
RESULT 1222
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 102.5; DB 4; Length 183;
Best Local Similarity 29.7%; Pred. No. 0.38;
RESULT 1223
ID ADX72128 standard; protein; 309 AA.
DE Plant full length insert polypeptide seqid 41494.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.5%; Score 102; DB 8; Length 309;
Best Local Similarity 24.6%; Pred. No. 0.87;
RESULT 1224
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 1225
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.

PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 101.5; DB 3; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.4;
RESULT 1226
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 6.4%; Score 101.5; DB 6; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.4;
RESULT 1227
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.4%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1228
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.4%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1229
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1230
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 6.4%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 1.8;
RESULT 1231
ID ABB68940 standard; protein; 1379 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 100.5; DB 4; Length 1379;
Best Local Similarity 20.2%; Pred. No. 9.4;
RESULT 1232
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYYA) UNIV YALE.
Query Match 6.3%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 1.8;
RESULT 1233
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Query Match 6.3%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 2.2;
RESULT 1234
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.93;
RESULT 1235
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.93;
RESULT 1236
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 4.2;
RESULT 1237
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 14;
RESULT 1238
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 98.5; DB 4; Length 1126;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 1239
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 29;
RESULT 1240
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 3; Length 2870;
Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1241
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 8; Length 2870;
Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1242
ID ADW79951 standard; protein; 2870 AA.
DE Nematode location of vulva (lov-1) mutant protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 9; Length 2870;
Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1243
ID AAY95556 standard; protein; 3178 AA.

DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 3; Length 3178;
Best Local Similarity 22.4%; Pred. No. 79;
RESULT 1244
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 8; Length 3178;
Best Local Similarity 22.4%; Pred. No. 79;
RESULT 1245
ID ADW79940 standard; protein; 3178 AA.
DE Nematode location of vulva (lov-1) protein.
PN US6849717-B1.
PD 01-FEB-2005.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.1%; Score 96; DB 9; Length 3178;
Best Local Similarity 22.4%; Pred. No. 79;
RESULT 1246
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.1%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 2.4;
RESULT 1247
ID ADQ67145 standard; protein; 803 AA.
DE Novel human protein sequence #2118.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.0%; Score 94; DB 8; Length 803;
Best Local Similarity 21.9%; Pred. No. 19;
RESULT 1248
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID No 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1249
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1250
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.9%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1251
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1252
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID No 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1253
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1254
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.9%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1255
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.4;
RESULT 1256
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 93.5; DB 4; Length 320;
Best Local Similarity 23.2%; Pred. No. 5.9;
RESULT 1257
ID ADE36618 standard; protein; 339 AA.
DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.3;
RESULT 1258
ID ADE36592 standard; protein; 339 AA.
DE Human NOV1a protein SEQ ID NO:2.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.3;
RESULT 1259
ID ABR58582 standard; protein; 359 AA.
DE Human cancer related protein SEQ ID NO:239.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1260
ID ABP70439 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;

RESULT 1261
ID ABP70441 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 4.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1262
ID ABP70438 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1263
ID ABR48174 standard; protein; 359 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:64.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1264
ID AAO26680 standard; protein; 359 AA.
DE KIM-1 related protein, SEQ ID No 8.
PN WO200298920-A1.
PD 12-DEC-2002.
PA (BIOJ) BIOGEN INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.9%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1265
ID ADE36594 standard; protein; 359 AA.
DE Human NOV1b protein SEQ ID NO:4.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 93.5; DB 7; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1266
ID ADN38984 standard; protein; 359 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 93.5; DB 7; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1267
ID ADQ76690 standard; protein; 359 AA.
DE Human kidney injury molecule-1 (KIM-1).
PN WO2004060041-A2.
PD 22-JUL-2004.
PA (BIOG-) BIOGEN IDEC MA INC.
Query Match 5.9%; Score 93.5; DB 8; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1268
ID ABR99971 standard; protein; 359 AA.
DE HAVCR1 protein, SEQ ID 25.
PN WO2005001092-A2.
PD 06-JAN-2005.
PA (AMHP) WYETH.
Query Match 5.9%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1269
ID ADY98071 standard; protein; 359 AA.
DE Human TIM-1 allele 1-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.9%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1270
ID ADY98077 standard; protein; 359 AA.
DE Human TIM-1 allele 4-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.9%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1271
ID ADY98073 standard; protein; 359 AA.
DE Human TIM-1 allele 2-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.9%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1272
ID ADZ79370 standard; protein; 359 AA.
DE Human kidney injury molecule-1(b) complete protein.
PN US2005112117-A1.
PD 26-MAY-2005.
PA (BAIL/) BAILLY V.
PA (BONV/) BONVENTRE J.
Query Match 5.9%; Score 93.5; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.9;
RESULT 1273
ID ABG07923 standard; protein; 366 AA.
DE Novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 93.5; DB 4; Length 366;
Best Local Similarity 23.2%; Pred. No. 7.1;
RESULT 1274
ID ADP04445 standard; protein; 1381 AA.
DE Sea squirt protein with tissue specific expression in development Seq40.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.9%; Score 93.5; DB 8; Length 1381;
Best Local Similarity 22.9%; Pred. No. 43;
RESULT 1275
ID ABR63235 standard; protein; 2055 AA.
DE Glucansucrase sequence from strain KG15.
PN WO2003008618-A2.
PD 30-JAN-2003.
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
Query Match 5.9%; Score 93.5; DB 6; Length 2055;
Best Local Similarity 23.3%; Pred. No. 75;
RESULT 1276
ID AAR88466 standard; protein; 629 AA.
DE Drosophila scavenger receptor class CI.
PN WO9600288-A2.
PD 04-JAN-1996.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.9%; Score 93; DB 2; Length 629;
Best Local Similarity 19.9%; Pred. No. 17;
RESULT 1277
ID ABG33057 standard; protein; 629 AA.
DE Fruit fly scavenger receptor type CI (dSR-CI).
PN US6429289-B1.
PD 06-AUG-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.9%; Score 93; DB 5; Length 629;
Best Local Similarity 19.9%; Pred. No. 17;
RESULT 1278
ID AAE21524 standard; protein; 629 AA.
DE Drosophila melanogaster scavenger receptor class CI (dSR-CI).
PN US6350859-B1.
PD 26-FEB-2002.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 5.9%; Score 93; DB 5; Length 629;
Best Local Similarity 19.9%; Pred. No. 17;
RESULT 1279
ID ABP73157 standard; protein; 40 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 5.9%; Score 92.5; DB 6; Length 40;
Best Local Similarity 54.1%; Pred. No. 0.42;
RESULT 1280
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.9%; Score 92.5; DB 2; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1281
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 5.9%; Score 92.5; DB 2; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1282
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 5.9%; Score 92.5; DB 7; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1283
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 5.9%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1284
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.9%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1285
ID ADU66693 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 5.9%; Score 92.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 6.7;
RESULT 1286
ID ABP70440 standard; protein; 365 AA.
DE Amino acid sequence of human TIM-1 allele 3.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.9%; Score 92.5; DB 6; Length 365;
Best Local Similarity 22.6%; Pred. No. 8.7;
RESULT 1287
ID ADY98075 standard; protein; 365 AA.
DE Human TIM-1 allele 3-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.9%; Score 92.5; DB 9; Length 365;
Best Local Similarity 22.6%; Pred. No. 8.7;
RESULT 1288
ID ABB50001 standard; protein; 569 AA.
DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.9%; Score 92.5; DB 5; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1289
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 92.5; DB 6; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1290
ID AAU48553 standard; protein; 706 AA.
DE Propionibacterium acnes immunogenic protein #9449.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.9%; Score 92.5; DB 4; Length 706;
Best Local Similarity 25.4%; Pred. No. 22;
RESULT 1291
ID ABM45072 standard; protein; 706 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.9%; Score 92.5; DB 6; Length 706;
Best Local Similarity 25.4%; Pred. No. 22;
RESULT 1292
ID ADN18863 standard; protein; 994 AA.
DE Bacterial polypeptide #1516.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 92.5; DB 8; Length 994;
Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1293
ID ABR53566 standard; protein; 1636 AA.
DE Protein sequence #SEQ ID 1997.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.9%; Score 92.5; DB 6; Length 1636;
Best Local Similarity 19.7%; Pred. No. 68;
RESULT 1294
ID ADK64364 standard; protein; 1636 AA.
DE Disease treating protein complex-derived protein #1193.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.9%; Score 92.5; DB 7; Length 1636;
Best Local Similarity 19.7%; Pred. No. 68;
RESULT 1295

ID ABP70442 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.8%; Score 92; DB 6; Length 364;
Best Local Similarity 21.6%; Pred. No. 9.7;
RESULT 1296
ID ADY98079 standard; protein; 364 AA.
DE Human TIM-1 allele 5-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.8%; Score 92; DB 9; Length 364;
Best Local Similarity 21.6%; Pred. No. 9.7;
RESULT 1297
ID ABG93047 standard; protein; 966 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.8%; Score 92; DB 5; Length 966;
Best Local Similarity 20.3%; Pred. No. 37;
RESULT 1298
ID ADT87298 standard; protein; 966 AA.
DE Yeast Stress-related protein from gene YBR112C.
PN WO2004092398-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 5.8%; Score 92; DB 8; Length 966;
Best Local Similarity 20.3%; Pred. No. 37;
RESULT 1299
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.7;
RESULT 1300
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.7;
RESULT 1301
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.8%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.7;
RESULT 1302
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.7;
RESULT 1303
ID AAB75555 standard; protein; 298 AA.
DE Gene 1 human secreted protein homologous amino acid sequence #109.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.8%; Score 91.5; DB 4; Length 298;
Best Local Similarity 26.8%; Pred. No. 8.2;
RESULT 1304
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.8%; Score 91.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 8.3;
RESULT 1305
ID AAM52302 standard; protein; 350 AA.
DE ActA protein fragment #2.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.8%; Score 91.5; DB 4; Length 350;
Best Local Similarity 22.0%; Pred. No. 10;
RESULT 1306
ID AAM52301 standard; protein; 376 AA.
DE ActA protein fragment #1.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.8%; Score 91.5; DB 4; Length 376;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 1307
ID AAM52300 standard; protein; 610 AA.
DE ActA protein.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.8%; Score 91.5; DB 4; Length 610;
Best Local Similarity 22.0%; Pred. No. 22;
RESULT 1308
ID AAG79171 standard; protein; 639 AA.
DE Amino acid sequence of an ActA fragment.
PN WO200174858-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.8%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1309
ID AAU09142 standard; protein; 639 AA.
DE Lysteria monocytogenes ActA.
PN WO200174853-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.8%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1310
ID ABB47677 standard; protein; 639 AA.
DE Listeria monocytogenes protein #381.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 91.5; DB 5; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1311
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 5.8%; Score 91.5; DB 8; Length 1103;
Best Local Similarity 24.3%; Pred. No. 49;
RESULT 1312
ID ABP60839 standard; protein; 246 AA.
DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.8%; Score 91; DB 5; Length 246;
Best Local Similarity 27.0%; Pred. No. 7.1;
RESULT 1313
ID AEA08149 standard; protein; 4262 AA.
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 5.8%; Score 91; DB 9; Length 4262;
Best Local Similarity 20.7%; Pred. No. 3.5e+02;
RESULT 1314
ID AEA08148 standard; protein; 4493 AA.
DE Human mucin 17 protein - SEQ ID 3.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match 5.8%; Score 91; DB 9; Length 4493;
Best Local Similarity 20.7%; Pred. No. 3.8e+02;
RESULT 1315
ID ADY11098 standard; protein; 463 AA.
DE Plant full length insert polypeptide seqid 66913.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.7%; Score 90.5; DB 8; Length 463;
Best Local Similarity 23.1%; Pred. No. 19;
RESULT 1316
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brsa-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match 5.7%; Score 90.5; DB 8; Length 505;
Best Local Similarity 27.0%; Pred. No. 21;
RESULT 1317
ID ABB60186 standard; protein; 1714 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 90.5; DB 4; Length 1714;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
RESULT 1318
ID ABB69419 standard; protein; 1976 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 90.5; DB 4; Length 1976;
Best Local Similarity 38.5%; Pred. No. 1.4e+02;
RESULT 1319
ID ABP70443 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 6.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.7%; Score 90; DB 6; Length 364;
Best Local Similarity 21.6%; Pred. No. 15;
RESULT 1320
ID ADY98081 standard; protein; 364 AA.
DE Human TIM-1 allele 5-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.7%; Score 90; DB 9; Length 364;
Best Local Similarity 21.6%; Pred. No. 15;
RESULT 1321
ID ABB59507 standard; protein; 629 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 90; DB 4; Length 629;
Best Local Similarity 20.7%; Pred. No. 32;
RESULT 1322
ID ADD47260 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12954.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 57;
RESULT 1323
ID ADE58049 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3917.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 57;
RESULT 1324
ID ADD47264 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12958.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 57;
RESULT 1325
ID ADE58045 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3913.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 57;
RESULT 1326
ID ADQ29696 standard; protein; 1217 AA.
DE Human colorectal cancer-associated protein #51.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 5.7%; Score 90; DB 8; Length 1217;
Best Local Similarity 18.3%; Pred. No. 79;
RESULT 1327
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 86;
RESULT 1328.

ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 86;
RESULT 1329
ID ABP70432 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.7%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1330
ID ABP70433 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.7%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1331
ID ADY98061 standard; protein; 305 AA.
DE Mouse TIM-2 variant.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.7%; Score 89.5; DB 9; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1332
ID ADY98059 standard; protein; 305 AA.
DE Mouse TIM-2.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.7%; Score 89.5; DB 9; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1333
ID AAR85213 standard; protein; 480 AA.
DE Blowfly larvae PM95 antigen.
PN AU9517609-A.
PD 02-NOV-1995.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.7%; Score 89.5; DB 2; Length 480;
Best Local Similarity 22.1%; Pred. No. 25;
RESULT 1334
ID ABO84994 standard; protein; 917 AA.
DE Murine cancer-associated protein (CAP) MP07-101.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.7%; Score 89.5; DB 8; Length 917;
Best Local Similarity 21.4%; Pred. No. 59;
RESULT 1335
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 15;
RESULT 1336
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 89; DB 5; Length 343;
Best Local Similarity 27.7%; Pred. No. 17;

RESULT 1337
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.7%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1338
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.
PD 18-NOV-1999.
PA (EPIM-) EPIMMUNE INC.
Query Match 5.7%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1339
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.7%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1340
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.7%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1341
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 5.7%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1342
ID ADP23231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.7%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1343
ID ADU60107 standard; protein; 416 AA.
DE Housekeeping gene protein, SEQ ID 68.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 5.7%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1344
ID ADW85920 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein-1.
PN WO2005012912-A2.
PD 10-FEB-2005.
PA (CHIR) CHIRON CORP.
Query Match 5.7%; Score 89; DB 9; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1345
ID ADR86408 standard; protein; 832 AA.
DE Aspergillus fumigatus essential gene protein #458.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.7%; Score 89; DB 8; Length 832;

Best Local Similarity 19.8%; Pred. No. 58;
RESULT 1346
ID ABB70039 standard; protein; 846 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36909.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 89; DB 4; Length 846;
Best Local Similarity 22.5%; Pred. No. 59;
RESULT 1347
ID ABB67102 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28098.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 89; DB 4; Length 882;
Best Local Similarity 22.5%; Pred. No. 63;
RESULT 1348
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 89; DB 8; Length 951;
Best Local Similarity 22.1%; Pred. No. 70;
RESULT 1349
ID ADM19804 standard; protein; 1076 AA.
DE Protein encoded by novel human channel/transporter gene #122.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 89; DB 4; Length 1076;
Best Local Similarity 21.1%; Pred. No. 83;
RESULT 1350
ID ADX97567 standard; protein; 2624 AA.
DE Pancreatic cancer associated human protein, SEQ ID 115.
PN EP1471075-A2.
PD 27-OCT-2004.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
Query Match 5.7%; Score 89; DB 8; Length 2624;
Best Local Similarity 27.7%; Pred. No. 2.8e+02;
RESULT 1351
ID AAG39194 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 88.5; DB 3; Length 193;
Best Local Similarity 21.4%; Pred. No. 8.8;
RESULT 1352
ID AAG39193 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 88.5; DB 3; Length 199;
Best Local Similarity 21.4%; Pred. No. 9.1;
RESULT 1353
ID ABG15314 standard; protein; 358 AA.
DE Novel human diagnostic protein #15305.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 88.5; DB 4; Length 358;
Best Local Similarity 20.2%; Pred. No. 20;
RESULT 1354
ID AAR11605 standard; protein; 392 AA.
DE Human 75kD TNF-binding protein.
PN EP417563-A.
PD 20-MAR-1991.
PA (HOFF) HOFFMANN-LA ROCHE AG.
Query Match 5.6%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 23;
RESULT 1355
ID AAY30935 standard; protein; 392 AA.
DE Human tumour necrosis factor binding protein fragment.
PN EP939121-A2.
PD 01-SEP-1999.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.6%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 23;
RESULT 1356
ID AAB86818 standard; protein; 392 AA.
DE Human TNFBP-associated protein #2.
PN EP1132471-A2.
PD 12-SEP-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.6%; Score 88.5; DB 4; Length 392;
Best Local Similarity 21.8%; Pred. No. 23;
RESULT 1357
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.6%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 28;
RESULT 1358
ID ABB63417 standard; protein; 481 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17043.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 88.5; DB 4; Length 481;
Best Local Similarity 21.2%; Pred. No. 31;
RESULT 1359
ID AAG64210 standard; protein; 596 AA.
DE Murine HSP47 interacting protein, M4.
PN JP2001145493-A.
PD 29-MAY-2001.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.6%; Score 88.5; DB 4; Length 596;
Best Local Similarity 21.3%; Pred. No. 41;
RESULT 1360
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.6%; Score 88.5; DB 2; Length 708;
Best Local Similarity 23.6%; Pred. No. 52;
RESULT 1361
ID ADE86597 standard; protein; 995 AA.
DE Frog tail resorption protein.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 5.6%; Score 88; DB 8; Length 995;
Best Local Similarity 19.9%; Pred. No. 92;
RESULT 1362
ID ADN23131 standard; protein; 3507 AA.
DE Bacterial polypeptide #5784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.6%; Score 88; DB 8; Length 3507;
Best Local Similarity 20.1%; Pred. No. 5.2e+02;
RESULT 1363
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 88; DB 5; Length 4315;
Best Local Similarity 23.8%; Pred. No. 6.9e+02;
RESULT 1364
ID ADL23265 standard; protein; 5703 AA.
DE Human MUC5B.
PN WO2004019041-A1.
PD 04-MAR-2004.
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
PA (PACK/) PACKER N H.
PA (KARL/) KARLSSON N.
PA (SCHU/) SCHULZ B L.
Query Match 5.6%; Score 88; DB 8; Length 5703;
Best Local Similarity 23.8%; Pred. No. 1e+03;
RESULT 1365
ID AEB56507 standard; protein; 5858 AA.
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.
PN WO2005073411-A1.
PD 11-AUG-2005.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.6%; Score 88; DB 9; Length 5858;
Best Local Similarity 23.8%; Pred. No. 1e+03;
RESULT 1366
ID AAG13468 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 87.5; DB 3; Length 310;
Best Local Similarity 23.2%; Pred. No. 21;
RESULT 1367
ID AAG13467 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 87.5; DB 3; Length 331;
Best Local Similarity 23.2%; Pred. No. 23;
RESULT 1368
ID AAY52525 standard; protein; 536 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 5.6%; Score 87.5; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 44;
RESULT 1369
ID AAU96329 standard; protein; 536 AA.
DE Der HMW-map polypeptide #16.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.6%; Score 87.5; DB 5; Length 536;
Best Local Similarity 23.9%; Pred. No. 44;
RESULT 1370
ID AAY52523 standard; protein; 555 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 5.6%; Score 87.5; DB 3; Length 555;
Best Local Similarity 23.9%; Pred. No. 46;
RESULT 1371
ID AAU96327 standard; protein; 555 AA.
DE Der HMW-map polypeptide #14.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.6%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 46;
RESULT 1372
ID AAU96328 standard; protein; 555 AA.
DE Der HMW-map polypeptide #15.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 5.6%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 46;
RESULT 1373
ID ADB64946 standard; protein; 717 AA.
DE Human protein encoded by clone PROST20036350.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.6%; Score 87.5; DB 7; Length 717;
Best Local Similarity 17.8%; Pred. No. 66;
RESULT 1374
ID ADH71768 standard; protein; 904 AA.
DE Human protein of the invention NOV28n SEQ ID NO:664.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 87.5; DB 8; Length 904;
Best Local Similarity 23.8%; Pred. No. 90;
RESULT 1375
ID AAW16313 standard; protein; 906 AA.
DE Yeast alpha factor-G-alpha protein fusion.
PN WO9711159-A1.
PD 27-MAR-1997.
PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.
Query Match 5.6%; Score 87.5; DB 2; Length 906;
Best Local Similarity 19.7%; Pred. No. 91;
RESULT 1376
ID ADZ03664 standard; protein; 981 AA.
DE PRG4-Lub:1 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.6%; Score 87.5; DB 9; Length 981;
Best Local Similarity 20.2%; Pred. No. 1e+02;
RESULT 1377
ID ADZ03672 standard; protein; 1038 AA.
DE PRG4-Lub:3 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.6%; Score 87.5; DB 9; Length 1038;
Best Local Similarity 22.3%; Pred. No. 1.1e+02;
RESULT 1378
ID ADZ03676 standard; protein; 1069 AA.
DE PRG4-Lub:4 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.6%; Score 87.5; DB 9; Length 1069;
Best Local Similarity 22.3%; Pred. No. 1.1e+02;
RESULT 1379
ID AAW54844 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.6%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1380
ID AAY41778 standard; protein; 1085 AA.

DE Bovine parathyroid calcium receptor 1 protein sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.6%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1381
ID AAW89563 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor BoPCaR 1.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.6%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1382
ID AAY51825 standard; protein; 1085 AA.
DE Bovine calcium receptor BoPCaR1 protein.
PN US6031003-A.
PD 29-FEB-2000.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 5.6%; Score 87.5; DB 3; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1383
ID AAB47820 standard; protein; 1085 AA.
DE BoPCaR1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSP-) NPS PHARM INC.
Query Match 5.6%; Score 87.5; DB 5; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1384
ID ADJ93194 standard; protein; 1085 AA.
DE Bovine extracellular Ca-sensing receptor.
PN WO200296946-A1.
PD 05-DEC-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.6%; Score 87.5; DB 7; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1385
ID ADI40961 standard; protein; 1085 AA.
DE Bovine GPCR CASR.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.6%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1386
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.6%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1387
ID ADZ03680 standard; protein; 1100 AA.
DE PRG4-Lub:5 protein.
PN WO2005016130-A2.
PD 24-FEB-2005.
PA (AMHP) WYETH.
Query Match 5.6%; Score 87.5; DB 9; Length 1100;
Best Local Similarity 22.3%; Pred. No. 1.2e+02;
RESULT 1388
ID ADS24007 standard; protein; 1322 AA.
DE Bacterial polypeptide #13040.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.6%; Score 87.5; DB 8; Length 1322;
Best Local Similarity 22.9%; Pred. No. 1.5e+02;
RESULT 1389
ID ADL72180 standard; protein; 2829 AA.
DE X. laevis mutated adenomatous polyposis coli (APC) protein.
PN WO2004018677-A1.
PD 04-MAR-2004.
PA (EISA) EISAI CO LTD.
Query Match 5.6%; Score 87.5; DB 8; Length 2829;
Best Local Similarity 21.2%; Pred. No. 4.3e+02;
RESULT 1390
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.5%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 16;
RESULT 1391
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.5%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;
RESULT 1392
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.5%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;
RESULT 1393
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.5%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;
RESULT 1394
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.5%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;
RESULT 1395
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.5%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;
RESULT 1396
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.5%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 21;

RESULT 1397
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.5%; Score 87; DB 8; Length 363;
Best Local Similarity 25.3%; Pred. No. 29;
RESULT 1398
ID ADY37611 standard; protein; 363 AA.
DE Lung cancer related protein, SEQ ID 87.
PN US2005048589-A1.
PD 03-MAR-2005.
PA (JEND/) JENDOUBI M.
Query Match 5.5%; Score 87; DB 9; Length 363;
Best Local Similarity 25.3%; Pred. No. 29;
RESULT 1399
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 5.5%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 35;
RESULT 1400
ID ADX91714 standard; protein; 611 AA.
DE Plant full length insert polypeptide seqid 54378.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.5%; Score 87; DB 8; Length 611;
Best Local Similarity 21.8%; Pred. No. 59;
RESULT 1401
ID AAG83274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 87; DB 4; Length 631;
Best Local Similarity 28.1%; Pred. No. 62;
RESULT 1402
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 87; DB 5; Length 631;
Best Local Similarity 28.1%; Pred. No. 62;
RESULT 1403
ID ADD42755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 87; DB 7; Length 664;
Best Local Similarity 28.1%; Pred. No. 66;
RESULT 1404
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kB agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.5%; Score 87; DB 2; Length 862;
Best Local Similarity 19.1%; Pred. No. 94;
RESULT 1405
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.5%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 99;
RESULT 1406
ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.5%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 99;
RESULT 1407
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PN WO200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 87; DB 4; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1408
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PN WO200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 5.5%; Score 87; DB 5; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1409
ID ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1410
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 95.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.5%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1411
ID ADW29028 standard; protein; 1016 AA.
DE C_trachomatis polymorphic membrane protein (PmpH) Seq 22.
PN WO2005002619-A2.
PD 13-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 5.5%; Score 87; DB 9; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1412
ID AEA19092 standard; protein; 1016 AA.
DE Chlamydia trachomatis protein - SEQ ID 95.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match 5.5%; Score 87; DB 9; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 1413
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.5%; Score 87; DB 2; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.1e+02;

RESULT 1414
ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 5.5%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.1e+02;
RESULT 1415
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2.1e+02;
RESULT 1416
ID ABB67362 standard; protein; 1575 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28878.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 87; DB 4; Length 1575;
Best Local Similarity 20.5%; Pred. No. 2.2e+02;
RESULT 1417
ID AAU39177 standard; protein; 238 AA.
DE Propionibacterium acnes immunogenic protein #73.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 86.5; DB 4; Length 238;
Best Local Similarity 22.7%; Pred. No. 18;
RESULT 1418
ID ABM35696 standard; protein; 238 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #372.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 86.5; DB 6; Length 238;
Best Local Similarity 22.7%; Pred. No. 18;
RESULT 1419
ID AAP91941 standard; peptide; 400 AA.
DE Sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.5%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 37;
RESULT 1420
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.5%; Score 86.5; DB 2; Length 410;
Best Local Similarity 20.7%; Pred. No. 38;
RESULT 1421
ID ADN19290 standard; protein; 503 AA.
DE Bacterial polypeptide #1943.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 86.5; DB 8; Length 503;
Best Local Similarity 22.1%; Pred. No. 50;

RESULT 1422
ID ADM48341 standard; protein; 681 AA.
DE Marburg virus glycoprotein, GP.
PN US2003215794-A1.
PD 20-NOV-2003.
PA (KAWA/) KAWAOKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Query Match 5.5%; Score 86.5; DB 8; Length 681;
Best Local Similarity 19.2%; Pred. No. 76;
RESULT 1423
ID ABU25742 standard; protein; 687 AA.
DE Protein encoded by Prokaryotic essential gene #11269.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 86.5; DB 6; Length 687;
Best Local Similarity 23.2%; Pred. No. 77;
RESULT 1424
ID ABG15647 standard; protein; 714 AA.
DE Novel human diagnostic protein #15638.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 81;
RESULT 1425
ID ABG15147 standard; protein; 714 AA.
DE Novel human diagnostic protein #15138.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 86.5; DB 4; Length 714;
Best Local Similarity 18.2%; Pred. No. 81;
RESULT 1426
ID AAY54466 standard; protein; 788 AA.
DE Amino acid sequence of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.5%; Score 86.5; DB 3; Length 788;
Best Local Similarity 27.2%; Pred. No. 93;
RESULT 1427
ID AAY54467 standard; protein; 807 AA.
DE Amini acid sequence of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 5.5%; Score 86.5; DB 3; Length 807;
Best Local Similarity 27.2%; Pred. No. 96;
RESULT 1428
ID ADA14416 standard; protein; 1579 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.
PN WO2003068969-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.5%; Score 86.5; DB 6; Length 1579;
Best Local Similarity 21.1%; Pred. No. 2.4e+02;
RESULT 1429
ID ADT07505 standard; protein; 2109 AA.
DE Human colon-specific polypeptide (CSP) #22.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.5%; Score 86.5; DB 8; Length 2109;
Best Local Similarity 26.1%; Pred. No. 3.6e+02;
RESULT 1430
ID ADT07506 standard; protein; 2254 AA.
DE Human colon-specific polypeptide (CSP) #23.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.5%; Score 86.5; DB 8; Length 2254;

Best Local Similarity 26.1%; Pred. No. 3.9e+02;
RESULT 1431
ID ADT07507 standard; protein; 2401 AA.
DE Human colon-specific polypeptide (CSP) #24.
PN WO2004089301-A2.
PD 21-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.5%; Score 86.5; DB 8; Length 2401;
Best Local Similarity 26.1%; Pred. No. 4.3e+02;
RESULT 1432
ID AAY57453 standard; protein; 2781 AA.
DE Human transcriptional regulatory factor SEQ ID NO:10.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.5%; Score 86.5; DB 3; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.2e+02;
RESULT 1433
ID ADF42724 standard; protein; 2781 AA.
DE Human BPTF amino acid sequence SEQ ID NO:30.
PN WO2003102163-A2.
PD 11-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.5%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.2e+02;
RESULT 1434
ID ADO00984 standard; protein; 2781 AA.
DE Human homologue of Fruit fly AD-related protein CG17135.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 5.5%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.2e+02;
RESULT 1435
ID ADQ18653 standard; protein; 2781 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.5%; Score 86.5; DB 8; Length 2781;
Best Local Similarity 20.8%; Pred. No. 5.2e+02;
RESULT 1436
ID AAY57452 standard; protein; 2907 AA.
DE Human transcriptional regulatory factor SEQ ID NO:1.
PN WO9957143-A1.
PD 11-NOV-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.5%; Score 86.5; DB 3; Length 2907;
Best Local Similarity 20.8%; Pred. No. 5.6e+02;
RESULT 1437
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.5%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 52;
RESULT 1438
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.5%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 52;
RESULT 1439
ID AAB98978 standard; protein; 551 AA.
DE Rabbit PCLP1.
PN WO200134797-A1.
PD 17-MAY-2001.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.5%; Score 86; DB 4; Length 551;
Best Local Similarity 26.4%; Pred. No. 64;
RESULT 1440
ID ADD18594 standard; protein; 601 AA.
DE Human disease related protein SeqID25.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.5%; Score 86; DB 7; Length 601;
Best Local Similarity 22.0%; Pred. No. 72;
RESULT 1441
ID AAY05477 standard; protein; 750 AA.
DE C. albicans Rbt1 protein sequence.
PN WO9918115-A1.
PD 15-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.5%; Score 86; DB 2; Length 750;
Best Local Similarity 23.4%; Pred. No. 97;
RESULT 1442
ID ADX76173 standard; protein; 857 AA.
DE Plant full length insert polypeptide seqid 45539.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.5%; Score 86; DB 8; Length 857;
Best Local Similarity 22.1%; Pred. No. 1.2e+02;
RESULT 1443
ID ADB79822 standard; protein; 1080 AA.
DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 5.5%; Score 86; DB 7; Length 1080;
Best Local Similarity 20.2%; Pred. No. 1.6e+02;
RESULT 1444
ID ABG28388 standard; protein; 1086 AA.
DE Novel human diagnostic protein #28379.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 86; DB 4; Length 1086;
Best Local Similarity 19.8%; Pred. No. 1.6e+02;
RESULT 1445
ID ABG05675 standard; protein; 1190 AA.
DE Novel human diagnostic protein #5666.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 86; DB 4; Length 1190;
Best Local Similarity 19.8%; Pred. No. 1.8e+02;
RESULT 1446
ID AAG23116 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 85.5; DB 3; Length 193;
Best Local Similarity 20.9%; Pred. No. 17;
RESULT 1447
ID AAG23115 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 85.5; DB 3; Length 199;
Best Local Similarity 20.9%; Pred. No. 18;
RESULT 1448
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.

Query Match 5.4%; Score 85.5; DB 3; Length 346;
Best Local Similarity 22.4%; Pred. No. 38;
RESULT 1449
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.4%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 38;
RESULT 1450
ID ABB08065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.4%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 38;
RESULT 1451
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.4%; Score 85.5; DB 6; Length 346;
Best Local Similarity 22.4%; Pred. No. 38;
RESULT 1452
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.4%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 39;
RESULT 1453
ID ABB93134 standard; protein; 649 AA.
DE Herbicidally active polypeptide SEQ ID NO 2345.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 85.5; DB 5; Length 649;
Best Local Similarity 23.4%; Pred. No. 89;
RESULT 1454
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.4%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 89;
RESULT 1455
ID ABU15839 standard; protein; 686 AA.
DE Protein encoded by Prokaryotic essential gene #1366.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.4%; Score 85.5; DB 6; Length 686;
Best Local Similarity 24.2%; Pred. No. 96;
RESULT 1456
ID ADN47243 standard; protein; 695 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.4%; Score 85.5; DB 8; Length 695;
Best Local Similarity 20.6%; Pred. No. 98;
RESULT 1457
ID ADD47689 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13385.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1458
ID ADD47692 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13388.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1459
ID AAB07743 standard; protein; 781 AA.
DE A snake venom protease (SVPH-4) polypeptide varaint SVPH-4b.
PN WO200043525-A2.
PD 27-JUL-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 5.4%; Score 85.5; DB 3; Length 781;
Best Local Similarity 17.9%; Pred. No. 1.1e+02;
RESULT 1460
ID ADE71292 standard; protein; 781 AA.
DE Novel human protein #46.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 5.4%; Score 85.5; DB 7; Length 781;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1461
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.4%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 1.3e+02;
RESULT 1462
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 85.5; DB 4; Length 843;
Best Local Similarity 22.5%; Pred. No. 1.3e+02;
RESULT 1463
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.4%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 1.6e+02;
RESULT 1464
ID ABU54710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.4%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 3.5e+02;
RESULT 1465
ID ABU54858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.4%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 3.6e+02;
RESULT 1466
ID ABU54707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.

Query Match 5.4%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 3.7e+02;
RESULT 1467
ID ADE40509 standard; protein; 2055 AA.
DE Human nuclear receptor coactivator ARAP3.
PN DE10135787-A1.
PD 13-FEB-2003.
PA (JENP) JENAPHARM GMBH & CO KG.
Query Match 5.4%; Score 85.5; DB 8; Length 2055;
Best Local Similarity 20.5%; Pred. No. 4.3e+02;
RESULT 1468
ID ABG95034 standard; protein; 2311 AA.
DE Human translocation (4; 11)(q21; q23) protein #1.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 5.4%; Score 85.5; DB 5; Length 2311;
Best Local Similarity 24.3%; Pred. No. 5.1e+02;
RESULT 1469
ID AEB29721 standard; protein; 2448 AA.
DE Human Mucin 5 (subtypes A and C).
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.4%; Score 85.5; DB 9; Length 2448;
Best Local Similarity 24.8%; Pred. No. 5.5e+02;
RESULT 1470
ID ABG31317 standard; protein; 2586 AA.
DE Human 5+3 corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1471
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.4%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1472
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1473
ID ADL02234 standard; protein; 2586 AA.
DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1474
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.4%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1475
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.4%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1476
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 8; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1477
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 5; Length 2589;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1478
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.4%; Score 85.5; DB 8; Length 2589;
Best Local Similarity 25.8%; Pred. No. 5.9e+02;
RESULT 1479
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.4%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 1.8e+03;
RESULT 1480
ID ABU54721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.4%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 4.7e+03;
RESULT 1481
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.4%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 1.1e+04;
RESULT 1482
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 85; DB 3; Length 280;
Best Local Similarity 23.2%; Pred. No. 31;
RESULT 1483
ID ABM91067 standard; protein; 318 AA.
DE M. xanthus protein sequence, seq id 10266.
PN US6833447-B1.

PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 5.4%; Score 85; DB 9; Length 318;
Best Local Similarity 23.7%; Pred. No. 37;
RESULT 1484
ID ABB71546 standard; protein; 326 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 85; DB 4; Length 326;
Best Local Similarity 22.8%; Pred. No. 39;
RESULT 1485
ID ADQ25899 standard; protein; 472 AA.
DE B amyloliquefaciens dipeptide synthesising protein SEQ ID NO: 7.
PN EP1433791-A2.
PD 30-JUN-2004.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 85; DB 8; Length 472;
Best Local Similarity 20.3%; Pred. No. 64;
RESULT 1486
ID ADZ77694 standard; protein; 472 AA.
DE Bacillus amyloliquefaciens IF03022 bacilysin synthetase enzyme Seq 25.
PN EP1529837-A2.
PD 11-MAY-2005.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 85; DB 9; Length 472;
Best Local Similarity 20.3%; Pred. No. 64;
RESULT 1487
ID AEA61455 standard; protein; 472 AA.
DE Dipeptide production microorganism protein, SEQ ID 7.
PN WO2005052153-A1.
PD 09-JUN-2005.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 85; DB 9; Length 472;
Best Local Similarity 20.3%; Pred. No. 64;
RESULT 1488
ID ADV99530 standard; protein; 503 AA.
DE Mouse stimulator of endothelial proliferation, mSEP.
PN WO2004111085-A1.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 5.4%; Score 85; DB 9; Length 503;
Best Local Similarity 23.0%; Pred. No. 70;
RESULT 1489
ID ADW43164 standard; protein; 503 AA.
DE House mouse membrane-bound angiogenic factor SEP protein.
PN WO2004111088-A2.
PD 23-DEC-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 5.4%; Score 85; DB 9; Length 503;
Best Local Similarity 23.0%; Pred. No. 70;
RESULT 1490
ID ABR53289 standard; protein; 576 AA.
DE Protein sequence #SEQ ID 1443.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.4%; Score 85; DB 6; Length 576;
Best Local Similarity 21.0%; Pred. No. 84;
RESULT 1491
ID ADK63572 standard; protein; 576 AA.
DE Disease treating protein complex-derived protein #867.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.4%; Score 85; DB 7; Length 576;
Best Local Similarity 21.0%; Pred. No. 84;
RESULT 1492
ID ABB55236 standard; protein; 627 AA.
DE Lactococcus lactis protein ytfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.4%; Score 85; DB 5; Length 627;
Best Local Similarity 21.5%; Pred. No. 95;
RESULT 1493
ID ADS29466 standard; protein; 627 AA.
DE Bacterial polypeptide #18499.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 85; DB 8; Length 627;
Best Local Similarity 21.5%; Pred. No. 95;
RESULT 1494
ID ADX95894 standard; protein; 635 AA.
DE Plant full length insert polypeptide seqid 58558.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.4%; Score 85; DB 8; Length 635;
Best Local Similarity 23.3%; Pred. No. 96;
RESULT 1495
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.4%; Score 85; DB 6; Length 637;
Best Local Similarity 21.7%; Pred. No. 97;
RESULT 1496
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PD 02-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 85; DB 3; Length 667;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1497
ID ADU06855 standard; protein; 674 AA.
DE Cell adhesion and extracellular matrix protein clone 7520409CD1.
PN WO2004094623-A2.
PD 04-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.4%; Score 85; DB 8; Length 674;
Best Local Similarity 22.4%; Pred. No. 1e+02;
RESULT 1498
ID ADT56202 standard; protein; 782 AA.
DE Plant polypeptide, SEQ ID 6279.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 5.4%; Score 85; DB 8; Length 782;
Best Local Similarity 19.7%; Pred. No. 1.3e+02;
RESULT 1499
ID ABB60387 standard; protein; 1049 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 85; DB 4; Length 1049;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1500
ID AAU14240 standard; protein; 1061 AA.
DE Human novel protein #111.
PN WO200155437-A2.

PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 85; DB 4; Length 1061;
Best Local Similarity 20.2%; Pred. No. 1.9e+02;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 51.9623 Seconds
(without alignments)
2460.550 Million cell updates/sec

Perfect score: 1575
Sequence: 1 TRLLVQGSLRAEELSIQVSC.....NPEESKSPSKTTVRCLEAEV 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
3	1575	100.0	322	3	US-09-905-291A-201	Sequence 201, App
93	1575	100.0	322	4	US-10-223-085-32	Sequence 32, Appl
94	1575	100.0	322	4	US-10-223-084-32	Sequence 32, Appl
95	1575	100.0	322	4	US-10-223-088-32	Sequence 32, Appl
96	1575	100.0	322	4	US-10-223-090-32	Sequence 32, Appl
98	1575	100.0	322	4	US-10-223-087-32	Sequence 32, Appl
101	1575	100.0	322	4	US-10-223-083-32	Sequence 32, Appl
102	1575	100.0	322	4	US-10-079-111-1	Sequence 1, Appli
103	1575	100.0	322	4	US-10-223-089-32	Sequence 32, Appl
108	1575	100.0	322	4	US-10-299-976-201	Sequence 201, App
136	1575	100.0	322	4	US-10-063-742-6	Sequence 6, Appli
211	1575	100.0	322	4	US-10-299-937-201	Sequence 201, App
214	1575	100.0	322	4	US-10-223-081-32	Sequence 32, Appl
224	1575	100.0	322	4	US-10-223-082-32	Sequence 32, Appl
230	1575	100.0	322	4	US-10-298-993-201	Sequence 201, App
231	1575	100.0	322	4	US-10-305-654-32	Sequence 32, Appl
232	1575	100.0	322	4	US-10-448-923-201	Sequence 201, App
233	1575	100.0	322	4	US-10-449-656-201	Sequence 201, App
234	1575	100.0	322	4	US-10-448-713-201	Sequence 201, App
235	1575	100.0	322	4	US-10-425-447-201	Sequence 201, App
236	1575	100.0	322	4	US-10-081-056-32	Sequence 32, Appl
238	1575	100.0	322	4	US-10-215-371-201	Sequence 201, App
239	1575	100.0	322	4	US-10-797-366-201	Sequence 201, App
240	1575	100.0	322	4	US-10-771-187-201	Sequence 201, App
241	1575	100.0	322	5	US-10-972-317-6	Sequence 6, Appli
242	1575	100.0	322	5	US-10-963-467-201	Sequence 201, App
243	1575	100.0	322	5	US-10-978-255-201	Sequence 201, App
244	1575	100.0	322	5	US-10-820-474A-64	Sequence 64, Appl
245	1575	100.0	322	5	US-10-756-149-5685	Sequence 5685, Ap
246	1575	100.0	322	5	US-10-970-823-201	Sequence 201, App
247	1572	99.8	344	4	US-10-276-774-2349	Sequence 2349, Ap
248	1569	99.6	322	4	US-10-291-634-2	Sequence 2, Appli
249	1569	99.6	322	4	US-10-264-237-2665	Sequence 2665, Ap
250	1556	98.8	322	5	US-10-723-860-3909	Sequence 3909, Ap
251	1429.5	90.8	297	4	US-10-138-588-2	Sequence 2, Appli
252	773	49.1	255	3	US-09-866-050A-700	Sequence 700, App
253	224	14.2	364	5	US-10-024-607-8	Sequence 8, Appli
254	222	14.1	365	3	US-09-870-759-73	Sequence 73, Appl
255	222	14.1	365	3	US-09-751-708A-73	Sequence 73, Appl
256	222	14.1	365	4	US-10-428-817A-69	Sequence 69, Appl
257	222	14.1	365	5	US-10-937-758A-50	Sequence 50, Appl
258	219.5	13.9	339	4	US-10-291-634-3	Sequence 3, Appli
259	208.5	13.2	668	4	US-10-741-601-341	Sequence 341, App
260	208.5	13.2	668	5	US-10-473-127-1285	Sequence 1285, Ap
261	208.5	13.2	668	5	US-10-741-600-1047	Sequence 1047, Ap
262	208.5	13.2	668	5	US-10-482-029-253	Sequence 253, App
263	207	13.1	361	3	US-09-836-544-32	Sequence 32, Appl
264	207	13.1	361	5	US-10-473-127-1276	Sequence 1276, Ap
265	207	13.1	361	5	US-10-473-127-1292	Sequence 1292, Ap
266	207	13.1	361	5	US-10-473-127-1296	Sequence 1296, Ap
267	207	13.1	361	5	US-10-473-127-1298	Sequence 1298, Ap
268	207	13.1	361	5	US-10-473-127-1300	Sequence 1300, Ap
269	207	13.1	361	5	US-10-473-127-1302	Sequence 1302, Ap
270	207	13.1	361	5	US-10-473-127-1304	Sequence 1304, Ap
271	205	13.0	361	5	US-10-473-127-1275	Sequence 1275, Ap
272	205	13.0	361	5	US-10-473-127-1309	Sequence 1309, Ap
273	205	13.0	361	5	US-10-473-127-1310	Sequence 1310, Ap
274	205	13.0	361	5	US-10-482-029-255	Sequence 255, App
275	205	13.0	361	5	US-10-852-335A-131	Sequence 131, App
276	204	13.0	361	4	US-10-741-601-340	Sequence 340, App
277	204	13.0	361	5	US-10-473-127-1288	Sequence 1288, Ap
278	204	13.0	361	5	US-10-741-600-1048	Sequence 1048, Ap
279	203.5	12.9	607	5	US-10-486-226-2	Sequence 2, Appli
280	203.5	12.9	700	5	US-10-473-127-1306	Sequence 1306, Ap
281	203.5	12.9	700	5	US-10-505-769-4	Sequence 4, Appli
282	203	12.9	361	5	US-10-505-769-2	Sequence 2, Appli
283	203	12.9	436	5	US-10-473-127-1308	Sequence 1308, Ap
284	203	12.9	742	4	US-10-648-593-176	Sequence 176, App
285	203	12.9	742	5	US-10-473-127-1282	Sequence 1282, Ap
286	203	12.9	742	5	US-10-473-127-1319	Sequence 1319, Ap
287	203	12.9	742	5	US-10-741-600-1054	Sequence 1054, Ap
288	203	12.9	742	5	US-10-287-436A-545	Sequence 545, App
289	203	12.9	742	5	US-10-287-436A-1236	Sequence 1236, Ap
290	202.5	12.9	431	5	US-10-473-127-1307	Sequence 1307, Ap
291	202	12.8	361	4	US-10-663-244-3	Sequence 3, Appli
292	202	12.8	361	5	US-10-473-127-1273	Sequence 1273, Ap
293	202	12.8	675	5	US-10-473-127-1284	Sequence 1284, Ap
294	202	12.8	691	4	US-10-741-601-344	Sequence 344, App
295	202	12.8	691	5	US-10-473-127-1287	Sequence 1287, Ap
296	202	12.8	691	5	US-10-741-600-1053	Sequence 1053, Ap
297	202	12.8	742	3	US-09-983-000A-16	Sequence 16, Appl
298	202	12.8	742	4	US-10-116-275-206	Sequence 206, App
299	202	12.8	742	4	US-10-663-244-1	Sequence 1, Appli
300	202	12.8	742	4	US-10-741-601-338	Sequence 338, App
301	202	12.8	742	4	US-10-741-601-339	Sequence 339, App
302	202	12.8	742	5	US-10-473-127-1286	Sequence 1286, Ap
303	202	12.8	742	5	US-10-473-127-1311	Sequence 1311, Ap
304	202	12.8	742	5	US-10-690-880-40	Sequence 40, Appl
305	202	12.8	742	5	US-10-741-600-1046	Sequence 1046, Ap
306	202	12.8	742	5	US-10-741-600-1049	Sequence 1049, Ap
307	202	12.8	742	5	US-10-652-981-16	Sequence 16, Appl
308	201	12.8	425	5	US-10-473-127-1283	Sequence 1283, Ap
309	200.5	12.7	699	5	US-10-505-769-6	Sequence 6, Appli
310	199.5	12.7	493	3	US-09-836-544-34	Sequence 34, Appl
311	199.5	12.7	493	4	US-10-663-244-2	Sequence 2, Appli
312	199.5	12.7	493	5	US-10-473-127-1278	Sequence 1278, Ap
313	199.5	12.7	493	5	US-10-473-127-1279	Sequence 1279, Ap
314	199.5	12.7	493	5	US-10-473-127-1289	Sequence 1289, Ap
315	199.5	12.7	493	5	US-10-473-127-1293	Sequence 1293, Ap
316	199.5	12.7	493	5	US-10-473-127-1297	Sequence 1297, Ap
317	199.5	12.7	493	5	US-10-473-127-1299	Sequence 1299, Ap

318	199.5	12.7	493	5	US-10-473-127-1301	Sequence 1301, Ap
319	199.5	12.7	493	5	US-10-473-127-1303	Sequence 1303, Ap
320	199.5	12.7	493	5	US-10-473-127-1305	Sequence 1305, Ap
321	199.5	12.7	493	6	US-11-037-713-34	Sequence 34, Appl
322	199.5	12.7	700	4	US-10-012-969C-2	Sequence 2, Appli
323	199	12.6	338	5	US-10-473-127-1271	Sequence 1271, Ap
324	199	12.6	338	5	US-10-473-127-1315	Sequence 1315, Ap
325	198	12.6	395	5	US-10-473-127-1281	Sequence 1281, Ap
326	197	12.5	719	5	US-10-473-127-1270	Sequence 1270, Ap
327	197	12.5	719	5	US-10-473-127-1316	Sequence 1316, Ap
328	196.5	12.5	535	4	US-10-741-601-336	Sequence 336, App
329	196.5	12.5	535	5	US-10-741-600-1044	Sequence 1044, Ap
330	196.5	12.5	699	5	US-10-473-127-1274	Sequence 1274, Ap
331	196.5	12.5	699	5	US-10-473-127-1280	Sequence 1280, Ap
332	196.5	12.5	699	5	US-10-473-127-1313	Sequence 1313, Ap
333	196.5	12.5	699	5	US-10-696-639-71	Sequence 71, Appl
334	196	12.4	293	5	US-10-473-127-1277	Sequence 1277, Ap
335	196	12.4	294	5	US-10-473-127-1290	Sequence 1290, Ap
336	196	12.4	294	5	US-10-473-127-1312	Sequence 1312, Ap
337	196	12.4	395	4	US-10-741-601-345	Sequence 345, App
338	196	12.4	395	5	US-10-741-600-1052	Sequence 1052, Ap
339	196	12.4	425	4	US-10-741-601-337	Sequence 337, App
340	196	12.4	425	5	US-10-741-600-1045	Sequence 1045, Ap
341	196	12.4	493	4	US-10-741-601-343	Sequence 343, App
342	196	12.4	493	5	US-10-741-600-1051	Sequence 1051, Ap
343	194.5	12.3	742	5	US-10-450-763-47430	Sequence 47430, A
344	191.5	12.2	676	5	US-10-473-127-1268	Sequence 1268, Ap
345	191.5	12.2	676	5	US-10-473-127-1318	Sequence 1318, Ap
346	191	12.1	271	5	US-10-473-127-1272	Sequence 1272, Ap
347	191	12.1	271	5	US-10-473-127-1314	Sequence 1314, Ap
348	191	12.1	470	5	US-10-473-127-1269	Sequence 1269, Ap
349	191	12.1	470	5	US-10-473-127-1317	Sequence 1317, Ap
350	187	11.9	112	5	US-10-487-620-2	Sequence 2, Appli
351	186.5	11.8	113	5	US-10-487-620-6	Sequence 6, Appli
352	185	11.7	112	5	US-10-487-620-8	Sequence 8, Appli
353	183	11.6	112	5	US-10-487-620-10	Sequence 10, Appl
354	182	11.6	112	5	US-10-487-620-4	Sequence 4, Appli
355	181	11.5	112	5	US-10-487-620-12	Sequence 12, Appl
356	175.5	11.1	920	5	US-10-450-763-47426	Sequence 47426, A
357	170	10.8	34	3	US-09-864-761-47905	Sequence 47905, A
358	161	10.2	90	3	US-09-799-118-3	Sequence 3, Appli
359	153.5	9.7	90	3	US-09-927-463-8	Sequence 8, Appli
360	153.5	9.7	90	4	US-10-837-671-8	Sequence 8, Appli
361	150	9.5	510	4	US-10-104-047-2580	Sequence 2580, Ap
362	148.5	9.4	80	5	US-10-487-620-23	Sequence 23, Appl
363	145	9.2	277	3	US-09-799-118-2	Sequence 2, Appli
364	145	9.2	277	4	US-10-247-671-185	Sequence 185, App
365	145	9.2	277	4	US-10-295-027-292	Sequence 292, App
366	145	9.2	277	4	US-10-295-027-1237	Sequence 1237, Ap
367	145	9.2	277	5	US-10-723-860-4326	Sequence 4326, Ap
368	145	9.2	1069	4	US-10-028-248A-39	Sequence 39, Appl
369	145	9.2	1069	4	US-10-107-782-39	Sequence 39, Appl
370	145	9.2	2626	4	US-10-634-574-4	Sequence 4, Appli
371	144	9.1	275	5	US-10-960-275-12	Sequence 12, Appl
372	143.5	9.1	95	4	US-10-424-599-248857	Sequence 248857,
373	134	8.5	897	4	US-10-028-248A-41	Sequence 41, Appl
374	134	8.5	897	4	US-10-028-248A-211	Sequence 211, App
375	134	8.5	897	4	US-10-107-782-41	Sequence 41, Appl
376	134	8.5	897	4	US-10-107-782-211	Sequence 211, App
377	134	8.5	2675	4	US-10-028-248A-2	Sequence 2, Appli
378	134	8.5	2675	4	US-10-107-782-2	Sequence 2, Appli
379	133	8.4	1192	4	US-10-028-248A-40	Sequence 40, Appl
380	133	8.4	1192	4	US-10-107-782-40	Sequence 40, Appl
381	133	8.4	1394	3	US-09-842-930A-25	Sequence 25, Appl
382	133	8.4	1394	5	US-10-990-844-25	Sequence 25, Appl
383	133	8.4	1416	4	US-10-133-172-4	Sequence 4, Appli
384	133	8.4	1431	3	US-09-842-930A-2	Sequence 2, Appli
385	133	8.4	1431	4	US-10-133-172-2	Sequence 2, Appli
386	133	8.4	1431	5	US-10-990-844-2	Sequence 2, Appli
387	133	8.4	1653	4	US-10-133-172-20	Sequence 20, Appl
388	131.5	8.3	883	4	US-10-195-970-3	Sequence 3, Appli
389	131.5	8.3	883	4	US-10-453-420-3	Sequence 3, Appli
390	131	8.3	649	3	US-09-759-130B-333	Sequence 333, App
391	131	8.3	649	4	US-10-189-123-63	Sequence 63, Appl
392	131	8.3	649	4	US-10-188-495-63	Sequence 63, Appl
393	131	8.3	649	4	US-10-741-790-333	Sequence 333, App
394	131	8.3	671	3	US-09-759-130B-331	Sequence 331, App
395	131	8.3	671	4	US-10-189-123-61	Sequence 61, Appl
396	131	8.3	671	4	US-10-188-495-61	Sequence 61, Appl
397	131	8.3	671	4	US-10-741-790-331	Sequence 331, App
406	131	8.3	911	4	US-10-237-535-52	Sequence 52, Appl
415	131	8.3	911	4	US-10-239-196-52	Sequence 52, Appl
506	131	8.3	911	4	US-10-312-352-24	Sequence 24, Appl
507	131	8.3	911	5	US-10-936-626-89	Sequence 89, Appl
508	131	8.3	911	5	US-10-938-061-89	Sequence 89, Appl
509	131	8.3	911	5	US-10-983-340-21	Sequence 21, Appl
510	130.5	8.3	883	3	US-09-759-130B-342	Sequence 342, App
511	130.5	8.3	883	4	US-10-195-970-6	Sequence 6, Appli
512	130.5	8.3	883	4	US-10-189-123-72	Sequence 72, Appl
513	130.5	8.3	883	4	US-10-188-495-72	Sequence 72, Appl
514	130.5	8.3	883	4	US-10-453-420-6	Sequence 6, Appli
515	130.5	8.3	883	4	US-10-741-790-342	Sequence 342, App
516	130.5	8.3	1082	4	US-10-264-237-2725	Sequence 2725, Ap
517	130.5	8.3	2316	5	US-10-287-436A-566	Sequence 566, App
518	129.5	8.2	457	5	US-10-960-275-5	Sequence 5, Appli
519	129.5	8.2	2157	5	US-10-960-275-2	Sequence 2, Appli
520	129.5	8.2	2570	4	US-10-028-248A-42	Sequence 42, Appl
521	129.5	8.2	2570	4	US-10-107-782-42	Sequence 42, Appl
522	128.5	8.2	95	5	US-10-473-127-1291	Sequence 1291, Ap
523	128	8.1	2212	4	US-10-028-248A-43	Sequence 43, Appl
524	128	8.1	2212	4	US-10-107-782-43	Sequence 43, Appl
525	127.5	8.1	671	3	US-09-983-000A-14	Sequence 14, Appl
526	127.5	8.1	671	5	US-10-652-981-14	Sequence 14, Appl
527	127.5	8.1	671	5	US-10-936-626-90	Sequence 90, Appl
528	127.5	8.1	671	5	US-10-938-061-90	Sequence 90, Appl
529	127.5	8.1	671	5	US-10-852-335A-97	Sequence 97, Appl
530	127.5	8.1	911	4	US-10-453-420-8	Sequence 8, Appli
531	127.5	8.1	911	4	US-10-295-027-260	Sequence 260, App
532	127	8.1	277	4	US-10-295-027-294	Sequence 294, App
533	127	8.1	277	4	US-10-755-889-118	Sequence 118, App
534	126.5	8.0	457	3	US-09-774-639-108	Sequence 108, App
535	126.5	8.0	457	3	US-09-969-730-110	Sequence 110, App
536	126.5	8.0	457	4	US-10-621-363-110	Sequence 110, App
537	124.5	7.9	482	4	US-10-104-047-3794	Sequence 3794, Ap
540	121.5	7.7	360	3	US-09-905-291A-213	Sequence 213, App
1071	121.5	7.7	360	4	US-10-174-587-28	Sequence 28, Appl
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1123	121.5	7.7	360	4	US-10-448-923-213	Sequence 213, App
1124	121.5	7.7	360	4	US-10-449-656-213	Sequence 213, App
1125	121.5	7.7	360	4	US-10-448-713-213	Sequence 213, App
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1139	121.5	7.7	360	5	US-10-978-255-213	Sequence 213, App
1143	121.5	7.7	360	5	US-10-970-823-213	Sequence 213, App
1144	121	7.7	528	3	US-09-759-130B-341	Sequence 341, App
1145	121	7.7	528	4	US-10-189-123-71	Sequence 71, Appl
1146	121	7.7	528	4	US-10-188-495-71	Sequence 71, Appl
1147	121	7.7	528	4	US-10-741-790-341	Sequence 341, App
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1150	118.5	7.5	1642	5	US-10-741-600-1178	Sequence 1178, Ap
1151	118.5	7.5	3396	4	US-10-788-792-170	Sequence 170, App
1152	118.5	7.5	3396	5	US-10-741-600-1172	Sequence 1172, Ap
1153	118.5	7.5	3396	5	US-10-741-600-1173	Sequence 1173, Ap
1154	118.5	7.5	3396	5	US-10-631-467-773	Sequence 773, App
1155	116	7.4	2397	5	US-10-631-467-1518	Sequence 1518, Ap
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1158	112.5	7.1	287	3	US-09-764-853-576	Sequence 576, App
1159	112.5	7.1	340	4	US-10-112-944-397	Sequence 397, App
1160	111.5	7.1	402	4	US-10-282-122A-64209	Sequence 64209, A

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1167	111	7.0	2409	5	US-10-741-600-1177	Sequence 1177, Ap
1168	111	7.0	2409	5	US-10-482-029-194	Sequence 194, App
1169	111	7.0	2409	5	US-10-852-335A-184	Sequence 184, App
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1171	109	6.9	1321	4	US-10-241-220-82	Sequence 82, Appl
1172	109	6.9	1321	4	US-10-295-027-262	Sequence 262, App
1173	109	6.9	1321	4	US-10-408-765A-1421	Sequence 1421, Ap
1174	109	6.9	1321	4	US-10-698-190-18	Sequence 18, Appl
1175	109	6.9	1321	5	US-10-872-972-82	Sequence 82, Appl
1176	109	6.9	1321	5	US-10-872-991-82	Sequence 82, Appl
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1178	108	6.9	322	4	US-10-120-907A-33	Sequence 33, Appl
1179	108	6.9	354	4	US-10-120-907A-3	Sequence 3, Appli
1180	108	6.9	354	4	US-10-120-907A-7	Sequence 7, Appli
1181	108	6.9	354	4	US-10-120-907A-9	Sequence 9, Appli
1182	108	6.9	354	4	US-10-120-907A-11	Sequence 11, Appl
1183	108	6.9	354	4	US-10-120-907A-13	Sequence 13, Appl
1184	108	6.9	354	4	US-10-120-907A-15	Sequence 15, Appl
1185	108	6.9	354	4	US-10-120-907A-17	Sequence 17, Appl
1186	108	6.9	354	4	US-10-120-907A-19	Sequence 19, Appl
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1188	108	6.9	354	4	US-10-120-907A-23	Sequence 23, Appl
1189	108	6.9	354	4	US-10-120-907A-24	Sequence 24, Appl
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1192	108	6.9	354	4	US-10-120-907A-30	Sequence 30, Appl
1193	108	6.9	354	4	US-10-120-907A-36	Sequence 36, Appl
1194	108	6.9	354	4	US-10-120-907A-38	Sequence 38, Appl
1195	108	6.9	354	4	US-10-120-907A-42	Sequence 42, Appl
1196	108	6.9	354	4	US-10-120-907A-64	Sequence 64, Appl
1197	108	6.9	354	4	US-10-120-907A-66	Sequence 66, Appl
1198	108	6.9	354	5	US-10-754-473-19	Sequence 19, Appl
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1202	108	6.9	721	4	US-10-120-907A-43	Sequence 43, Appl
1203	108	6.9	721	4	US-10-120-907A-65	Sequence 65, Appl
1204	108	6.9	721	4	US-10-120-907A-67	Sequence 67, Appl
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1214	107	6.8	2420	4	US-10-028-248A-4	Sequence 4, Appli
1215	107	6.8	2420	4	US-10-107-782-4	Sequence 4, Appli
1216	105.5	6.7	341	3	US-09-948-820-48	Sequence 48, Appl
1217	105.5	6.7	341	5	US-10-613-076-48	Sequence 48, Appl
1218	105	6.7	354	4	US-10-120-907A-37	Sequence 37, Appl
1219	105	6.7	354	5	US-10-754-473-18	Sequence 18, Appl
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1223	104	6.6	139	5	US-10-473-127-2040	Sequence 2040, Ap
1224	104	6.6	139	5	US-10-741-600-1050	Sequence 1050, Ap
1225	104	6.6	1712	6	US-11-097-143-8400	Sequence 8400, Ap
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1230	101.5	6.4	590	6	US-11-058-709-12	Sequence 12, Appl
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1232	100.5	6.4	402	4	US-10-257-174-47	Sequence 47, Appl
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1242	99	6.3	5376	4	US-10-107-782-74	Sequence 74, Appl
1243	98.5	6.3	1126	6	US-11-097-143-35952	Sequence 35952, A
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1247	95.5	6.1	5374	4	US-10-028-248A-75	Sequence 75, Appl
1248	95.5	6.1	5374	4	US-10-107-782-75	Sequence 75, Appl
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1250	93.5	5.9	258	4	US-10-091-438-205	Sequence 205, App
1251	93.5	5.9	261	3	US-09-764-853-669	Sequence 669, App
1252	93.5	5.9	261	4	US-10-091-438-144	Sequence 144, App
1253	93.5	5.9	320	5	US-10-450-763-31869	Sequence 31869, A
1254	93.5	5.9	339	5	US-10-391-939A-2	Sequence 2, Appli
1255	93.5	5.9	339	5	US-10-391-939A-28	Sequence 28, Appl
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1257	93.5	5.9	359	4	US-10-188-012-19	Sequence 19, Appl
1258	93.5	5.9	359	4	US-10-188-012-23	Sequence 23, Appl
1259	93.5	5.9	359	4	US-10-295-027-302	Sequence 302, App
1260	93.5	5.9	359	4	US-10-188-832-64	Sequence 64, Appl
1261	93.5	5.9	359	5	US-10-391-939A-4	Sequence 4, Appli
1262	93.5	5.9	359	5	US-10-663-497-17	Sequence 17, Appl
1263	93.5	5.9	359	5	US-10-663-497-19	Sequence 19, Appl
1264	93.5	5.9	359	5	US-10-663-497-23	Sequence 23, Appl
1265	93.5	5.9	359	5	US-10-718-321-8	Sequence 8, Appli
1266	93.5	5.9	359	5	US-10-847-918-25	Sequence 25, Appl
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1270	92.5	5.9	300	3	US-09-953-499-10	Sequence 10, Appl
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1272	92.5	5.9	300	4	US-10-633-008-10	Sequence 10, Appl
1273	92.5	5.9	300	4	US-10-785-220-10	Sequence 10, Appl
1274	92.5	5.9	300	4	US-10-785-221-10	Sequence 10, Appl
1275	92.5	5.9	300	4	US-10-785-433-10	Sequence 10, Appl
1276	92.5	5.9	300	4	US-10-767-904-10	Sequence 10, Appl
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1278	92.5	5.9	300	5	US-10-785-607-10	Sequence 10, Appl
1279	92.5	5.9	300	5	US-10-785-351-12	Sequence 12, Appl
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1281	92.5	5.9	365	5	US-10-663-497-21	Sequence 21, Appl
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1285	92	5.8	364	5	US-10-663-497-25	Sequence 25, Appl
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1287	92	5.8	966	4	US-10-451-467A-52	Sequence 52, Appl
1288	91.5	5.8	166	3	US-09-764-853-777	Sequence 777, App
1289	91.5	5.8	166	4	US-10-091-438-181	Sequence 181, App
1290	91.5	5.8	350	4	US-10-239-431A-6	Sequence 6, Appli
1291	91.5	5.8	376	4	US-10-239-431A-4	Sequence 4, Appli
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1293	91.5	5.8	639	3	US-09-825-144-9	Sequence 9, Appli
1294	91.5	5.8	639	3	US-09-823-240-5	Sequence 5, Appli
1295	91.5	5.8	1103	4	US-10-369-493-3228	Sequence 3228, Ap
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1302	90.5	5.7	505	4	US-10-442-017-17	Sequence 17, Appl
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47	107	6.8	556	6	US-10-453-372-210	Sequence 210, App
48	107	6.8	2313	7	US-11-128-059-80	Sequence 80, Appl
49	107	6.8	2417	6	US-10-453-372-228	Sequence 228, App
50	106	6.7	552	6	US-10-453-372-234	Sequence 234, App
51	104	6.6	139	6	US-10-995-561-613	Sequence 613, App
52	104	6.6	139	7	US-11-169-041-201	Sequence 201, App
53	104	6.6	552	6	US-10-453-372-248	Sequence 248, App
54	100.5	6.4	402	7	US-11-174-150-47	Sequence 47, Appl
55	93.5	5.9	359	6	US-10-055-877-265	Sequence 265, App
56	93.5	5.9	359	7	US-11-080-091-1	Sequence 1, Appli
57	93.5	5.9	359	7	US-11-116-939-15	Sequence 15, Appl
58	93.5	5.9	359	7	US-11-087-177-23	Sequence 23, Appl
59	93.5	5.9	359	7	US-11-087-177-25	Sequence 25, Appl
60	93.5	5.9	359	7	US-11-087-177-29	Sequence 29, Appl
61	92.5	5.9	365	7	US-11-087-177-27	Sequence 27, Appl
62	92	5.8	364	7	US-11-087-177-31	Sequence 31, Appl
63	91.5	5.8	305	7	US-11-080-091-13	Sequence 13, Appl
64	90	5.7	364	7	US-11-087-177-33	Sequence 33, Appl
65	89.5	5.7	300	7	US-11-025-834A-21	Sequence 21, Appl
66	89.5	5.7	305	7	US-11-087-177-11	Sequence 11, Appl
67	89.5	5.7	305	7	US-11-087-177-13	Sequence 13, Appl
68	89	5.7	438	6	US-10-821-234-1051	Sequence 1051, Ap
69	87.5	5.6	717	7	US-11-072-512-3100	Sequence 3100, Ap
70	87	5.5	1016	7	US-11-103-957-41	Sequence 41, Appl
71	87	5.5	1016	7	US-11-018-868-22	Sequence 22, Appl
72	86	5.5	390	7	US-11-087-099-4671	Sequence 4671, Ap
73	85	5.4	472	7	US-11-165-211-7	Sequence 7, Appli
74	85	5.4	472	7	US-11-165-226-7	Sequence 7, Appli
75	85	5.4	637	7	US-11-124-367A-321	Sequence 321, App
76	85	5.4	1052	7	US-11-124-367A-323	Sequence 323, App
77	85	5.4	1061	7	US-11-000-463-347	Sequence 347, App
78	85	5.4	1061	7	US-11-124-367A-325	Sequence 325, App
79	85	5.4	1091	7	US-11-000-463-348	Sequence 348, App
80	85	5.4	1419	7	US-11-124-367A-324	Sequence 324, App
81	85	5.4	1428	7	US-11-124-367A-320	Sequence 320, App
82	84	5.3	331	7	US-11-096-568A-11026	Sequence 11026, A
83	84	5.3	332	7	US-11-096-568A-11025	Sequence 11025, A
84	84	5.3	341	7	US-11-096-568A-11024	Sequence 11024, A
85	84	5.3	834	6	US-10-453-372-658	Sequence 658, App
86	83.5	5.3	5179	7	US-11-108-172-1068	Sequence 1068, Ap
87	83	5.3	409	6	US-10-878-556A-55	Sequence 55, Appl
88	83	5.3	775	6	US-10-453-372-656	Sequence 656, App
89	83	5.3	793	6	US-10-995-561-925	Sequence 925, App
90	83	5.3	804	6	US-10-453-372-650	Sequence 650, App
91	83	5.3	847	6	US-10-453-372-654	Sequence 654, App
92	83	5.3	857	6	US-10-453-372-652	Sequence 652, App
93	83	5.3	905	6	US-10-453-372-638	Sequence 638, App
94	83	5.3	905	6	US-10-453-372-662	Sequence 662, App
95	83	5.3	905	6	US-10-453-372-664	Sequence 664, App
96	83	5.3	963	6	US-10-995-561-923	Sequence 923, App
97	83	5.3	963	6	US-10-453-372-660	Sequence 660, App
98	83	5.3	1012	6	US-10-453-372-646	Sequence 646, App
99	83	5.3	1448	6	US-10-485-517-212	Sequence 212, App
100	82.5	5.2	280	7	US-11-096-568A-23463	Sequence 23463, A

102	82.5	5.2	790	6	US-10-973-115B-204	Sequence 204, App
103	82.5	5.2	1690	6	US-10-330-773-389	Sequence 389, App
105	82	5.2	208	6	US-10-973-115B-510	Sequence 510, App
106	82	5.2	312	7	US-11-096-568A-12515	Sequence 12515, A
107	82	5.2	825	6	US-10-453-372-644	Sequence 644, App
108	82	5.2	957	7	US-11-108-172-1065	Sequence 1065, Ap
109	81.5	5.2	432	7	US-11-124-367A-326	Sequence 326, App
110	81.5	5.2	463	6	US-10-467-657-6352	Sequence 6352, Ap
111	81.5	5.2	463	6	US-10-467-657-7604	Sequence 7604, Ap
112	81.5	5.2	1445	7	US-11-169-041-181	Sequence 181, App
113	80.5	5.1	238	7	US-11-096-568A-25154	Sequence 25154, A
114	80.5	5.1	595	7	US-11-182-946-9	Sequence 9, Appli
115	80	5.1	366	7	US-11-096-568A-6733	Sequence 6733, Ap
116	79.5	5.0	336	6	US-10-453-372-640	Sequence 640, App
117	79.5	5.0	461	7	US-11-132-285-6	Sequence 6, Appli
118	79.5	5.0	461	7	US-11-182-946-4	Sequence 4, Appli
119	79.5	5.0	461	7	US-11-183-205-32	Sequence 32, Appl
120	79.5	5.0	721	7	US-11-060-920-5	Sequence 5, Appli
121	79.5	5.0	2591	6	US-10-453-372-718	Sequence 718, App
122	79.5	5.0	2602	6	US-10-453-372-716	Sequence 716, App
123	79.5	5.0	2617	6	US-10-453-372-666	Sequence 666, App
124	79.5	5.0	2617	6	US-10-453-372-732	Sequence 732, App
125	79.5	5.0	2617	6	US-10-453-372-734	Sequence 734, App
126	79.5	5.0	2617	6	US-10-453-372-736	Sequence 736, App
127	79.5	5.0	2617	6	US-10-453-372-738	Sequence 738, App
128	79.5	5.0	2617	6	US-10-453-372-740	Sequence 740, App
129	79.5	5.0	2617	6	US-10-453-372-742	Sequence 742, App
130	79.5	5.0	2617	6	US-10-453-372-744	Sequence 744, App
131	79.5	5.0	2617	6	US-10-453-372-746	Sequence 746, App
132	79.5	5.0	2617	6	US-10-453-372-748	Sequence 748, App
133	79.5	5.0	2617	6	US-10-453-372-750	Sequence 750, App
134	79	5.0	92	7	US-11-128-059-70	Sequence 70, Appl
135	79	5.0	374	7	US-11-072-175-148	Sequence 148, App
136	79	5.0	784	6	US-10-330-773-671	Sequence 671, App
137	78.5	5.0	181	7	US-11-087-099-9675	Sequence 9675, Ap
138	78.5	5.0	181	7	US-11-096-568A-12137	Sequence 12137, A
139	78.5	5.0	409	7	US-11-096-568A-7532	Sequence 7532, Ap
140	78.5	5.0	574	7	US-11-053-100-40	Sequence 40, Appl
141	78.5	5.0	724	7	US-11-053-100-41	Sequence 41, Appl
142	78.5	5.0	874	7	US-11-053-100-42	Sequence 42, Appl
143	78.5	5.0	1174	7	US-11-053-100-43	Sequence 43, Appl
144	78.5	5.0	1722	6	US-10-714-995-48	Sequence 48, Appl
145	78	5.0	280	6	US-10-967-457-75	Sequence 75, Appl
146	78	5.0	453	7	US-11-087-099-7775	Sequence 7775, Ap
147	77.5	4.9	348	7	US-11-096-568A-6734	Sequence 6734, Ap
148	77.5	4.9	472	7	US-11-165-211-6	Sequence 6, Appli
149	77.5	4.9	472	7	US-11-165-226-6	Sequence 6, Appli
150	77.5	4.9	477	6	US-10-540-091-2	Sequence 2, Appli
151	77.5	4.9	630	6	US-10-517-939-42	Sequence 42, Appl
152	77.5	4.9	1249	7	US-11-126-022-30	Sequence 30, Appl
153	77	4.9	771	6	US-10-821-234-1271	Sequence 1271, Ap
154	77	4.9	1007	6	US-10-517-939-84	Sequence 84, Appl
155	77	4.9	1150	7	US-11-139-435-1	Sequence 1, Appli
156	76.5	4.9	279	7	US-11-096-568A-8112	Sequence 8112, Ap
157	76.5	4.9	283	7	US-11-096-568A-8111	Sequence 8111, Ap
158	76.5	4.9	298	7	US-11-096-568A-8110	Sequence 8110, Ap
159	76.5	4.9	311	7	US-11-096-568A-22963	Sequence 22963, A
160	76.5	4.9	536	6	US-10-453-372-6	Sequence 6, Appli
161	76.5	4.9	536	6	US-10-453-372-22	Sequence 22, Appl
162	76.5	4.9	536	6	US-10-453-372-24	Sequence 24, Appl
163	76.5	4.9	536	6	US-10-453-372-26	Sequence 26, Appl
164	76.5	4.9	536	6	US-10-453-372-28	Sequence 28, Appl
166	76.5	4.9	653	6	US-10-917-905-2	Sequence 2, Appli
167	76.5	4.9	653	6	US-10-973-115B-438	Sequence 438, App
168	76.5	4.9	653	7	US-11-135-855-25	Sequence 25, Appl
169	76.5	4.9	773	7	US-11-010-239-63	Sequence 63, Appl
170	76.5	4.9	1249	7	US-11-126-022-25	Sequence 25, Appl
171	76.5	4.9	1307	7	US-11-072-512-2438	Sequence 2438, Ap
172	76	4.8	336	7	US-11-096-568A-34180	Sequence 34180, A
173	76	4.8	367	7	US-11-096-568A-34179	Sequence 34179, A
174	76	4.8	393	7	US-11-096-568A-34178	Sequence 34178, A
175	76	4.8	400	7	US-11-087-099-8803	Sequence 8803, Ap
176	76	4.8	499	7	US-11-096-568A-32028	Sequence 32028, A
177	76	4.8	509	7	US-11-124-327-2	Sequence 2, Appli
178	76	4.8	536	6	US-10-453-372-30	Sequence 30, Appl
179	76	4.8	542	6	US-10-453-372-10	Sequence 10, Appl
180	76	4.8	552	6	US-10-453-372-14	Sequence 14, Appl
181	76	4.8	560	7	US-11-080-991-62	Sequence 62, Appl
182	76	4.8	572	6	US-10-453-372-16	Sequence 16, Appl
183	76	4.8	578	7	US-11-096-568A-27923	Sequence 27923, A
184	76	4.8	588	6	US-10-453-372-8	Sequence 8, Appli
185	76	4.8	588	6	US-10-453-372-12	Sequence 12, Appl
186	76	4.8	594	7	US-11-096-568A-27922	Sequence 27922, A
187	76	4.8	714	7	US-11-096-568A-27921	Sequence 27921, A
188	76	4.8	1014	7	US-11-204-187-20	Sequence 20, Appl
189	75.5	4.8	484	7	US-11-096-568A-6203	Sequence 6203, Ap
190	75.5	4.8	488	7	US-11-096-568A-6202	Sequence 6202, Ap
191	75.5	4.8	499	7	US-11-096-568A-6201	Sequence 6201, Ap
192	75.5	4.8	2343	6	US-10-330-773-904	Sequence 904, App
193	75	4.8	335	7	US-11-096-568A-21687	Sequence 21687, A
194	75	4.8	336	7	US-11-096-568A-21686	Sequence 21686, A
195	75	4.8	941	7	US-11-169-232-14	Sequence 14, Appl
196	75	4.8	1022	7	US-11-169-232-84	Sequence 84, Appl
197	75	4.8	1038	7	US-11-169-232-74	Sequence 74, Appl
198	75	4.8	1049	7	US-11-169-232-58	Sequence 58, Appl
199	75	4.8	1140	7	US-11-169-232-104	Sequence 104, App
200	75	4.8	1270	7	US-11-169-232-44	Sequence 44, Appl
201	75	4.8	1311	7	US-11-169-232-42	Sequence 42, Appl
202	75	4.8	1313	7	US-11-169-232-142	Sequence 142, App
203	75	4.8	1314	7	US-11-169-232-50	Sequence 50, Appl
204	75	4.8	1320	7	US-11-169-232-46	Sequence 46, Appl
205	75	4.8	1320	7	US-11-169-232-60	Sequence 60, Appl
206	75	4.8	1354	7	US-11-169-232-48	Sequence 48, Appl
207	75	4.8	1361	7	US-11-169-232-40	Sequence 40, Appl
208	75	4.8	1363	7	US-11-169-232-52	Sequence 52, Appl
209	75	4.8	1404	7	US-11-169-232-2	Sequence 2, Appli
210	75	4.8	1404	7	US-11-169-232-62	Sequence 62, Appl
211	75	4.8	1874	6	US-10-821-234-1182	Sequence 1182, Ap
212	74.5	4.7	249	7	US-11-128-059-56	Sequence 56, Appl
213	74.5	4.7	441	7	US-11-096-568A-30300	Sequence 30300, A
214	74.5	4.7	671	7	US-11-087-099-8628	Sequence 8628, Ap
215	74.5	4.7	681	7	US-11-096-568A-2501	Sequence 2501, Ap
216	74.5	4.7	733	7	US-11-096-568A-24028	Sequence 24028, A
217	74.5	4.7	759	7	US-11-096-568A-24027	Sequence 24027, A
218	74.5	4.7	764	7	US-11-096-568A-24026	Sequence 24026, A
219	74.5	4.7	998	6	US-10-510-524-1	Sequence 1, Appli
220	74.5	4.7	998	7	US-11-203-251A-88	Sequence 88, Appl
221	74.5	4.7	2801	6	US-10-330-773-630	Sequence 630, App
222	74	4.7	124	7	US-11-128-059-64	Sequence 64, Appl
223	74	4.7	339	6	US-10-498-026-35	Sequence 35, Appl
224	74	4.7	339	6	US-10-498-026-36	Sequence 36, Appl
225	74	4.7	397	7	US-11-096-568A-20883	Sequence 20883, A
226	74	4.7	717	7	US-11-096-568A-28799	Sequence 28799, A
227	74	4.7	860	7	US-11-022-562-217	Sequence 217, App
228	74	4.7	1694	7	US-11-052-554A-83	Sequence 83, Appl
229	73.5	4.7	232	6	US-10-527-500-37	Sequence 37, Appl
230	73.5	4.7	713	7	US-11-256-548-2	Sequence 2, Appli
231	73.5	4.7	826	6	US-10-873-528-194	Sequence 194, App
232	73	4.6	304	7	US-11-087-177-4	Sequence 4, Appli
233	73	4.6	311	7	US-11-096-568A-11193	Sequence 11193, A
234	73	4.6	329	6	US-10-995-561-694	Sequence 694, App
235	73	4.6	353	7	US-11-096-568A-11192	Sequence 11192, A
236	73	4.6	488	7	US-11-202-330-5	Sequence 5, Appli
237	73	4.6	512	7	US-11-108-172-1093	Sequence 1093, Ap
238	73	4.6	558	7	US-11-052-554A-20	Sequence 20, Appl
239	73	4.6	558	7	US-11-134-563-12	Sequence 12, Appl
240	73	4.6	646	6	US-10-995-561-695	Sequence 695, App
241	73	4.6	708	6	US-10-636-320-2	Sequence 2, Appli
242	73	4.6	750	7	US-11-124-368A-244	Sequence 244, App
243	73	4.6	750	7	US-11-124-368A-249	Sequence 249, App
244	73	4.6	918	6	US-10-995-561-696	Sequence 696, App
245	73	4.6	948	6	US-10-523-503-68	Sequence 68, Appl
246	73	4.6	1158	6	US-10-467-657-3112	Sequence 3112, Ap
247	73	4.6	1166	6	US-10-501-035-205	Sequence 205, App
248	73	4.6	1207	6	US-10-821-234-1109	Sequence 1109, Ap
249	72.5	4.6	281	7	US-11-087-177-3	Sequence 3, Appli

250	72.5	4.6	302	7	US-11-096-568A-15531	Sequence 15531, A
251	72.5	4.6	389	7	US-11-096-568A-6654	Sequence 6654, Ap
252	72.5	4.6	445	6	US-10-793-626-1294	Sequence 1294, Ap
253	72.5	4.6	498	6	US-10-510-947-9	Sequence 9, Appli
254	72.5	4.6	582	7	US-11-096-568A-24623	Sequence 24623, A
255	72.5	4.6	605	7	US-11-096-568A-24622	Sequence 24622, A
256	72.5	4.6	673	7	US-11-096-568A-24621	Sequence 24621, A
257	72.5	4.6	758	7	US-11-043-693-1	Sequence 1, Appli
258	72.5	4.6	1152	6	US-10-501-035-222	Sequence 222, App
259	72.5	4.6	1338	6	US-10-821-234-1622	Sequence 1622, Ap
260	72.5	4.6	1338	7	US-11-109-156-23	Sequence 23, Appl
261	72.5	4.6	1338	7	US-11-075-047A-2	Sequence 2, Appli
262	72.5	4.6	2314	7	US-11-097-728-2	Sequence 2, Appli
263	72.5	4.6	2353	7	US-11-097-728-6	Sequence 6, Appli
264	72.5	4.6	2801	7	US-11-124-368A-305	Sequence 305, App
265	72.5	4.6	2801	7	US-11-124-367A-433	Sequence 433, App
266	72.5	4.6	2896	7	US-11-124-368A-306	Sequence 306, App
267	72.5	4.6	2896	7	US-11-124-367A-434	Sequence 434, App
268	72.5	4.6	2910	6	US-10-330-773-39	Sequence 39, Appl
269	72.5	4.6	3256	7	US-11-124-368A-304	Sequence 304, App
270	72.5	4.6	3256	7	US-11-124-367A-432	Sequence 432, App
271	72	4.6	245	7	US-11-087-099-299	Sequence 299, App
272	72	4.6	245	7	US-11-096-568A-33799	Sequence 33799, A
273	72	4.6	255	7	US-11-096-568A-7533	Sequence 7533, Ap
274	72	4.6	308	7	US-11-072-512-3898	Sequence 3898, Ap
275	72	4.6	458	6	US-10-540-091-24	Sequence 24, Appl
276	72	4.6	747	7	US-11-182-592-2	Sequence 2, Appli
277	72	4.6	784	6	US-10-467-657-5968	Sequence 5968, Ap
278	72	4.6	1009	6	US-10-514-531-11	Sequence 11, Appl
279	71.5	4.5	232	6	US-10-884-730-366	Sequence 366, App
280	71.5	4.5	353	7	US-11-096-568A-12810	Sequence 12810, A
281	71.5	4.5	447	6	US-10-641-678-58	Sequence 58, Appl
282	71.5	4.5	541	7	US-11-201-916-4	Sequence 4, Appli
283	71	4.5	250	7	US-11-128-059-62	Sequence 62, Appl
284	71	4.5	343	7	US-11-080-091-4	Sequence 4, Appli
285	71	4.5	345	7	US-11-087-177-19	Sequence 19, Appl
286	71	4.5	354	7	US-11-189-817-2	Sequence 2, Appli
287	71	4.5	554	5	US-09-978-360A-410	Sequence 410, App
288	71	4.5	578	7	US-11-087-099-542	Sequence 542, App
289	71	4.5	579	7	US-11-087-099-6979	Sequence 6979, Ap
290	71	4.5	579	7	US-11-087-099-7852	Sequence 7852, Ap
291	71	4.5	581	7	US-11-087-099-2154	Sequence 2154, Ap
292	71	4.5	581	7	US-11-087-099-2375	Sequence 2375, Ap
293	71	4.5	581	7	US-11-087-099-3070	Sequence 3070, Ap
294	71	4.5	581	7	US-11-087-099-3227	Sequence 3227, Ap
295	71	4.5	581	7	US-11-087-099-3736	Sequence 3736, Ap
296	71	4.5	581	7	US-11-087-099-5261	Sequence 5261, Ap
297	71	4.5	581	7	US-11-087-099-7613	Sequence 7613, Ap
298	71	4.5	581	7	US-11-087-099-8783	Sequence 8783, Ap
299	71	4.5	581	7	US-11-087-099-9181	Sequence 9181, Ap
300	71	4.5	581	7	US-11-087-099-10957	Sequence 10957, A
301	71	4.5	581	7	US-11-087-099-11208	Sequence 11208, A
302	71	4.5	581	7	US-11-087-099-11354	Sequence 11354, A
303	71	4.5	581	7	US-11-087-099-12146	Sequence 12146, A
304	71	4.5	582	7	US-11-087-099-4567	Sequence 4567, Ap
305	71	4.5	626	7	US-11-010-748A-1	Sequence 1, Appli
306	71	4.5	1118	7	US-11-113-751-42	Sequence 42, Appl
307	71	4.5	1153	7	US-11-113-751-44	Sequence 44, Appl
308	71	4.5	1164	7	US-11-087-099-2278	Sequence 2278, Ap
309	71	4.5	1164	7	US-11-087-099-9070	Sequence 9070, Ap
310	70.5	4.5	163	7	US-11-096-568A-4288	Sequence 4288, Ap
311	70.5	4.5	231	7	US-11-096-568A-1421	Sequence 1421, Ap
312	70.5	4.5	232	6	US-10-884-730-363	Sequence 363, App
313	70.5	4.5	232	6	US-10-884-730-364	Sequence 364, App
314	70.5	4.5	232	6	US-10-884-730-365	Sequence 365, App
315	70.5	4.5	292	7	US-11-073-226-6	Sequence 6, Appli
316	70.5	4.5	308	7	US-11-096-568A-20980	Sequence 20980, A
317	70.5	4.5	348	7	US-11-096-568A-20979	Sequence 20979, A
318	70.5	4.5	368	7	US-11-096-568A-20978	Sequence 20978, A
319	70.5	4.5	497	7	US-11-072-512-3603	Sequence 3603, Ap
320	70.5	4.5	512	6	US-10-821-234-1032	Sequence 1032, Ap
322	70.5	4.5	678	7	US-11-102-240-34	Sequence 34, Appl
323	70.5	4.5	678	7	US-11-103-195-34	Sequence 34, Appl
324	70.5	4.5	750	7	US-11-096-568A-30499	Sequence 30499, A
325	70.5	4.5	885	7	US-11-096-568A-30498	Sequence 30498, A
326	70.5	4.5	911	7	US-11-096-568A-30497	Sequence 30497, A
327	70.5	4.5	989	6	US-10-821-234-975	Sequence 975, App
328	70.5	4.5	1980	7	US-11-179-624-3	Sequence 3, Appli
329	70	4.4	221	7	US-11-096-568A-28866	Sequence 28866, A
330	70	4.4	224	7	US-11-096-568A-7141	Sequence 7141, Ap
331	70	4.4	256	7	US-11-096-568A-7140	Sequence 7140, Ap
332	70	4.4	289	7	US-11-096-568A-28865	Sequence 28865, A
333	70	4.4	323	7	US-11-096-568A-21688	Sequence 21688, A
334	70	4.4	393	5	US-09-930-864-1	Sequence 1, Appli
335	70	4.4	427	7	US-11-096-568A-28864	Sequence 28864, A
336	70	4.4	467	7	US-11-087-099-2054	Sequence 2054, Ap
337	70	4.4	485	6	US-10-501-035-349	Sequence 349, App
338	70	4.4	531	7	US-11-096-568A-19343	Sequence 19343, A
339	70	4.4	578	6	US-10-821-234-1039	Sequence 1039, Ap
340	70	4.4	609	7	US-11-110-082-40	Sequence 40, Appl
341	70	4.4	733	7	US-11-096-568A-29646	Sequence 29646, A
342	70	4.4	735	7	US-11-096-568A-29645	Sequence 29645, A
343	70	4.4	735	7	US-11-096-568A-31569	Sequence 31569, A
344	70	4.4	768	7	US-11-096-568A-29644	Sequence 29644, A
345	70	4.4	768	7	US-11-096-568A-31568	Sequence 31568, A
346	70	4.4	770	7	US-11-096-568A-31567	Sequence 31567, A
347	70	4.4	1256	6	US-10-517-696-111	Sequence 111, App
348	70	4.4	1416	7	US-11-128-059-60	Sequence 60, Appl
349	70	4.4	2011	7	US-11-080-991-56	Sequence 56, Appl
350	69.5	4.4	106	7	US-11-096-568A-19298	Sequence 19298, A
351	69.5	4.4	162	7	US-11-096-568A-641	Sequence 641, App
352	69.5	4.4	173	7	US-11-096-568A-452	Sequence 452, App
353	69.5	4.4	173	7	US-11-096-568A-453	Sequence 453, App
354	69.5	4.4	175	7	US-11-087-099-6466	Sequence 6466, Ap
355	69.5	4.4	215	6	US-10-467-657-476	Sequence 476, App
357	69.5	4.4	312	6	US-10-973-115B-336	Sequence 336, App
358	69.5	4.4	349	7	US-11-096-568A-10641	Sequence 10641, A
359	69.5	4.4	453	7	US-11-052-554A-224	Sequence 224, App
360	69.5	4.4	461	7	US-11-096-568A-10640	Sequence 10640, A
361	69.5	4.4	519	7	US-11-087-099-9352	Sequence 9352, Ap
362	69.5	4.4	533	6	US-10-330-773-666	Sequence 666, App
363	69.5	4.4	618	7	US-11-087-099-9161	Sequence 9161, Ap
364	69.5	4.4	626	7	US-11-072-512-2827	Sequence 2827, Ap
365	69.5	4.4	646	7	US-11-087-099-6754	Sequence 6754, Ap
366	69.5	4.4	713	6	US-10-330-773-668	Sequence 668, App
367	69.5	4.4	862	7	US-11-051-720-1443	Sequence 1443, Ap
368	69.5	4.4	1007	7	US-11-051-720-1445	Sequence 1445, Ap
369	69.5	4.4	1120	7	US-11-051-720-1733	Sequence 1733, Ap
370	69.5	4.4	1305	7	US-11-051-720-1370	Sequence 1370, Ap
371	69.5	4.4	16990	7	US-11-175-689-7	Sequence 7, Appli
372	69	4.4	143	7	US-11-096-568A-8463	Sequence 8463, Ap
373	69	4.4	180	7	US-11-096-568A-12758	Sequence 12758, A
374	69	4.4	443	7	US-11-087-099-7683	Sequence 7683, Ap
375	69	4.4	476	7	US-11-055-822-540	Sequence 540, App
376	69	4.4	476	7	US-11-055-822-542	Sequence 542, App
377	69	4.4	476	7	US-11-055-822-1122	Sequence 1122, Ap
378	69	4.4	476	7	US-11-055-822-1124	Sequence 1124, Ap
379	69	4.4	545	7	US-11-201-916-8	Sequence 8, Appli
380	69	4.4	654	6	US-10-528-031-1	Sequence 1, Appli
381	69	4.4	694	7	US-11-096-568A-29818	Sequence 29818, A
382	69	4.4	696	7	US-11-256-548-23	Sequence 23, Appl
383	69	4.4	705	7	US-11-087-099-10564	Sequence 10564, A
384	69	4.4	720	7	US-11-256-548-6	Sequence 6, Appli
385	69	4.4	761	6	US-10-485-517-252	Sequence 252, App
386	69	4.4	802	7	US-11-087-099-4882	Sequence 4882, Ap
387	69	4.4	820	7	US-11-087-099-12246	Sequence 12246, A
388	69	4.4	910	7	US-11-206-587-17	Sequence 17, Appl
389	69	4.4	1158	7	US-11-075-646-6	Sequence 6, Appli
390	68.5	4.3	245	7	US-11-096-568A-21710	Sequence 21710, A
391	68.5	4.3	330	7	US-11-098-686-10903	Sequence 10903, A
392	68.5	4.3	339	7	US-11-096-568A-21709	Sequence 21709, A
393	68.5	4.3	341	7	US-11-096-568A-21708	Sequence 21708, A
394	68.5	4.3	411	7	US-11-096-568A-7197	Sequence 7197, Ap
395	68.5	4.3	436	7	US-11-124-368A-236	Sequence 236, App
396	68.5	4.3	451	7	US-11-096-568A-7196	Sequence 7196, Ap
397	68.5	4.3	455	7	US-11-087-099-10931	Sequence 10931, A

398	68.5	4.3	464	7	US-11-096-568A-7530	Sequence 7530, Ap
399	68.5	4.3	467	7	US-11-096-568A-7195	Sequence 7195, Ap
400	68.5	4.3	467	7	US-11-096-568A-7529	Sequence 7529, Ap
401	68.5	4.3	509	7	US-11-096-568A-7528	Sequence 7528, Ap
402	68.5	4.3	529	7	US-11-210-316-28	Sequence 28, Appl
403	68.5	4.3	589	7	US-11-096-568A-9189	Sequence 9189, Ap
404	68.5	4.3	589	7	US-11-096-568A-9191	Sequence 9191, Ap
405	68.5	4.3	605	7	US-11-096-568A-9188	Sequence 9188, Ap
406	68.5	4.3	696	7	US-11-052-554A-100	Sequence 100, App
407	68.5	4.3	696	7	US-11-052-554A-101	Sequence 101, App
408	68.5	4.3	709	7	US-11-072-512-2349	Sequence 2349, Ap
409	68.5	4.3	748	6	US-10-330-773-394	Sequence 394, App
410	68.5	4.3	825	7	US-11-087-099-1341	Sequence 1341, Ap
411	68.5	4.3	886	7	US-11-087-099-11456	Sequence 11456, A
412	68.5	4.3	897	7	US-11-137-465-35	Sequence 35, Appl
413	68.5	4.3	1070	7	US-11-087-099-5657	Sequence 5657, Ap
414	68.5	4.3	1344	7	US-11-072-512-2452	Sequence 2452, Ap
415	68.5	4.3	1669	6	US-10-330-773-392	Sequence 392, App
416	68.5	4.3	2244	7	US-11-131-263-41	Sequence 41, Appl
417	68	4.3	246	7	US-11-052-554A-50	Sequence 50, Appl
418	68	4.3	263	7	US-11-096-568A-9712	Sequence 9712, Ap
419	68	4.3	269	6	US-10-839-799-109	Sequence 109, App
420	68	4.3	312	6	US-10-986-501-124	Sequence 124, App
421	68	4.3	347	7	US-11-096-568A-16579	Sequence 16579, A
422	68	4.3	406	7	US-11-096-568A-15346	Sequence 15346, A
423	68	4.3	415	7	US-11-096-568A-15345	Sequence 15345, A
424	68	4.3	422	7	US-11-169-041-224	Sequence 224, App
425	68	4.3	472	7	US-11-165-211-4	Sequence 4, Appli
426	68	4.3	472	7	US-11-165-226-4	Sequence 4, Appli
427	68	4.3	550	7	US-11-087-099-5463	Sequence 5463, Ap
428	68	4.3	648	7	US-11-096-568A-27576	Sequence 27576, A
429	68	4.3	693	6	US-10-714-995-24	Sequence 24, Appl
430	68	4.3	1323	6	US-10-517-939-312	Sequence 312, App
431	68	4.3	1340	7	US-11-098-686-11135	Sequence 11135, A
432	68	4.3	2053	7	US-11-013-759-9	Sequence 9, Appli
433	68	4.3	2426	7	US-11-203-806A-11	Sequence 11, Appl
434	68	4.3	3712	7	US-11-019-711-48	Sequence 48, Appl
435	68	4.3	3712	7	US-11-019-711-51	Sequence 51, Appl
436	67.5	4.3	96	7	US-11-096-568A-6177	Sequence 6177, Ap
437	67.5	4.3	163	7	US-11-096-568A-9622	Sequence 9622, Ap
438	67.5	4.3	173	7	US-11-096-568A-9621	Sequence 9621, Ap
439	67.5	4.3	176	7	US-11-096-568A-9620	Sequence 9620, Ap
440	67.5	4.3	238	7	US-11-096-568A-26721	Sequence 26721, A
441	67.5	4.3	400	7	US-11-096-568A-3236	Sequence 3236, Ap
442	67.5	4.3	411	7	US-11-024-959-330	Sequence 330, App
443	67.5	4.3	413	7	US-11-096-568A-20771	Sequence 20771, A
444	67.5	4.3	418	7	US-11-096-568A-3235	Sequence 3235, Ap
445	67.5	4.3	423	7	US-11-098-686-10135	Sequence 10135, A
446	67.5	4.3	436	7	US-11-096-568A-3234	Sequence 3234, Ap
447	67.5	4.3	497	7	US-11-072-512-3773	Sequence 3773, Ap
448	67.5	4.3	532	7	US-11-087-099-8860	Sequence 8860, Ap
449	67.5	4.3	577	7	US-11-201-916-31	Sequence 31, Appl
450	67.5	4.3	600	7	US-11-072-512-3397	Sequence 3397, Ap
451	67.5	4.3	618	7	US-11-087-099-6625	Sequence 6625, Ap
452	67.5	4.3	623	7	US-11-096-568A-26597	Sequence 26597, A
453	67.5	4.3	630	7	US-11-236-198-5	Sequence 5, Appli
454	67.5	4.3	637	7	US-11-096-568A-27876	Sequence 27876, A
455	67.5	4.3	649	7	US-11-236-198-3	Sequence 3, Appli
456	67.5	4.3	704	7	US-11-096-568A-27875	Sequence 27875, A
457	67.5	4.3	725	7	US-11-096-568A-26596	Sequence 26596, A
458	67.5	4.3	732	7	US-11-096-568A-27874	Sequence 27874, A
459	67.5	4.3	758	7	US-11-096-568A-26595	Sequence 26595, A
460	67.5	4.3	961	7	US-11-113-424-35	Sequence 35, Appl
461	67.5	4.3	1026	7	US-11-169-041-205	Sequence 205, App
462	67.5	4.3	1122	7	US-11-191-374-3	Sequence 3, Appli
463	67.5	4.3	1122	7	US-11-191-375-3	Sequence 3, Appli
464	67.5	4.3	1122	7	US-11-191-588-3	Sequence 3, Appli
465	67.5	4.3	1267	7	US-11-096-568A-28960	Sequence 28960, A
466	67.5	4.3	1274	7	US-11-096-568A-28959	Sequence 28959, A
467	67.5	4.3	1480	7	US-11-096-568A-28958	Sequence 28958, A
468	67.5	4.3	1574	7	US-11-212-443-179	Sequence 179, App
469	67.5	4.3	1678	7	US-11-124-367A-340	Sequence 340, App
470	67.5	4.3	1678	7	US-11-124-367A-341	Sequence 341, App
471	67.5	4.3	1978	7	US-11-212-443-60	Sequence 60, Appl
472	67.5	4.3	4374	7	US-11-128-572-2	Sequence 2, Appli
473	67	4.3	137	7	US-11-072-512-2849	Sequence 2849, Ap
474	67	4.3	149	7	US-11-096-568A-12138	Sequence 12138, A
475	67	4.3	208	7	US-11-072-512-2188	Sequence 2188, Ap
476	67	4.3	209	7	US-11-096-568A-3341	Sequence 3341, Ap
477	67	4.3	246	7	US-11-073-226-1	Sequence 1, Appli
478	67	4.3	304	7	US-11-080-091-10	Sequence 10, Appl
479	67	4.3	309	6	US-10-873-528-156	Sequence 156, App
480	67	4.3	317	7	US-11-087-099-9345	Sequence 9345, Ap
481	67	4.3	332	7	US-11-096-568A-14684	Sequence 14684, A
482	67	4.3	336	7	US-11-087-099-4886	Sequence 4886, Ap
483	67	4.3	336	7	US-11-096-568A-5652	Sequence 5652, Ap
484	67	4.3	344	7	US-11-174-816-47	Sequence 47, Appl
485	67	4.3	344	7	US-11-174-819-32	Sequence 32, Appl
486	67	4.3	345	7	US-11-087-177-21	Sequence 21, Appl
487	67	4.3	362	7	US-11-080-091-12	Sequence 12, Appl
488	67	4.3	389	7	US-11-188-743-23	Sequence 23, Appl
489	67	4.3	402	7	US-11-096-568A-14683	Sequence 14683, A
490	67	4.3	413	7	US-11-096-568A-14682	Sequence 14682, A
491	67	4.3	472	7	US-11-165-211-1	Sequence 1, Appli
492	67	4.3	472	7	US-11-165-211-2	Sequence 2, Appli
493	67	4.3	472	7	US-11-165-211-3	Sequence 3, Appli
494	67	4.3	472	7	US-11-165-211-5	Sequence 5, Appli
495	67	4.3	472	7	US-11-165-226-1	Sequence 1, Appli
496	67	4.3	472	7	US-11-165-226-2	Sequence 2, Appli
497	67	4.3	472	7	US-11-165-226-3	Sequence 3, Appli
498	67	4.3	472	7	US-11-165-226-5	Sequence 5, Appli
499	67	4.3	514	7	US-11-195-739-1	Sequence 1, Appli
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501	67	4.3	536	7	US-11-018-868-42	Sequence 42, Appl
502	67	4.3	543	7	US-11-096-568A-31276	Sequence 31276, A
503	67	4.3	552	7	US-11-087-099-10983	Sequence 10983, A
504	67	4.3	581	7	US-11-096-568A-31275	Sequence 31275, A
505	67	4.3	619	6	US-10-517-939-352	Sequence 352, App
506	67	4.3	644	7	US-11-087-099-11826	Sequence 11826, A
507	67	4.3	645	7	US-11-072-512-3227	Sequence 3227, Ap
508	67	4.3	681	7	US-11-067-121-9	Sequence 9, Appli
509	67	4.3	765	7	US-11-087-099-905	Sequence 905, App
510	67	4.3	823	7	US-11-087-099-1971	Sequence 1971, Ap
511	67	4.3	976	6	US-10-966-483-2	Sequence 2, Appli
512	67	4.3	976	6	US-10-511-273-1	Sequence 1, Appli
513	67	4.3	976	7	US-11-233-796-2	Sequence 2, Appli
514	67	4.3	976	7	US-11-072-175-138	Sequence 138, App
515	67	4.3	976	7	US-11-203-251A-77	Sequence 77, Appl
516	67	4.3	1218	7	US-11-052-554A-123	Sequence 123, App
517	67	4.3	1279	6	US-10-793-626-3188	Sequence 3188, Ap
518	67	4.3	4384	6	US-10-821-234-1120	Sequence 1120, Ap
519	66.5	4.2	160	7	US-11-087-099-4973	Sequence 4973, Ap
520	66.5	4.2	180	7	US-11-096-568A-3993	Sequence 3993, Ap
521	66.5	4.2	191	7	US-11-096-568A-3992	Sequence 3992, Ap
522	66.5	4.2	221	6	US-10-714-887-144	Sequence 144, App
523	66.5	4.2	235	5	US-09-978-360A-782	Sequence 782, App
524	66.5	4.2	298	7	US-11-080-091-9	Sequence 9, Appli
526	66.5	4.2	310	6	US-10-973-115B-152	Sequence 152, App
527	66.5	4.2	310	7	US-11-043-806-394	Sequence 394, App
528	66.5	4.2	310	7	US-11-043-806-395	Sequence 395, App
529	66.5	4.2	310	7	US-11-043-806-397	Sequence 397, App
530	66.5	4.2	314	7	US-11-096-568A-3237	Sequence 3237, Ap
531	66.5	4.2	319	7	US-11-096-568A-24347	Sequence 24347, A
532	66.5	4.2	362	7	US-11-256-548-3	Sequence 3, Appli
533	66.5	4.2	380	7	US-11-087-099-1300	Sequence 1300, Ap
534	66.5	4.2	502	7	US-11-098-686-10593	Sequence 10593, A
535	66.5	4.2	648	6	US-10-917-905-6	Sequence 6, Appli
536	66.5	4.2	673	6	US-10-330-773-674	Sequence 674, App
537	66.5	4.2	786	6	US-10-467-962B-103	Sequence 103, App
538	66.5	4.2	812	7	US-11-120-308-126	Sequence 126, App
539	66.5	4.2	897	7	US-11-087-099-11042	Sequence 11042, A
540	66.5	4.2	1267	7	US-11-109-156-35	Sequence 35, Appl
541	66	4.2	149	7	US-11-087-099-7791	Sequence 7791, Ap
542	66	4.2	212	7	US-11-025-834A-16	Sequence 16, Appl
543	66	4.2	292	7	US-11-129-143-96	Sequence 96, Appl
544	66	4.2	300	7	US-11-096-568A-27037	Sequence 27037, A

545	66	4.2	333	7	US-11-096-568A-21892	Sequence 21892, A
546	66	4.2	334	7	US-11-096-568A-21891	Sequence 21891, A
547	66	4.2	337	7	US-11-087-099-3435	Sequence 3435, Ap
548	66	4.2	340	6	US-10-501-035-354	Sequence 354, App
549	66	4.2	343	7	US-11-016-564-17	Sequence 17, Appl
550	66	4.2	344	7	US-11-174-816-46	Sequence 46, Appl
551	66	4.2	344	7	US-11-174-819-30	Sequence 30, Appl
552	66	4.2	367	7	US-11-072-512-2763	Sequence 2763, Ap
553	66	4.2	380	7	US-11-087-099-6673	Sequence 6673, Ap
554	66	4.2	434	7	US-11-096-568A-21798	Sequence 21798, A
555	66	4.2	462	7	US-11-177-648-27	Sequence 27, Appl
556	66	4.2	462	7	US-11-177-648-92	Sequence 92, Appl
557	66	4.2	462	7	US-11-177-648-93	Sequence 93, Appl
558	66	4.2	462	7	US-11-177-648-94	Sequence 94, Appl
559	66	4.2	462	7	US-11-177-648-95	Sequence 95, Appl
560	66	4.2	464	7	US-11-096-568A-21797	Sequence 21797, A
562	66	4.2	490	6	US-10-973-115B-356	Sequence 356, App
563	66	4.2	508	7	US-11-087-099-10016	Sequence 10016, A
564	66	4.2	525	7	US-11-074-176-146	Sequence 146, App
565	66	4.2	567	7	US-11-016-503-2	Sequence 2, Appli
567	66	4.2	607	6	US-10-973-115B-344	Sequence 344, App
568	66	4.2	607	7	US-11-176-863-2	Sequence 2, Appli
569	66	4.2	648	7	US-11-098-686-10873	Sequence 10873, A
570	66	4.2	690	6	US-10-613-744-19	Sequence 19, Appl
571	66	4.2	690	6	US-10-511-657-2	Sequence 2, Appli
572	66	4.2	738	6	US-10-880-881-23	Sequence 23, Appl
573	66	4.2	780	7	US-11-087-099-251	Sequence 251, App
574	66	4.2	793	7	US-11-060-914-2	Sequence 2, Appli
575	66	4.2	799	6	US-10-493-909-8	Sequence 8, Appli
576	66	4.2	822	6	US-10-493-909-48	Sequence 48, Appl
577	66	4.2	823	7	US-11-087-099-11109	Sequence 11109, A
578	66	4.2	874	6	US-10-510-386-28	Sequence 28, Appl
579	66	4.2	928	7	US-11-130-594-8	Sequence 8, Appli
580	66	4.2	928	7	US-11-201-801-8	Sequence 8, Appli
581	66	4.2	931	7	US-11-230-145-2	Sequence 2, Appli
582	66	4.2	1035	6	US-10-966-483-20	Sequence 20, Appl
583	66	4.2	1035	7	US-11-021-441-4	Sequence 4, Appli
584	66	4.2	1047	6	US-10-510-386-200	Sequence 200, App
585	66	4.2	1161	7	US-11-075-646-8	Sequence 8, Appli
586	66	4.2	1551	7	US-11-087-099-10366	Sequence 10366, A
587	66	4.2	1647	7	US-11-052-554A-260	Sequence 260, App
588	65.5	4.2	145	6	US-10-793-626-1504	Sequence 1504, Ap
589	65.5	4.2	192	7	US-11-096-568A-3893	Sequence 3893, Ap
590	65.5	4.2	205	7	US-11-096-568A-3892	Sequence 3892, Ap
591	65.5	4.2	257	7	US-11-096-568A-25250	Sequence 25250, A
592	65.5	4.2	436	7	US-11-024-959-394	Sequence 394, App
593	65.5	4.2	445	6	US-10-467-657-5092	Sequence 5092, Ap
594	65.5	4.2	470	6	US-10-878-556A-101	Sequence 101, App
595	65.5	4.2	485	7	US-11-096-568A-26552	Sequence 26552, A
596	65.5	4.2	539	7	US-11-096-568A-13358	Sequence 13358, A
597	65.5	4.2	541	7	US-11-201-916-17	Sequence 17, Appl
598	65.5	4.2	560	7	US-11-018-868-40	Sequence 40, Appl
599	65.5	4.2	567	6	US-10-485-517-216	Sequence 216, App
600	65.5	4.2	612	6	US-10-467-657-3988	Sequence 3988, Ap
601	65.5	4.2	652	6	US-10-821-234-1016	Sequence 1016, Ap
602	65.5	4.2	683	7	US-11-124-368A-243	Sequence 243, App
603	65.5	4.2	707	7	US-11-072-512-3162	Sequence 3162, Ap
604	65.5	4.2	777	7	US-11-124-368A-238	Sequence 238, App
605	65.5	4.2	778	7	US-11-124-368A-240	Sequence 240, App
606	65.5	4.2	791	7	US-11-124-368A-245	Sequence 245, App
607	65.5	4.2	836	7	US-11-124-368A-246	Sequence 246, App
608	65.5	4.2	877	6	US-10-485-517-200	Sequence 200, App
609	65.5	4.2	925	6	US-10-453-372-1124	Sequence 1124, Ap
610	65.5	4.2	966	6	US-10-877-346-32	Sequence 32, Appl
611	65.5	4.2	972	6	US-10-453-372-1128	Sequence 1128, Ap
612	65.5	4.2	997	7	US-11-080-991-50	Sequence 50, Appl
613	65.5	4.2	999	7	US-11-113-424-36	Sequence 36, Appl
614	65.5	4.2	2432	6	US-10-821-234-899	Sequence 899, App
615	65.5	4.2	2551	7	US-11-052-554A-368	Sequence 368, App
616	65.5	4.2	3069	7	US-11-235-732-2	Sequence 2, Appli
617	65.5	4.2	3095	7	US-11-235-732-4	Sequence 4, Appli
618	65.5	4.2	3100	7	US-11-235-732-7	Sequence 7, Appli
619	65.5	4.2	3567	6	US-10-453-372-1112	Sequence 1112, Ap
620	65.5	4.2	14130	7	US-11-175-689-9	Sequence 9, Appli
621	65	4.1	162	6	US-10-467-657-9046	Sequence 9046, Ap
622	65	4.1	181	6	US-10-746-959C-10	Sequence 10, Appl
623	65	4.1	196	7	US-11-096-568A-24825	Sequence 24825, A
624	65	4.1	204	7	US-11-052-554A-377	Sequence 377, App
625	65	4.1	211	7	US-11-096-568A-24824	Sequence 24824, A
626	65	4.1	234	7	US-11-096-568A-21717	Sequence 21717, A
627	65	4.1	244	7	US-11-052-554A-60	Sequence 60, Appl
628	65	4.1	244	7	US-11-096-568A-9713	Sequence 9713, Ap
629	65	4.1	248	7	US-11-096-568A-13135	Sequence 13135, A
630	65	4.1	253	7	US-11-096-568A-21716	Sequence 21716, A
631	65	4.1	305	6	US-10-055-877-126	Sequence 126, App
632	65	4.1	305	6	US-10-055-877-264	Sequence 264, App
633	65	4.1	305	7	US-11-080-091-2	Sequence 2, Appli
634	65	4.1	305	7	US-11-087-177-7	Sequence 7, Appli
635	65	4.1	309	7	US-11-037-243-118	Sequence 118, App
636	65	4.1	379	7	US-11-087-099-10889	Sequence 10889, A
637	65	4.1	380	7	US-11-087-099-4525	Sequence 4525, Ap
638	65	4.1	380	7	US-11-087-099-4810	Sequence 4810, Ap
639	65	4.1	432	7	US-11-055-822-1096	Sequence 1096, Ap
640	65	4.1	445	7	US-11-072-512-2209	Sequence 2209, Ap
642	65	4.1	449	6	US-10-973-115B-224	Sequence 224, App
643	65	4.1	462	7	US-11-177-648-96	Sequence 96, Appl
644	65	4.1	509	7	US-11-008-727-16	Sequence 16, Appl
645	65	4.1	555	7	US-11-072-512-2530	Sequence 2530, Ap
646	65	4.1	557	7	US-11-016-503-4	Sequence 4, Appli
647	65	4.1	567	7	US-11-016-503-10	Sequence 10, Appl
648	65	4.1	619	7	US-11-136-244-3	Sequence 3, Appli
649	65	4.1	625	7	US-11-072-512-3210	Sequence 3210, Ap
650	65	4.1	628	7	US-11-037-243-86	Sequence 86, Appl
651	65	4.1	640	7	US-11-136-244-4	Sequence 4, Appli
652	65	4.1	653	6	US-10-501-035-358	Sequence 358, App
653	65	4.1	764	7	US-11-072-512-2379	Sequence 2379, Ap
654	65	4.1	814	7	US-11-124-368A-186	Sequence 186, App
655	65	4.1	922	7	US-11-072-512-2694	Sequence 2694, Ap
656	65	4.1	1036	7	US-11-096-568A-28315	Sequence 28315, A
657	65	4.1	1070	7	US-11-096-568A-28314	Sequence 28314, A
658	65	4.1	1131	7	US-11-072-512-2866	Sequence 2866, Ap
659	65	4.1	1198	6	US-10-451-375-4	Sequence 4, Appli
660	65	4.1	1276	7	US-11-096-568A-28313	Sequence 28313, A
661	65	4.1	1981	6	US-10-374-954-23	Sequence 23, Appl
662	65	4.1	1992	7	US-11-013-759-3	Sequence 3, Appli
663	65	4.1	1992	7	US-11-013-759-13	Sequence 13, Appl
664	65	4.1	1998	6	US-10-374-954-21	Sequence 21, Appl
665	65	4.1	2009	6	US-10-374-954-2	Sequence 2, Appli
666	65	4.1	2047	7	US-11-013-759-4	Sequence 4, Appli
667	65	4.1	2047	7	US-11-013-759-7	Sequence 7, Appli
668	64.5	4.1	160	6	US-10-533-811-13	Sequence 13, Appl
669	64.5	4.1	223	7	US-11-087-099-7197	Sequence 7197, Ap
670	64.5	4.1	250	7	US-11-096-568A-3195	Sequence 3195, Ap
671	64.5	4.1	264	7	US-11-096-568A-5205	Sequence 5205, Ap
672	64.5	4.1	282	6	US-10-055-877-127	Sequence 127, App
673	64.5	4.1	282	7	US-11-087-177-9	Sequence 9, Appli
674	64.5	4.1	315	7	US-11-072-512-2198	Sequence 2198, Ap
675	64.5	4.1	370	7	US-11-096-568A-3216	Sequence 3216, Ap
676	64.5	4.1	370	7	US-11-096-568A-3217	Sequence 3217, Ap
677	64.5	4.1	371	6	US-10-467-657-1926	Sequence 1926, Ap
678	64.5	4.1	378	7	US-11-087-099-8872	Sequence 8872, Ap
679	64.5	4.1	378	7	US-11-087-099-11183	Sequence 11183, A
680	64.5	4.1	380	7	US-11-087-099-5374	Sequence 5374, Ap
681	64.5	4.1	381	7	US-11-087-099-12159	Sequence 12159, A
682	64.5	4.1	388	7	US-11-087-099-4330	Sequence 4330, Ap
683	64.5	4.1	393	7	US-11-096-568A-3215	Sequence 3215, Ap
684	64.5	4.1	407	7	US-11-096-568A-5204	Sequence 5204, Ap
685	64.5	4.1	433	7	US-11-096-568A-5203	Sequence 5203, Ap
686	64.5	4.1	482	6	US-10-821-234-972	Sequence 972, App
687	64.5	4.1	519	7	US-11-087-099-5406	Sequence 5406, Ap
688	64.5	4.1	579	7	US-11-072-512-2360	Sequence 2360, Ap
689	64.5	4.1	645	7	US-11-072-512-3418	Sequence 3418, Ap
691	64.5	4.1	649	7	US-11-102-240-132	Sequence 132, App
692	64.5	4.1	649	7	US-11-103-195-132	Sequence 132, App
693	64.5	4.1	651	7	US-11-198-819-22	Sequence 22, Appl
694	64.5	4.1	729	7	US-11-096-568A-19858	Sequence 19858, A

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696	64.5	4.1	791	7	US-11-096-568A-19857	Sequence 19857, A
697	64.5	4.1	848	7	US-11-096-568A-19856	Sequence 19856, A
698	64.5	4.1	1075	7	US-11-098-686-10295	Sequence 10295, A
699	64.5	4.1	1124	7	US-11-087-099-4425	Sequence 4425, Ap
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701	64.5	4.1	2910	7	US-11-087-084-2	Sequence 2, Appli
702	64.5	4.1	2910	7	US-11-087-085-2	Sequence 2, Appli
703	64	4.1	122	7	US-11-087-099-6151	Sequence 6151, Ap
704	64	4.1	131	7	US-11-096-568A-12238	Sequence 12238, A
705	64	4.1	145	7	US-11-152-601-43	Sequence 43, Appl
706	64	4.1	187	7	US-11-096-568A-11277	Sequence 11277, A
707	64	4.1	198	7	US-11-087-099-11173	Sequence 11173, A
708	64	4.1	203	7	US-11-050-857-488	Sequence 488, App
709	64	4.1	203	7	US-11-043-806-370	Sequence 370, App
710	64	4.1	262	7	US-11-096-568A-11276	Sequence 11276, A
711	64	4.1	266	7	US-11-096-568A-11275	Sequence 11275, A
712	64	4.1	276	7	US-11-096-568A-30981	Sequence 30981, A
713	64	4.1	303	7	US-11-096-568A-27931	Sequence 27931, A
714	64	4.1	319	6	US-10-793-626-792	Sequence 792, App
715	64	4.1	319	6	US-10-793-626-2008	Sequence 2008, Ap
716	64	4.1	335	6	US-10-873-528-4	Sequence 4, Appli
717	64	4.1	338	7	US-11-096-568A-30980	Sequence 30980, A
718	64	4.1	342	6	US-10-980-388-118	Sequence 118, App
719	64	4.1	342	7	US-11-174-816-18	Sequence 18, Appl
720	64	4.1	342	7	US-11-174-819-71	Sequence 71, Appl
721	64	4.1	346	7	US-11-096-568A-30979	Sequence 30979, A
723	64	4.1	349	6	US-10-973-115B-424	Sequence 424, App
724	64	4.1	373	6	US-10-498-026-113	Sequence 113, App
725	64	4.1	379	7	US-11-087-099-8341	Sequence 8341, Ap
726	64	4.1	381	7	US-11-096-568A-17861	Sequence 17861, A
727	64	4.1	382	7	US-11-096-568A-17860	Sequence 17860, A
728	64	4.1	386	7	US-11-096-568A-13774	Sequence 13774, A
729	64	4.1	387	6	US-10-895-064-611	Sequence 611, App
730	64	4.1	387	7	US-11-129-741-611	Sequence 611, App
731	64	4.1	387	7	US-11-096-568A-13773	Sequence 13773, A
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733	64	4.1	388	7	US-11-096-568A-27930	Sequence 27930, A
734	64	4.1	389	7	US-11-096-568A-27929	Sequence 27929, A
735	64	4.1	392	7	US-11-096-568A-34392	Sequence 34392, A
736	64	4.1	417	7	US-11-096-568A-34391	Sequence 34391, A
737	64	4.1	446	7	US-11-087-099-8235	Sequence 8235, Ap
738	64	4.1	447	6	US-10-967-527A-14	Sequence 14, Appl
739	64	4.1	462	7	US-11-177-648-97	Sequence 97, Appl
740	64	4.1	482	7	US-11-087-099-6811	Sequence 6811, Ap
741	64	4.1	513	7	US-11-096-568A-12983	Sequence 12983, A
742	64	4.1	537	7	US-11-087-099-4695	Sequence 4695, Ap
743	64	4.1	548	7	US-11-096-568A-12982	Sequence 12982, A
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746	64	4.1	640	6	US-10-999-886-4	Sequence 4, Appli
747	64	4.1	756	6	US-10-055-877-188	Sequence 188, App
748	64	4.1	860	7	US-11-087-099-6246	Sequence 6246, Ap
749	64	4.1	972	7	US-11-177-894-17	Sequence 17, Appl
750	64	4.1	976	7	US-11-148-770-31	Sequence 31, Appl
751	64	4.1	976	7	US-11-177-894-15	Sequence 15, Appl
752	64	4.1	976	7	US-11-177-894-16	Sequence 16, Appl
753	64	4.1	976	7	US-11-177-894-18	Sequence 18, Appl
754	64	4.1	976	7	US-11-177-894-19	Sequence 19, Appl
755	64	4.1	976	7	US-11-177-894-20	Sequence 20, Appl
756	64	4.1	976	7	US-11-177-894-21	Sequence 21, Appl
757	64	4.1	1078	7	US-11-096-568A-30451	Sequence 30451, A
758	64	4.1	1116	7	US-11-096-568A-30450	Sequence 30450, A
759	64	4.1	1123	7	US-11-037-243-77	Sequence 77, Appl
760	64	4.1	1123	7	US-11-096-568A-30449	Sequence 30449, A
761	64	4.1	1613	6	US-10-055-877-145	Sequence 145, App
762	64	4.1	1637	6	US-10-055-877-144	Sequence 144, App
763	64	4.1	4868	7	US-11-044-111-24	Sequence 24, Appl
764	63.5	4.0	173	7	US-11-096-568A-7049	Sequence 7049, Ap
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766	63.5	4.0	273	6	US-10-353-783-54	Sequence 54, Appl
767	63.5	4.0	273	7	US-11-096-568A-18389	Sequence 18389, A
768	63.5	4.0	273	7	US-11-096-568A-22109	Sequence 22109, A
769	63.5	4.0	290	7	US-11-096-568A-18388	Sequence 18388, A
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771	63.5	4.0	316	6	US-10-517-696-126	Sequence 126, App
772	63.5	4.0	319	7	US-11-087-099-9069	Sequence 9069, Ap
773	63.5	4.0	325	6	US-10-517-696-148	Sequence 148, App
774	63.5	4.0	335	7	US-11-087-099-4668	Sequence 4668, Ap
775	63.5	4.0	336	6	US-10-517-696-153	Sequence 153, App
776	63.5	4.0	336	7	US-11-096-568A-5367	Sequence 5367, Ap
777	63.5	4.0	350	6	US-10-517-696-125	Sequence 125, App
778	63.5	4.0	358	7	US-11-096-568A-21943	Sequence 21943, A
779	63.5	4.0	372	6	US-10-517-696-129	Sequence 129, App
780	63.5	4.0	372	7	US-11-096-568A-5366	Sequence 5366, Ap
781	63.5	4.0	375	7	US-11-096-568A-21942	Sequence 21942, A
782	63.5	4.0	379	6	US-10-517-696-150	Sequence 150, App
783	63.5	4.0	384	7	US-11-096-568A-33509	Sequence 33509, A
784	63.5	4.0	388	7	US-11-096-568A-33508	Sequence 33508, A
785	63.5	4.0	393	7	US-11-052-554A-254	Sequence 254, App
786	63.5	4.0	396	6	US-10-517-696-147	Sequence 147, App
787	63.5	4.0	396	7	US-11-096-568A-33507	Sequence 33507, A
788	63.5	4.0	397	7	US-11-230-180-6	Sequence 6, Appli
789	63.5	4.0	398	6	US-10-517-696-136	Sequence 136, App
790	63.5	4.0	409	6	US-10-517-696-149	Sequence 149, App
791	63.5	4.0	420	6	US-10-517-696-141	Sequence 141, App
792	63.5	4.0	446	7	US-11-102-621-138	Sequence 138, App
793	63.5	4.0	458	7	US-11-096-568A-21941	Sequence 21941, A
794	63.5	4.0	463	6	US-10-517-696-121	Sequence 121, App
795	63.5	4.0	475	6	US-10-501-035-309	Sequence 309, App
796	63.5	4.0	475	6	US-10-517-696-117	Sequence 117, App
797	63.5	4.0	483	6	US-10-517-696-132	Sequence 132, App
798	63.5	4.0	484	6	US-10-517-696-120	Sequence 120, App
799	63.5	4.0	485	6	US-10-517-696-142	Sequence 142, App
800	63.5	4.0	492	6	US-10-517-696-131	Sequence 131, App
801	63.5	4.0	492	7	US-11-098-686-11360	Sequence 11360, A
802	63.5	4.0	517	6	US-10-517-696-144	Sequence 144, App
803	63.5	4.0	524	6	US-10-517-696-122	Sequence 122, App
804	63.5	4.0	524	7	US-11-087-099-12268	Sequence 12268, A
805	63.5	4.0	538	6	US-10-493-909-99	Sequence 99, Appl
806	63.5	4.0	541	7	US-11-201-916-14	Sequence 14, Appl
807	63.5	4.0	578	7	US-11-096-568A-33961	Sequence 33961, A
808	63.5	4.0	583	7	US-11-080-991-64	Sequence 64, Appl
809	63.5	4.0	590	7	US-11-096-568A-33960	Sequence 33960, A
810	63.5	4.0	610	7	US-11-096-568A-33959	Sequence 33959, A
811	63.5	4.0	614	6	US-10-517-696-128	Sequence 128, App
812	63.5	4.0	654	6	US-10-510-947-6	Sequence 6, Appli
813	63.5	4.0	693	6	US-10-995-561-632	Sequence 632, App
814	63.5	4.0	736	7	US-11-085-185-4	Sequence 4, Appli
815	63.5	4.0	778	6	US-10-821-234-1276	Sequence 1276, Ap
816	63.5	4.0	1009	6	US-10-912-971-16	Sequence 16, Appl
817	63.5	4.0	1053	6	US-10-517-939-52	Sequence 52, Appl
818	63.5	4.0	1230	7	US-11-087-099-1702	Sequence 1702, Ap
819	63.5	4.0	1230	7	US-11-087-099-8922	Sequence 8922, Ap
820	63.5	4.0	1255	7	US-11-050-857-487	Sequence 487, App
821	63.5	4.0	1255	7	US-11-043-806-398	Sequence 398, App
822	63.5	4.0	1315	6	US-10-995-561-630	Sequence 630, App
823	63.5	4.0	1607	7	US-11-098-686-10178	Sequence 10178, A
824	63.5	4.0	1992	7	US-11-069-834-58	Sequence 58, Appl
825	63.5	4.0	2000	7	US-11-069-834-56	Sequence 56, Appl
826	63.5	4.0	2015	7	US-11-052-554A-374	Sequence 374, App
827	63.5	4.0	2145	7	US-11-087-099-10331	Sequence 10331, A
828	63.5	4.0	2176	7	US-11-193-561-25	Sequence 25, Appl
829	63.5	4.0	2176	7	US-11-193-771-25	Sequence 25, Appl
830	63.5	4.0	2176	7	US-11-193-789-25	Sequence 25, Appl
831	63.5	4.0	2176	7	US-11-193-806-25	Sequence 25, Appl
832	63.5	4.0	2176	7	US-11-193-857-25	Sequence 25, Appl
833	63.5	4.0	2296	6	US-10-995-561-633	Sequence 633, App
834	63.5	4.0	2296	7	US-11-193-561-23	Sequence 23, Appl
835	63.5	4.0	2296	7	US-11-193-771-23	Sequence 23, Appl
836	63.5	4.0	2296	7	US-11-193-789-23	Sequence 23, Appl
837	63.5	4.0	2296	7	US-11-193-806-23	Sequence 23, Appl
838	63.5	4.0	2296	7	US-11-193-857-23	Sequence 23, Appl
839	63.5	4.0	2392	6	US-10-330-773-907	Sequence 907, App
840	63.5	4.0	3487	7	US-11-087-099-10423	Sequence 10423, A
841	63	4.0	148	7	US-11-052-554A-359	Sequence 359, App

842	63	4.0	192	7	US-11-072-512-3585	Sequence 3585, Ap
843	63	4.0	193	7	US-11-096-568A-24769	Sequence 24769, A
844	63	4.0	246	6	US-10-467-657-2424	Sequence 2424, Ap
845	63	4.0	257	7	US-11-067-121-18	Sequence 18, Appl
846	63	4.0	290	7	US-11-087-099-4115	Sequence 4115, Ap
847	63	4.0	307	6	US-10-498-026-111	Sequence 111, App
848	63	4.0	327	6	US-10-055-877-183	Sequence 183, App
849	63	4.0	331	7	US-11-096-568A-16226	Sequence 16226, A
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852	63	4.0	344	7	US-11-174-819-28	Sequence 28, Appl
853	63	4.0	359	7	US-11-087-099-7177	Sequence 7177, Ap
854	63	4.0	362	7	US-11-087-099-7379	Sequence 7379, Ap
855	63	4.0	363	7	US-11-087-099-9842	Sequence 9842, Ap
856	63	4.0	371	7	US-11-096-568A-31340	Sequence 31340, A
857	63	4.0	386	7	US-11-055-822-586	Sequence 586, App
858	63	4.0	408	7	US-11-096-568A-31339	Sequence 31339, A
859	63	4.0	471	7	US-11-087-099-8817	Sequence 8817, Ap
860	63	4.0	472	7	US-11-165-226-10	Sequence 10, Appl
861	63	4.0	472	7	US-11-165-226-11	Sequence 11, Appl
862	63	4.0	472	7	US-11-165-226-12	Sequence 12, Appl
863	63	4.0	472	7	US-11-165-226-13	Sequence 13, Appl
864	63	4.0	475	7	US-11-087-099-4508	Sequence 4508, Ap
865	63	4.0	485	7	US-11-043-889-52	Sequence 52, Appl
866	63	4.0	497	6	US-10-501-035-337	Sequence 337, App
867	63	4.0	501	6	US-10-485-517-381	Sequence 381, App
868	63	4.0	513	6	US-10-641-678-66	Sequence 66, Appl
869	63	4.0	514	6	US-10-641-678-67	Sequence 67, Appl
870	63	4.0	546	7	US-11-072-512-2051	Sequence 2051, Ap
871	63	4.0	548	7	US-11-096-568A-402	Sequence 402, App
872	63	4.0	581	7	US-11-236-198-7	Sequence 7, Appli
873	63	4.0	615	7	US-11-096-568A-401	Sequence 401, App
874	63	4.0	615	7	US-11-096-568A-403	Sequence 403, App
875	63	4.0	629	7	US-11-096-568A-29173	Sequence 29173, A
876	63	4.0	643	7	US-11-096-568A-400	Sequence 400, App
877	63	4.0	645	6	US-10-485-517-244	Sequence 244, App
878	63	4.0	678	7	US-11-096-568A-29172	Sequence 29172, A
879	63	4.0	706	7	US-11-087-099-4237	Sequence 4237, Ap
880	63	4.0	719	7	US-11-096-568A-29171	Sequence 29171, A
881	63	4.0	726	7	US-11-096-568A-28626	Sequence 28626, A
882	63	4.0	728	6	US-10-530-340-14	Sequence 14, Appl
883	63	4.0	743	7	US-11-072-512-2340	Sequence 2340, Ap
884	63	4.0	756	7	US-11-096-568A-28625	Sequence 28625, A
885	63	4.0	786	7	US-11-096-568A-32685	Sequence 32685, A
886	63	4.0	793	7	US-11-096-568A-28222	Sequence 28222, A
887	63	4.0	798	7	US-11-096-568A-28221	Sequence 28221, A
888	63	4.0	801	7	US-11-096-568A-28220	Sequence 28220, A
889	63	4.0	808	7	US-11-087-099-7073	Sequence 7073, Ap
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892	63	4.0	1083	7	US-11-113-751-40	Sequence 40, Appl
893	63	4.0	1393	7	US-11-096-568A-32145	Sequence 32145, A
894	63	4.0	1637	6	US-10-821-234-1204	Sequence 1204, Ap
895	63	4.0	1645	7	US-11-043-806-364	Sequence 364, App
896	63	4.0	1928	6	US-10-480-330-30	Sequence 30, Appl
897	63	4.0	1965	6	US-10-480-330-4	Sequence 4, Appli
898	63	4.0	1966	6	US-10-480-330-2	Sequence 2, Appli
899	63	4.0	1966	6	US-10-480-330-6	Sequence 6, Appli
900	63	4.0	1966	6	US-10-480-330-8	Sequence 8, Appli
901	63	4.0	1966	6	US-10-480-330-10	Sequence 10, Appl
902	63	4.0	1966	6	US-10-480-330-12	Sequence 12, Appl
903	63	4.0	1966	6	US-10-480-330-14	Sequence 14, Appl
904	63	4.0	1966	6	US-10-480-330-16	Sequence 16, Appl
905	63	4.0	1966	6	US-10-480-330-18	Sequence 18, Appl
906	63	4.0	1966	6	US-10-480-330-20	Sequence 20, Appl
907	63	4.0	1966	6	US-10-480-330-22	Sequence 22, Appl
908	63	4.0	1966	6	US-10-480-330-24	Sequence 24, Appl
909	63	4.0	1966	6	US-10-480-330-26	Sequence 26, Appl
910	63	4.0	1966	6	US-10-480-330-28	Sequence 28, Appl
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912	63	4.0	2105	7	US-11-052-554A-173	Sequence 173, App
913	63	4.0	2221	7	US-11-126-313-30	Sequence 30, Appl
914	63	4.0	2224	7	US-11-043-806-392	Sequence 392, App
915	63	4.0	2224	7	US-11-043-806-393	Sequence 393, App
916	62.5	4.0	146	6	US-10-467-657-5594	Sequence 5594, Ap
917	62.5	4.0	158	7	US-11-096-568A-7142	Sequence 7142, Ap
918	62.5	4.0	180	7	US-11-096-568A-3506	Sequence 3506, Ap
919	62.5	4.0	232	5	US-09-978-360A-642	Sequence 642, App
920	62.5	4.0	246	7	US-11-096-568A-26953	Sequence 26953, A
921	62.5	4.0	271	6	US-10-353-783-52	Sequence 52, Appl
922	62.5	4.0	277	7	US-11-096-568A-26952	Sequence 26952, A
924	62.5	4.0	299	6	US-10-973-115B-366	Sequence 366, App
925	62.5	4.0	299	7	US-11-000-463-275	Sequence 275, App
926	62.5	4.0	299	7	US-11-000-463-747	Sequence 747, App
927	62.5	4.0	299	7	US-11-000-463-748	Sequence 748, App
928	62.5	4.0	299	7	US-11-173-037-7	Sequence 7, Appli
929	62.5	4.0	343	7	US-11-098-686-11280	Sequence 11280, A
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931	62.5	4.0	414	7	US-11-089-551A-28	Sequence 28, Appl
932	62.5	4.0	440	7	US-11-087-099-8456	Sequence 8456, Ap
933	62.5	4.0	442	7	US-11-102-621-126	Sequence 126, App
934	62.5	4.0	446	7	US-11-096-568A-28876	Sequence 28876, A
935	62.5	4.0	457	7	US-11-096-568A-32234	Sequence 32234, A
936	62.5	4.0	467	7	US-11-096-568A-7912	Sequence 7912, Ap
937	62.5	4.0	489	7	US-11-096-568A-32213	Sequence 32213, A
938	62.5	4.0	499	7	US-11-096-568A-25749	Sequence 25749, A
939	62.5	4.0	504	7	US-11-087-099-1053	Sequence 1053, Ap
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941	62.5	4.0	524	6	US-10-517-696-113	Sequence 113, App
942	62.5	4.0	539	7	US-11-096-568A-32212	Sequence 32212, A
943	62.5	4.0	542	7	US-11-074-176-30	Sequence 30, Appl
944	62.5	4.0	545	7	US-11-096-568A-32211	Sequence 32211, A
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948	62.5	4.0	577	7	US-11-124-368A-232	Sequence 232, App
949	62.5	4.0	585	7	US-11-108-172-1067	Sequence 1067, Ap
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951	62.5	4.0	603	7	US-11-096-568A-25747	Sequence 25747, A
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953	62.5	4.0	915	7	US-11-156-084-119	Sequence 119, App
954	62.5	4.0	965	7	US-11-113-424-2	Sequence 2, Appli
955	62.5	4.0	1001	6	US-10-330-773-510	Sequence 510, App
956	62.5	4.0	1162	6	US-10-451-375-3	Sequence 3, Appli
957	62.5	4.0	2059	7	US-11-087-100-4	Sequence 4, Appli
958	62.5	4.0	2059	7	US-11-087-084-4	Sequence 4, Appli
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964	62.5	4.0	3002	6	US-10-821-234-916	Sequence 916, App
965	62.5	4.0	3487	7	US-11-087-099-9068	Sequence 9068, Ap
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970	62	3.9	195	7	US-11-096-568A-14743	Sequence 14743, A
971	62	3.9	195	7	US-11-096-568A-21216	Sequence 21216, A
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973	62	3.9	231	7	US-11-132-285-61	Sequence 61, Appl
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976	62	3.9	235	7	US-11-219-359-5	Sequence 5, Appli
977	62	3.9	243	7	US-11-096-568A-14742	Sequence 14742, A
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979	62	3.9	284	7	US-11-096-568A-9853	Sequence 9853, Ap
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981	62	3.9	321	7	US-11-096-568A-21893	Sequence 21893, A
982	62	3.9	325	7	US-11-096-568A-23538	Sequence 23538, A
983	62	3.9	339	7	US-11-124-367A-265	Sequence 265, App
984	62	3.9	341	7	US-11-240-769-72	Sequence 72, Appl
985	62	3.9	341	7	US-11-096-568A-23537	Sequence 23537, A
986	62	3.9	341	7	US-11-151-868-2	Sequence 2, Appli
987	62	3.9	342	7	US-11-008-570-47	Sequence 47, Appl
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990	62	3.9	346	6	US-10-973-115B-432	Sequence 432, App
991	62	3.9	352	5	US-09-978-360A-437	Sequence 437, App
992	62	3.9	352	7	US-11-124-367A-267	Sequence 267, App
993	62	3.9	362	7	US-11-096-568A-25696	Sequence 25696, A
994	62	3.9	370	7	US-11-096-568A-6789	Sequence 6789, Ap
995	62	3.9	379	7	US-11-087-099-8218	Sequence 8218, Ap
996	62	3.9	379	7	US-11-096-568A-25695	Sequence 25695, A
997	62	3.9	380	7	US-11-196-475-118	Sequence 118, App
998	62	3.9	385	7	US-11-087-099-2954	Sequence 2954, Ap
999	62	3.9	395	7	US-11-124-367A-322	Sequence 322, App
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1002	62	3.9	462	7	US-11-177-648-98	Sequence 98, Appl
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1018	62	3.9	926	7	US-11-024-959-518	Sequence 518, App
1019	62	3.9	1075	7	US-11-100-640-12	Sequence 12, Appl
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1027	62	3.9	1532	7	US-11-124-367A-403	Sequence 403, App
1028	62	3.9	1532	7	US-11-124-367A-404	Sequence 404, App
1029	62	3.9	1532	7	US-11-124-367A-405	Sequence 405, App
1030	62	3.9	1532	7	US-11-124-367A-407	Sequence 407, App
1031	62	3.9	1535	7	US-11-124-367A-408	Sequence 408, App
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1036	61.5	3.9	211	7	US-11-124-368A-187	Sequence 187, App
1037	61.5	3.9	226	7	US-11-104-111-18	Sequence 18, Appl
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1041	61.5	3.9	246	7	US-11-096-568A-4926	Sequence 4926, Ap
1042	61.5	3.9	251	7	US-11-096-568A-14887	Sequence 14887, A
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1044	61.5	3.9	261	7	US-11-096-568A-17990	Sequence 17990, A
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1047	61.5	3.9	296	7	US-11-096-568A-1922	Sequence 1922, Ap
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1049	61.5	3.9	311	7	US-11-087-099-5603	Sequence 5603, Ap
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1051	61.5	3.9	344	7	US-11-174-816-62	Sequence 62, Appl
1052	61.5	3.9	344	7	US-11-174-819-81	Sequence 81, Appl
1053	61.5	3.9	357	7	US-11-087-099-8457	Sequence 8457, Ap
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1059	61.5	3.9	384	7	US-11-080-991-26	Sequence 26, Appl
1060	61.5	3.9	384	7	US-11-183-615-4	Sequence 4, Appli
1061	61.5	3.9	393	7	US-11-196-475-114	Sequence 114, App
1062	61.5	3.9	396	7	US-11-087-099-7395	Sequence 7395, Ap
1063	61.5	3.9	431	7	US-11-096-568A-6443	Sequence 6443, Ap
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1072	61.5	3.9	511	6	US-10-641-678-42	Sequence 42, Appl
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1075	61.5	3.9	516	7	US-11-096-568A-31882	Sequence 31882, A
1076	61.5	3.9	540	6	US-10-641-678-44	Sequence 44, Appl
1077	61.5	3.9	540	7	US-11-212-443-168	Sequence 168, App
1078	61.5	3.9	541	7	US-11-169-041-136	Sequence 136, App
1079	61.5	3.9	549	7	US-11-096-568A-33577	Sequence 33577, A
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1087	61.5	3.9	684	7	US-11-096-568A-26673	Sequence 26673, A
1088	61.5	3.9	690	7	US-11-096-568A-31869	Sequence 31869, A
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1090	61.5	3.9	730	7	US-11-082-389-358	Sequence 358, App
1091	61.5	3.9	731	7	US-11-098-686-10415	Sequence 10415, A
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1093	61.5	3.9	877	7	US-11-074-176-322	Sequence 322, App
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1096	61.5	3.9	1076	7	US-11-098-686-11338	Sequence 11338, A
1097	61.5	3.9	1107	6	US-10-485-517-145	Sequence 145, App
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1099	61.5	3.9	1129	7	US-11-077-550-56	Sequence 56, Appl
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1105	61	3.9	265	7	US-11-087-099-5324	Sequence 5324, Ap
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1107	61	3.9	273	7	US-11-087-099-2253	Sequence 2253, Ap
1108	61	3.9	277	7	US-11-098-686-11027	Sequence 11027, A
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1119	61	3.9	336	7	US-11-096-568A-15586	Sequence 15586, A
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1147	61	3.9	547	7	US-11-087-099-3034	Sequence 3034, Ap
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1225	60.5	3.8	417	6	US-10-793-626-950	Sequence 950, App
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1237	60.5	3.8	511	7	US-11-096-568A-146	Sequence 146, App
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1243	60.5	3.8	608	7	US-11-241-347-9	Sequence 9, Appli
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1257	60.5	3.8	871	7	US-11-077-550-8	Sequence 8, Appli
1258	60.5	3.8	871	7	US-11-077-550-26	Sequence 26, Appl
1259	60.5	3.8	871	7	US-11-077-550-153	Sequence 153, App
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1262	60.5	3.8	873	7	US-11-077-550-151	Sequence 151, App
1263	60.5	3.8	879	7	US-11-077-550-159	Sequence 159, App
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1269	60.5	3.8	1129	7	US-11-077-550-42	Sequence 42, Appl
1270	60.5	3.8	1137	7	US-11-012-762-70	Sequence 70, Appl
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1276	60.5	3.8	1532	7	US-11-212-443-62	Sequence 62, Appl
1277	60.5	3.8	1995	7	US-11-069-834-60	Sequence 60, Appl
1278	60.5	3.8	2244	7	US-11-131-263-9	Sequence 9, Appli
1279	60.5	3.8	2244	7	US-11-131-263-18	Sequence 18, Appl
1280	60.5	3.8	2244	7	US-11-131-263-30	Sequence 30, Appl
1281	60.5	3.8	2314	7	US-11-013-759-11	Sequence 11, Appl
1282	60.5	3.8	2766	6	US-10-877-346-62	Sequence 62, Appl
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1331	60	3.8	438	7	US-11-074-176-152	Sequence 152, App
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1335	60	3.8	456	7	US-11-000-463-923	Sequence 923, App
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SUMMARIES

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119	89	5.7	353	1	US-08-073-807A-17	Sequence 17, Appl
120	89	5.7	380	1	US-08-073-807A-18	Sequence 18, Appl
121	89	5.7	416	1	US-08-073-807A-2	Sequence 2, Appli
122	89	5.7	416	2	US-09-311-784A-26	Sequence 26, Appl
123	89	5.7	471	2	US-09-949-016-9525	Sequence 9525, Ap
124	88.5	5.6	265	2	US-09-248-796A-21903	Sequence 21903, A
125	88.5	5.6	376	2	US-09-487-558B-206	Sequence 206, App
126	88.5	5.6	451	2	US-09-252-991A-17201	Sequence 17201, A
127	88	5.6	261	2	US-09-248-796A-14279	Sequence 14279, A
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130	87.5	5.6	555	2	US-09-292-225-15	Sequence 15, Appl
131	87.5	5.6	555	2	US-09-292-225-18	Sequence 18, Appl
132	87.5	5.6	717	2	US-10-104-047-3100	Sequence 3100, Ap
133	87.5	5.6	795	2	US-09-270-767-43662	Sequence 43662, A
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135	87.5	5.6	1085	1	US-08-484-565-5	Sequence 5, Appli
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137	87.5	5.6	1085	1	US-08-943-986-5	Sequence 5, Appli
138	87.5	5.6	1085	2	US-08-353-784-5	Sequence 5, Appli
139	87.5	5.6	1085	2	US-08-484-719B-5	Sequence 5, Appli
140	87.5	5.6	1085	2	US-08-484-159-5	Sequence 5, Appli
141	87	5.5	288	2	US-09-216-393B-341	Sequence 341, App
142	87	5.5	288	2	US-09-216-393B-344	Sequence 344, App
143	87	5.5	631	2	US-09-620-412C-325	Sequence 325, App
144	87	5.5	631	2	US-09-598-419-325	Sequence 325, App
145	87	5.5	664	2	US-10-197-220-168	Sequence 168, App
146	87	5.5	862	1	US-08-325-267A-4	Sequence 4, Appli
147	87	5.5	894	2	US-08-362-525-22	Sequence 22, Appl
148	87	5.5	894	2	US-08-971-692-15	Sequence 15, Appl
149	87	5.5	1016	2	US-10-197-220-95	Sequence 95, Appl
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151	87	5.5	1537	2	US-09-487-558B-104	Sequence 104, App
152	86.5	5.5	503	2	US-09-487-558B-424	Sequence 424, App
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154	86.5	5.5	807	2	US-09-294-663-4	Sequence 4, Appli
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157	86	5.5	750	2	US-09-165-239A-4	Sequence 4, Appli
158	86	5.5	786	2	US-09-103-429A-3	Sequence 3, Appli
159	86	5.5	805	2	US-09-103-429A-4	Sequence 4, Appli
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163	84.5	5.4	270	2	US-09-248-796A-14475	Sequence 14475, A
164	84.5	5.4	507	2	US-09-949-016-8889	Sequence 8889, Ap
165	84.5	5.4	507	2	US-09-949-016-8897	Sequence 8897, Ap
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167	84	5.3	216	2	US-08-928-361B-27	Sequence 27, Appl
168	84	5.3	216	2	US-09-588-995A-8	Sequence 8, Appli
169	84	5.3	1075	2	US-09-487-558B-110	Sequence 110, App
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181	83.5	5.3	879	1	US-08-413-118-3	Sequence 3, Appli
182	83.5	5.3	879	1	US-08-413-118-106	Sequence 106, App
183	83.5	5.3	879	2	US-08-473-446-2	Sequence 2, Appli
184	83.5	5.3	879	2	US-08-473-446-3	Sequence 3, Appli
185	83.5	5.3	879	2	US-08-473-446-106	Sequence 106, App
186	83.5	5.3	5179	2	US-09-538-092-1258	Sequence 1258, Ap
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189	83	5.3	175	2	US-09-270-767-48770	Sequence 48770, A
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192	83	5.3	409	2	US-09-538-092-1214	Sequence 1214, Ap
193	83	5.3	409	2	US-09-949-016-6281	Sequence 6281, Ap
194	83	5.3	454	2	US-09-949-016-11120	Sequence 11120, A
195	83	5.3	605	2	US-09-487-558B-428	Sequence 428, App
196	83	5.3	736	2	US-09-457-040B-26	Sequence 26, Appl
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207	82.5	5.2	790	2	US-09-949-016-8169	Sequence 8169, Ap
208	82.5	5.2	790	2	US-09-949-016-8170	Sequence 8170, Ap
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210	82	5.2	208	2	US-09-990-444-416	Sequence 416, App
211	82	5.2	208	2	US-09-832-129-36	Sequence 36, Appl
212	82	5.2	208	2	US-09-997-333-416	Sequence 416, App
213	82	5.2	208	2	US-09-992-598-416	Sequence 416, App
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227	81.5	5.2	687	2	US-08-521-872-4	Sequence 4, Appli
228	81.5	5.2	687	2	US-08-590-399-4	Sequence 4, Appli
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236	81	5.1	855	2	US-08-885-291-2	Sequence 2, Appli
237	81	5.1	855	2	US-09-496-672-2	Sequence 2, Appli
238	81	5.1	855	2	US-09-618-425-11	Sequence 11, Appl
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241	81	5.1	1322	2	US-09-487-558B-114	Sequence 114, App
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244	80.5	5.1	478	2	US-09-862-027-51	Sequence 51, Appl
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249	80.5	5.1	595	2	US-09-006-353A-9	Sequence 9, Appli
250	80.5	5.1	595	2	US-09-573-986-9	Sequence 9, Appli
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252	80.5	5.1	642	2	US-09-949-016-8043	Sequence 8043, Ap
253	80.5	5.1	673	2	US-09-949-016-7388	Sequence 7388, Ap
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255	80	5.1	52	4	PCT-US95-04353-10	Sequence 10, Appl
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258	80	5.1	257	2	US-09-902-540-15102	Sequence 15102, A
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260	80	5.1	404	2	US-09-270-767-41751	Sequence 41751, A
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262	80	5.1	451	4	PCT-US95-09941-2	Sequence 2, Appli
263	80	5.1	468	1	US-08-959-011-3	Sequence 3, Appli
264	79.5	5.0	153	2	US-09-252-991A-17880	Sequence 17880, A
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266	79.5	5.0	154	2	US-09-270-767-55692	Sequence 55692, A
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268	79.5	5.0	374	2	US-09-248-796A-17283	Sequence 17283, A
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272	79.5	5.0	461	1	US-08-650-000-2	Sequence 2, Appli
273	79.5	5.0	461	2	US-09-042-785A-7	Sequence 7, Appli
274	79.5	5.0	461	2	US-08-477-347-3	Sequence 3, Appli
275	79.5	5.0	461	2	US-09-006-353A-4	Sequence 4, Appli
276	79.5	5.0	461	2	US-08-476-862-2	Sequence 2, Appli
277	79.5	5.0	461	2	US-09-573-986-4	Sequence 4, Appli
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281	79.5	5.0	461	2	US-09-800-908-3	Sequence 3, Appli
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285	79.5	5.0	461	6	5395760-2	Patent No. 5395760
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287	79.5	5.0	515	2	US-09-198-452A-1094	Sequence 1094, Ap
288	79.5	5.0	515	2	US-09-438-185A-1021	Sequence 1021, Ap
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293	79.5	5.0	985	2	US-09-993-777-66	Sequence 66, Appl
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295	79.5	5.0	985	4	PCT-US96-03916-66	Sequence 66, Appl
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298	79.5	5.0	1177	2	US-09-262-537-2	Sequence 2, Appli
299	79.5	5.0	1403	2	US-09-262-537-6	Sequence 6, Appli
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302	79	5.0	175	2	US-09-588-995A-17	Sequence 17, Appl
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304	79	5.0	374	2	US-09-489-847-166	Sequence 166, App
305	79	5.0	382	2	US-09-907-794A-137	Sequence 137, App
306	79	5.0	382	2	US-09-905-125A-137	Sequence 137, App
307	79	5.0	382	2	US-09-902-775A-137	Sequence 137, App
308	79	5.0	382	2	US-09-906-700-137	Sequence 137, App
309	79	5.0	382	2	US-09-903-603A-137	Sequence 137, App
310	79	5.0	382	2	US-09-904-920A-137	Sequence 137, App
311	79	5.0	382	2	US-09-909-064-137	Sequence 137, App
312	79	5.0	382	2	US-09-905-381A-137	Sequence 137, App
313	79	5.0	382	2	US-09-906-618-137	Sequence 137, App
314	79	5.0	382	2	US-09-906-646-137	Sequence 137, App
315	79	5.0	382	2	US-09-904-462-137	Sequence 137, App
316	79	5.0	382	2	US-09-902-736A-137	Sequence 137, App
317	79	5.0	382	2	US-09-906-722A-137	Sequence 137, App
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325	79	5.0	1011	2	US-09-457-571-2	Sequence 2, Appli
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327	79	5.0	1312	2	US-10-071-179-29	Sequence 29, Appl
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329	79	5.0	1848	2	US-09-839-996-6	Sequence 6, Appli
330	79	5.0	1848	2	US-10-080-505-6	Sequence 6, Appli
331	79	5.0	1848	2	US-10-645-655-6	Sequence 6, Appli
332	79	5.0	1848	4	PCT-US95-10661A-6	Sequence 6, Appli
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334	79	5.0	1984	2	US-09-457-571-10	Sequence 10, Appl
335	79	5.0	1989	2	US-08-836-325-12	Sequence 12, Appl
336	79	5.0	1989	2	US-09-457-571-12	Sequence 12, Appl
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347	78.5	5.0	595	1	US-08-580-014-2	Sequence 2, Appli
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352	78.5	5.0	653	2	US-09-957-187-10	Sequence 10, Appl
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355	78	5.0	280	2	US-09-905-125A-325	Sequence 325, App
356	78	5.0	280	2	US-09-902-775A-325	Sequence 325, App
357	78	5.0	280	2	US-09-906-700-325	Sequence 325, App
358	78	5.0	280	2	US-09-903-603A-325	Sequence 325, App
359	78	5.0	280	2	US-09-904-920A-325	Sequence 325, App
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363	78	5.0	280	2	US-09-906-618-325	Sequence 325, App
364	78	5.0	280	2	US-09-906-646-325	Sequence 325, App
365	78	5.0	280	2	US-09-904-462-325	Sequence 325, App
366	78	5.0	280	2	US-09-902-736A-325	Sequence 325, App
367	78	5.0	280	2	US-09-906-722A-325	Sequence 325, App
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372	78	5.0	609	2	US-09-198-452A-579	Sequence 579, App
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374	78	5.0	849	2	US-08-487-691-18	Sequence 18, Appl
375	78	5.0	849	2	US-08-189-738A-19	Sequence 19, Appl
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377	78	5.0	905	2	US-08-487-691-2	Sequence 2, Appli
378	78	5.0	905	2	US-08-666-221B-4	Sequence 4, Appli
379	78	5.0	905	2	US-08-189-738A-2	Sequence 2, Appli
380	78	5.0	1006	2	US-09-949-016-7897	Sequence 7897, Ap
381	78	5.0	1442	1	US-08-015-986A-3	Sequence 3, Appli
382	78	5.0	1442	1	US-08-446-363-3	Sequence 3, Appli
383	78	5.0	1744	2	US-09-438-185A-542	Sequence 542, App
384	78	5.0	2176	2	US-09-949-016-9923	Sequence 9923, Ap
385	77.5	4.9	497	2	US-09-377-557-10	Sequence 10, Appl
386	77.5	4.9	514	2	US-08-738-168B-15	Sequence 15, Appl
387	77.5	4.9	1262	2	US-09-107-433-5067	Sequence 5067, Ap
388	77.5	4.9	1475	2	US-09-538-092-1160	Sequence 1160, Ap
389	77.5	4.9	3969	2	US-08-061-376-5	Sequence 5, Appli
390	77.5	4.9	3969	2	US-09-538-092-1262	Sequence 1262, Ap
391	77	4.9	162	2	US-09-068-140A-2	Sequence 2, Appli
392	77	4.9	173	2	US-09-068-140A-13	Sequence 13, Appl

393	77	4.9	249	2	US-08-700-651-15	Sequence 15, Appl
394	77	4.9	249	2	US-08-928-361B-20	Sequence 20, Appl
395	77	4.9	249	2	US-09-588-995A-20	Sequence 20, Appl
396	77	4.9	624	2	US-09-877-730-24	Sequence 24, Appl
397	77	4.9	712	2	US-09-877-730-22	Sequence 22, Appl
398	77	4.9	714	2	US-09-949-016-7038	Sequence 7038, Ap
399	77	4.9	793	2	US-09-877-730-28	Sequence 28, Appl
400	77	4.9	905	2	US-08-666-221B-10	Sequence 10, Appl
401	77	4.9	908	2	US-09-949-016-7580	Sequence 7580, Ap
402	77	4.9	991	2	US-09-877-730-12	Sequence 12, Appl
403	77	4.9	1069	2	US-09-877-730-2	Sequence 2, Appli
404	77	4.9	1072	2	US-09-877-730-18	Sequence 18, Appl
405	77	4.9	1140	2	US-09-538-092-647	Sequence 647, App
406	77	4.9	1150	2	US-09-877-730-8	Sequence 8, Appli
407	77	4.9	1401	2	US-09-127-670-6	Sequence 6, Appli
408	77	4.9	2123	2	US-08-968-685A-10	Sequence 10, Appl
409	76.5	4.9	134	2	US-09-248-796A-27317	Sequence 27317, A
410	76.5	4.9	240	1	US-08-114-555A-8	Sequence 8, Appli
411	76.5	4.9	240	2	US-08-559-397A-14	Sequence 14, Appl
412	76.5	4.9	303	2	US-09-248-796A-14269	Sequence 14269, A
413	76.5	4.9	334	2	US-10-012-231A-41	Sequence 41, Appl
414	76.5	4.9	334	2	US-10-015-389A-41	Sequence 41, Appl
415	76.5	4.9	334	2	US-10-006-768A-41	Sequence 41, Appl
416	76.5	4.9	334	2	US-10-015-671A-41	Sequence 41, Appl
417	76.5	4.9	334	2	US-10-015-393A-41	Sequence 41, Appl
418	76.5	4.9	334	2	US-10-011-833A-41	Sequence 41, Appl
419	76.5	4.9	334	2	US-10-006-041A-41	Sequence 41, Appl
420	76.5	4.9	334	2	US-10-012-064A-41	Sequence 41, Appl
421	76.5	4.9	348	2	US-09-216-295-16	Sequence 16, Appl
422	76.5	4.9	348	2	US-09-632-570-16	Sequence 16, Appl
423	76.5	4.9	348	2	US-09-632-575-46	Sequence 46, Appl
424	76.5	4.9	382	1	US-08-415-818-7	Sequence 7, Appli
425	76.5	4.9	382	1	US-08-894-236-7	Sequence 7, Appli
426	76.5	4.9	382	1	US-08-555-268A-14	Sequence 14, Appl
427	76.5	4.9	382	2	US-09-430-775-36	Sequence 36, Appl
428	76.5	4.9	382	4	PCT-US96-01444-7	Sequence 7, Appli
429	76.5	4.9	397	2	US-09-198-452A-201	Sequence 201, App
430	76.5	4.9	397	2	US-09-438-185A-188	Sequence 188, App
431	76.5	4.9	452	2	US-09-248-796A-16219	Sequence 16219, A
432	76.5	4.9	653	2	US-09-991-181-229	Sequence 229, App
433	76.5	4.9	653	2	US-09-990-444-229	Sequence 229, App
434	76.5	4.9	653	2	US-09-997-333-229	Sequence 229, App
435	76.5	4.9	653	2	US-09-992-598-229	Sequence 229, App
436	76.5	4.9	901	2	US-09-248-796A-14747	Sequence 14747, A
437	76.5	4.9	1013	2	US-08-860-886-2	Sequence 2, Appli
438	76.5	4.9	1307	2	US-10-104-047-2438	Sequence 2438, Ap
439	76.5	4.9	5037	2	US-09-424-783-4	Sequence 4, Appli
440	76	4.8	154	2	US-09-270-767-61124	Sequence 61124, A
441	76	4.8	299	2	US-09-270-767-44350	Sequence 44350, A
442	76	4.8	321	2	US-09-248-796A-20146	Sequence 20146, A
443	76	4.8	345	2	US-09-543-681A-6150	Sequence 6150, Ap
444	76	4.8	380	2	US-09-134-001C-4558	Sequence 4558, Ap
445	76	4.8	386	2	US-09-328-352-4722	Sequence 4722, Ap
446	76	4.8	402	2	US-09-270-767-45612	Sequence 45612, A
447	76	4.8	509	2	US-09-907-794A-315	Sequence 315, App
448	76	4.8	509	2	US-09-905-125A-315	Sequence 315, App
449	76	4.8	509	2	US-09-902-775A-315	Sequence 315, App
450	76	4.8	509	2	US-09-906-700-315	Sequence 315, App
451	76	4.8	509	2	US-09-903-603A-315	Sequence 315, App
452	76	4.8	509	2	US-09-904-920A-315	Sequence 315, App
453	76	4.8	509	2	US-09-909-064-315	Sequence 315, App
454	76	4.8	509	2	US-09-905-381A-315	Sequence 315, App
455	76	4.8	509	2	US-09-906-618-315	Sequence 315, App
456	76	4.8	509	2	US-09-906-646-315	Sequence 315, App
457	76	4.8	509	2	US-09-904-462-315	Sequence 315, App
458	76	4.8	509	2	US-09-902-736A-315	Sequence 315, App
459	76	4.8	509	2	US-09-906-722A-315	Sequence 315, App
460	76	4.8	563	2	US-09-949-016-10405	Sequence 10405, A
461	76	4.8	985	2	US-09-248-796A-16090	Sequence 16090, A
462	76	4.8	1014	2	US-09-078-347A-3	Sequence 3, Appli
463	76	4.8	1014	2	US-09-596-248D-25	Sequence 25, Appl
464	76	4.8	1014	2	US-09-296-662-35	Sequence 35, Appl
465	76	4.8	1063	2	US-09-596-248D-47	Sequence 47, Appl
466	76	4.8	1401	2	US-08-781-891-206	Sequence 206, App
467	76	4.8	1401	2	US-09-618-166-206	Sequence 206, App
468	76	4.8	1426	2	US-09-136-574A-43	Sequence 43, Appl
469	76	4.8	1645	2	US-09-976-594-769	Sequence 769, App
470	75.5	4.8	258	2	US-08-961-083-90	Sequence 90, Appl
471	75.5	4.8	258	2	US-09-536-784-90	Sequence 90, Appl
472	75.5	4.8	258	2	US-09-765-271-90	Sequence 90, Appl
473	75.5	4.8	258	2	US-09-765-272A-90	Sequence 90, Appl
474	75.5	4.8	348	1	US-08-035-392-2	Sequence 2, Appli
475	75.5	4.8	348	1	US-08-504-511A-2	Sequence 2, Appli
476	75.5	4.8	430	1	US-08-035-392-4	Sequence 4, Appli
477	75.5	4.8	430	1	US-08-504-511A-4	Sequence 4, Appli
478	75.5	4.8	451	2	US-09-134-001C-4461	Sequence 4461, Ap
479	75.5	4.8	453	2	US-09-230-225B-4	Sequence 4, Appli
480	75.5	4.8	484	1	US-08-127-499A-26	Sequence 26, Appl
481	75.5	4.8	484	1	US-08-482-847-26	Sequence 26, Appl
482	75.5	4.8	510	2	US-09-270-767-43633	Sequence 43633, A
483	75.5	4.8	511	1	US-08-220-151-17	Sequence 17, Appl
484	75.5	4.8	511	1	US-08-413-118-17	Sequence 17, Appl
485	75.5	4.8	511	2	US-08-473-446-17	Sequence 17, Appl
486	75.5	4.8	565	2	US-08-961-083-218	Sequence 218, App
487	75.5	4.8	565	2	US-09-536-784-218	Sequence 218, App
488	75.5	4.8	565	2	US-09-765-271-218	Sequence 218, App
489	75.5	4.8	565	2	US-09-765-272A-218	Sequence 218, App
490	75.5	4.8	639	2	US-09-949-016-6812	Sequence 6812, Ap
491	75.5	4.8	641	2	US-10-164-595-46	Sequence 46, Appl
492	75.5	4.8	652	2	US-09-949-016-7323	Sequence 7323, Ap
493	75	4.8	210	2	US-09-270-767-32951	Sequence 32951, A
494	75	4.8	210	2	US-09-270-767-48168	Sequence 48168, A
495	75	4.8	424	1	US-08-419-414-2	Sequence 2, Appli
496	75	4.8	425	2	US-09-748-537-14	Sequence 14, Appl
497	75	4.8	554	1	US-08-524-051-2	Sequence 2, Appli
498	75	4.8	554	2	US-09-052-778-16	Sequence 16, Appl
499	75	4.8	557	2	US-09-248-796A-26892	Sequence 26892, A
500	75	4.8	904	2	US-09-198-484-2	Sequence 2, Appli
501	75	4.8	920	1	US-07-718-575-10	Sequence 10, Appl
502	75	4.8	920	1	US-08-481-206-10	Sequence 10, Appl
503	75	4.8	920	1	US-08-486-269A-10	Sequence 10, Appl
504	75	4.8	941	2	US-07-757-022B-14	Sequence 14, Appl
505	75	4.8	1022	2	US-07-757-022B-84	Sequence 84, Appl
506	75	4.8	1038	2	US-07-757-022B-74	Sequence 74, Appl
507	75	4.8	1049	2	US-07-757-022B-58	Sequence 58, Appl
508	75	4.8	1140	2	US-07-757-022B-104	Sequence 104, App
509	75	4.8	1151	1	US-08-286-889-37	Sequence 37, Appl
510	75	4.8	1151	1	US-08-485-618-37	Sequence 37, Appl
511	75	4.8	1151	1	US-08-362-652-37	Sequence 37, Appl
512	75	4.8	1151	1	US-08-605-672-37	Sequence 37, Appl
513	75	4.8	1151	1	US-08-482-293A-37	Sequence 37, Appl
514	75	4.8	1151	1	US-08-943-363-37	Sequence 37, Appl
515	75	4.8	1151	2	US-09-193-043-37	Sequence 37, Appl
516	75	4.8	1151	2	US-09-688-307A-37	Sequence 37, Appl
517	75	4.8	1151	2	US-09-350-259-37	Sequence 37, Appl
518	75	4.8	1161	2	US-09-193-043-55	Sequence 55, Appl
519	75	4.8	1161	2	US-09-688-307A-55	Sequence 55, Appl
520	75	4.8	1161	2	US-09-350-259-55	Sequence 55, Appl
521	75	4.8	1162	1	US-08-728-323A-2	Sequence 2, Appli
522	75	4.8	1162	2	US-09-298-568-2	Sequence 2, Appli
523	75	4.8	1162	2	US-09-410-399-2	Sequence 2, Appli
524	75	4.8	1162	2	US-09-894-273-2	Sequence 2, Appli
525	75	4.8	1270	2	US-07-757-022B-44	Sequence 44, Appl
526	75	4.8	1311	2	US-07-757-022B-42	Sequence 42, Appl
527	75	4.8	1313	2	US-07-757-022B-142	Sequence 142, App
528	75	4.8	1314	2	US-07-757-022B-50	Sequence 50, Appl
529	75	4.8	1320	2	US-07-757-022B-46	Sequence 46, Appl
530	75	4.8	1320	2	US-07-757-022B-60	Sequence 60, Appl
531	75	4.8	1320	2	US-10-164-595-58	Sequence 58, Appl
532	75	4.8	1354	2	US-07-757-022B-48	Sequence 48, Appl
533	75	4.8	1361	2	US-07-757-022B-40	Sequence 40, Appl
534	75	4.8	1363	2	US-07-757-022B-52	Sequence 52, Appl
535	75	4.8	1404	2	US-07-757-022B-2	Sequence 2, Appli
536	75	4.8	1404	2	US-07-757-022B-62	Sequence 62, Appl
537	75	4.8	1404	2	US-10-164-595-78	Sequence 78, Appl
538	75	4.8	1404	2	US-09-298-970A-1	Sequence 1, Appli

539	75	4.8	1404	2	US-09-897-188-1	Sequence 1, Appli
540	75	4.8	1411	2	US-09-949-016-10827	Sequence 10827, A
541	74.5	4.7	109	2	US-09-107-532A-4999	Sequence 4999, Ap
542	74.5	4.7	145	2	US-08-808-599A-41	Sequence 41, Appl
543	74.5	4.7	186	2	US-09-252-991A-20433	Sequence 20433, A
544	74.5	4.7	216	2	US-09-248-796A-25076	Sequence 25076, A
545	74.5	4.7	270	2	US-09-134-000C-3553	Sequence 3553, Ap
546	74.5	4.7	312	2	US-09-248-796A-20143	Sequence 20143, A
547	74.5	4.7	333	2	US-09-107-532A-6475	Sequence 6475, Ap
548	74.5	4.7	386	2	US-09-270-767-44120	Sequence 44120, A
549	74.5	4.7	429	2	US-09-949-016-8183	Sequence 8183, Ap
550	74.5	4.7	429	2	US-09-949-016-8184	Sequence 8184, Ap
551	74.5	4.7	478	1	US-08-456-670B-40	Sequence 40, Appl
552	74.5	4.7	478	2	US-09-372-036-40	Sequence 40, Appl
553	74.5	4.7	530	2	US-09-912-935-38	Sequence 38, Appl
554	74.5	4.7	564	2	US-09-949-016-6898	Sequence 6898, Ap
555	74.5	4.7	565	2	US-09-949-016-6902	Sequence 6902, Ap
556	74.5	4.7	587	2	US-09-815-923-4	Sequence 4, Appli
557	74.5	4.7	639	2	US-09-248-796A-20583	Sequence 20583, A
558	74.5	4.7	758	2	US-09-949-016-8288	Sequence 8288, Ap
559	74.5	4.7	794	2	US-09-252-991A-28569	Sequence 28569, A
560	74.5	4.7	998	1	US-08-449-645A-20	Sequence 20, Appl
561	74.5	4.7	998	1	US-08-702-367A-20	Sequence 20, Appl
562	74.5	4.7	998	4	PCT-US95-04681-20	Sequence 20, Appl
563	74.5	4.7	1638	2	US-09-071-035-258	Sequence 258, App
564	74.5	4.7	1638	2	US-09-071-035-262	Sequence 262, App
565	74.5	4.7	1638	2	US-09-071-035-266	Sequence 266, App
566	74.5	4.7	1638	2	US-10-206-576-258	Sequence 258, App
567	74.5	4.7	1638	2	US-10-206-576-262	Sequence 262, App
568	74.5	4.7	1638	2	US-10-206-576-266	Sequence 266, App
569	74.5	4.7	1747	2	US-09-134-000C-5999	Sequence 5999, Ap
570	74	4.7	197	2	US-09-513-999C-7852	Sequence 7852, Ap
571	74	4.7	257	2	US-09-567-458A-2	Sequence 2, Appli
572	74	4.7	279	2	US-09-248-796A-16859	Sequence 16859, A
573	74	4.7	299	2	US-09-107-433-3811	Sequence 3811, Ap
574	74	4.7	323	2	US-09-270-767-44688	Sequence 44688, A
575	74	4.7	339	1	US-08-433-854-4	Sequence 4, Appli
576	74	4.7	339	1	US-08-174-745A-4	Sequence 4, Appli
577	74	4.7	339	1	US-08-195-947-4	Sequence 4, Appli
578	74	4.7	339	1	US-08-433-885-4	Sequence 4, Appli
579	74	4.7	339	1	US-08-433-908B-4	Sequence 4, Appli
580	74	4.7	339	2	US-08-410-614-4	Sequence 4, Appli
581	74	4.7	370	2	US-09-270-767-37418	Sequence 37418, A
582	74	4.7	370	2	US-09-270-767-52635	Sequence 52635, A
583	74	4.7	395	2	US-09-949-016-9564	Sequence 9564, Ap
584	74	4.7	422	2	US-09-949-016-8251	Sequence 8251, Ap
585	74	4.7	428	2	US-09-134-000C-6457	Sequence 6457, Ap
586	74	4.7	472	2	US-09-625-188-6	Sequence 6, Appli
587	74	4.7	493	2	US-09-248-796A-17819	Sequence 17819, A
588	74	4.7	778	2	US-09-248-796A-16358	Sequence 16358, A
589	74	4.7	823	2	US-09-248-796A-16699	Sequence 16699, A
590	74	4.7	910	2	US-09-270-767-42083	Sequence 42083, A
591	74	4.7	1021	2	US-09-902-540-16773	Sequence 16773, A
592	74	4.7	1693	2	US-08-840-316-1	Sequence 1, Appli
593	74	4.7	1693	2	US-08-809-523-1	Sequence 1, Appli
594	74	4.7	1693	2	US-08-471-971-1	Sequence 1, Appli
595	74	4.7	1693	2	US-09-402-776-1	Sequence 1, Appli
596	74	4.7	1693	2	US-08-470-246-1	Sequence 1, Appli
597	74	4.7	1693	2	US-08-316-765-1	Sequence 1, Appli
598	74	4.7	1693	2	US-09-724-475-1	Sequence 1, Appli
599	74	4.7	1693	4	PCT-US93-08849A-1	Sequence 1, Appli
600	74	4.7	1693	4	PCT-US93-08849-1	Sequence 1, Appli
601	74	4.7	1729	2	US-09-134-000C-5675	Sequence 5675, Ap
602	74	4.7	2414	1	US-08-227-536-2	Sequence 2, Appli
603	74	4.7	2414	2	US-09-538-092-1289	Sequence 1289, Ap
604	74	4.7	2414	4	PCT-US95-04682-2	Sequence 2, Appli
605	74	4.7	3224	1	US-08-705-660-34	Sequence 34, Appl
606	74	4.7	3224	2	US-08-989-045-34	Sequence 34, Appl
607	74	4.7	3224	2	US-09-538-092-1161	Sequence 1161, Ap
608	74	4.7	3224	2	US-09-315-355A-34	Sequence 34, Appl
609	73.5	4.7	124	2	US-08-700-651-11	Sequence 11, Appl
610	73.5	4.7	124	2	US-08-928-361B-16	Sequence 16, Appl
611	73.5	4.7	124	2	US-09-588-995A-16	Sequence 16, Appl
612	73.5	4.7	128	2	US-08-700-651-7	Sequence 7, Appli
613	73.5	4.7	128	2	US-08-928-361B-12	Sequence 12, Appl
614	73.5	4.7	128	2	US-09-588-995A-12	Sequence 12, Appl
615	73.5	4.7	130	2	US-08-700-651-8	Sequence 8, Appli
616	73.5	4.7	130	2	US-08-928-361B-13	Sequence 13, Appl
617	73.5	4.7	130	2	US-09-588-995A-13	Sequence 13, Appl
618	73.5	4.7	138	2	US-08-700-651-10	Sequence 10, Appl
619	73.5	4.7	138	2	US-08-928-361B-15	Sequence 15, Appl
620	73.5	4.7	138	2	US-09-588-995A-15	Sequence 15, Appl
621	73.5	4.7	217	2	US-09-949-016-11174	Sequence 11174, A
622	73.5	4.7	262	2	US-09-248-796A-21451	Sequence 21451, A
623	73.5	4.7	382	2	US-09-248-796A-17276	Sequence 17276, A
624	73.5	4.7	397	2	US-08-991-426-4	Sequence 4, Appli
625	73.5	4.7	397	2	US-09-143-470-4	Sequence 4, Appli
626	73.5	4.7	397	2	US-08-649-006A-4	Sequence 4, Appli
627	73.5	4.7	397	2	US-09-771-023-4	Sequence 4, Appli
628	73.5	4.7	427	1	US-08-282-197C-53	Sequence 53, Appl
629	73.5	4.7	499	2	US-09-561-763-2	Sequence 2, Appli
630	73.5	4.7	499	2	US-09-431-367B-2	Sequence 2, Appli
631	73.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App
632	73.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App
633	73.5	4.7	570	2	US-09-874-923-104	Sequence 104, App
634	73.5	4.7	638	1	US-08-463-262A-11	Sequence 11, Appl
635	73.5	4.7	638	1	US-08-463-989-11	Sequence 11, Appl
636	73.5	4.7	638	2	US-09-003-574-11	Sequence 11, Appl
637	73.5	4.7	638	2	US-09-003-570-11	Sequence 11, Appl
638	73.5	4.7	638	2	US-09-864-541A-11	Sequence 11, Appl
639	73.5	4.7	646	2	US-09-902-540-12044	Sequence 12044, A
640	73.5	4.7	712	2	US-09-949-016-10600	Sequence 10600, A
641	73.5	4.7	713	2	US-08-899-437-2	Sequence 2, Appli
642	73.5	4.7	713	2	US-09-126-121-2	Sequence 2, Appli
643	73.5	4.7	763	2	US-08-961-083-66	Sequence 66, Appl
644	73.5	4.7	763	2	US-09-536-784-66	Sequence 66, Appl
645	73.5	4.7	763	2	US-09-765-271-66	Sequence 66, Appl
646	73.5	4.7	763	2	US-09-765-272A-66	Sequence 66, Appl
647	73.5	4.7	780	2	US-09-248-796A-16702	Sequence 16702, A
648	73.5	4.7	795	2	US-09-193-562D-11	Sequence 11, Appl
649	73.5	4.7	795	2	US-10-055-412B-11	Sequence 11, Appl
650	73.5	4.7	819	2	US-09-468-656A-10	Sequence 10, Appl
651	73.5	4.7	821	2	US-09-193-562D-12	Sequence 12, Appl
652	73.5	4.7	821	2	US-10-055-412B-12	Sequence 12, Appl
653	73.5	4.7	826	2	US-09-769-787-194	Sequence 194, App
654	73.5	4.7	866	1	US-08-405-392-17	Sequence 17, Appl
655	73.5	4.7	866	2	US-08-487-691-17	Sequence 17, Appl
656	73.5	4.7	905	2	US-09-193-562D-2	Sequence 2, Appli
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658	73.5	4.7	919	2	US-09-949-016-6954	Sequence 6954, Ap
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662	73.5	4.7	1876	2	US-09-839-479-70	Sequence 70, Appl
663	73.5	4.7	1878	2	US-09-418-710-13	Sequence 13, Appl
664	73.5	4.7	1878	2	US-09-839-479-13	Sequence 13, Appl
665	73	4.6	155	2	US-09-252-991A-22634	Sequence 22634, A
666	73	4.6	162	2	US-08-700-651-13	Sequence 13, Appl
667	73	4.6	326	2	US-09-248-796A-19891	Sequence 19891, A
668	73	4.6	332	2	US-09-313-942-10	Sequence 10, Appl
669	73	4.6	332	2	US-10-282-162-10	Sequence 10, Appl
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671	73	4.6	380	2	US-09-270-767-43987	Sequence 43987, A
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673	73	4.6	482	2	US-09-990-444-513	Sequence 513, App
674	73	4.6	482	2	US-09-997-333-513	Sequence 513, App
675	73	4.6	482	2	US-09-992-598-513	Sequence 513, App
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677	73	4.6	488	2	US-09-069-781B-5	Sequence 5, Appli
678	73	4.6	488	2	US-09-137-132-5	Sequence 5, Appli
679	73	4.6	488	2	US-08-864-564A-5	Sequence 5, Appli
680	73	4.6	488	2	US-09-094-410-5	Sequence 5, Appli
681	73	4.6	488	2	US-08-708-123D-5	Sequence 5, Appli
682	73	4.6	488	2	US-08-583-153A-5	Sequence 5, Appli
683	73	4.6	488	2	US-08-638-524B-5	Sequence 5, Appli
684	73	4.6	497	2	US-08-956-171E-5234	Sequence 5234, Ap

685	73	4.6	497	2	US-08-781-986A-5234	Sequence 5234, Ap
686	73	4.6	579	2	US-09-198-452A-918	Sequence 918, App
687	73	4.6	606	2	US-09-438-185A-853	Sequence 853, App
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691	73	4.6	658	2	US-09-312-611-4	Sequence 4, Appli
692	73	4.6	708	1	US-07-797-556-2	Sequence 2, Appli
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695	73	4.6	708	1	US-09-059-099-2	Sequence 2, Appli
696	73	4.6	708	2	US-09-058-264-2	Sequence 2, Appli
697	73	4.6	708	2	US-09-455-962-2	Sequence 2, Appli
698	73	4.6	708	4	PCT-US95-06530-2	Sequence 2, Appli
699	73	4.6	830	2	US-09-107-433-4309	Sequence 4309, Ap
700	73	4.6	851	2	US-09-583-110-3850	Sequence 3850, Ap
701	73	4.6	852	2	US-09-206-551-19	Sequence 19, Appl
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703	73	4.6	859	2	US-10-282-162-7	Sequence 7, Appli
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705	73	4.6	918	2	US-09-312-611-6	Sequence 6, Appli
706	73	4.6	918	2	US-09-853-180B-3	Sequence 3, Appli
707	73	4.6	918	2	US-09-949-002-333	Sequence 333, App
708	73	4.6	933	1	US-08-682-847-2	Sequence 2, Appli
709	73	4.6	937	2	US-09-949-002-536	Sequence 536, App
710	73	4.6	951	2	US-09-313-942-9	Sequence 9, Appli
711	73	4.6	951	2	US-10-282-162-9	Sequence 9, Appli
712	73	4.6	1158	2	US-09-313-942-26	Sequence 26, Appl
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714	73	4.6	1168	2	US-09-313-942-24	Sequence 24, Appl
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717	73	4.6	1702	2	US-09-839-996-5	Sequence 5, Appli
718	73	4.6	1702	2	US-10-080-505-5	Sequence 5, Appli
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721	73	4.6	2285	2	US-09-308-375-2	Sequence 2, Appli
722	73	4.6	2285	2	US-09-932-183A-2	Sequence 2, Appli
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726	72.5	4.6	167	2	US-08-956-171E-5216	Sequence 5216, Ap
727	72.5	4.6	167	2	US-08-781-986A-5216	Sequence 5216, Ap
728	72.5	4.6	185	2	US-09-248-796A-18311	Sequence 18311, A
729	72.5	4.6	204	2	US-09-902-540-14080	Sequence 14080, A
730	72.5	4.6	206	2	US-09-198-452A-879	Sequence 879, App
731	72.5	4.6	206	2	US-09-438-185A-822	Sequence 822, App
732	72.5	4.6	293	2	US-09-496-320-5	Sequence 5, Appli
733	72.5	4.6	315	2	US-09-328-352-5948	Sequence 5948, Ap
734	72.5	4.6	328	2	US-09-489-039A-12803	Sequence 12803, A
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736	72.5	4.6	378	2	US-09-248-796A-18526	Sequence 18526, A
737	72.5	4.6	428	2	US-09-489-039A-10901	Sequence 10901, A
738	72.5	4.6	445	2	US-09-710-279-1294	Sequence 1294, Ap
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741	72.5	4.6	494	2	US-09-902-540-9960	Sequence 9960, Ap
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744	72.5	4.6	608	2	US-09-949-016-11149	Sequence 11149, A
745	72.5	4.6	608	2	US-09-949-016-11150	Sequence 11150, A
746	72.5	4.6	608	2	US-09-949-016-11151	Sequence 11151, A
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748	72.5	4.6	652	2	US-08-842-248A-4	Sequence 4, Appli
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756	72.5	4.6	758	2	US-08-643-839-1	Sequence 1, Appli
757	72.5	4.6	758	2	US-09-051-363-24	Sequence 24, Appl
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759	72.5	4.6	758	2	US-10-105-901A-1	Sequence 1, Appli
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761	72.5	4.6	780	1	US-08-786-164-14	Sequence 14, Appl
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769	72.5	4.6	907	2	US-09-328-599A-1	Sequence 1, Appli
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777	72.5	4.6	2308	1	US-08-448-164-1	Sequence 1, Appli
778	72.5	4.6	2308	2	US-08-081-929-2	Sequence 2, Appli
779	72.5	4.6	2308	2	US-10-000-954-2	Sequence 2, Appli
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782	72.5	4.6	3256	2	US-09-919-172-98	Sequence 98, Appl
783	72.5	4.6	3256	2	US-09-976-594-22	Sequence 22, Appl
784	72.5	4.6	3256	2	US-09-919-039-21	Sequence 21, Appl
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787	72	4.6	303	2	US-09-270-767-57613	Sequence 57613, A
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791	72	4.6	342	2	US-09-949-016-10365	Sequence 10365, A
792	72	4.6	401	2	US-09-270-767-44680	Sequence 44680, A
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794	72	4.6	456	2	US-09-611-781-2	Sequence 2, Appli
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798	72	4.6	559	2	US-09-545-814-14	Sequence 14, Appl
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805	72	4.6	785	2	US-09-539-879A-3	Sequence 3, Appli
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807	72	4.6	813	2	US-09-964-899-25	Sequence 25, Appl
808	72	4.6	903	2	US-09-193-562D-46	Sequence 46, Appl
809	72	4.6	903	2	US-09-623-624-18	Sequence 18, Appl
810	72	4.6	903	2	US-10-055-412B-46	Sequence 46, Appl
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817	72	4.6	2441	2	US-08-961-739-2	Sequence 2, Appli
818	72	4.6	2441	2	US-09-514-247A-8	Sequence 8, Appli
819	72	4.6	2441	2	US-09-686-316-2	Sequence 2, Appli
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824	71.5	4.5	232	2	US-09-746-311B-366	Sequence 366, App
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835	71.5	4.5	540	2	US-09-538-092-793	Sequence 793, App
836	71.5	4.5	556	2	US-09-949-016-11052	Sequence 11052, A
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841	71.5	4.5	681	2	US-09-336-910A-2	Sequence 2, Appli
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844	71.5	4.5	1709	2	US-09-949-016-11345	Sequence 11345, A
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846	71.5	4.5	1751	2	US-09-136-574A-44	Sequence 44, Appl
847	71.5	4.5	3174	1	US-08-477-451-3	Sequence 3, Appli
848	71	4.5	144	2	US-09-252-991A-23388	Sequence 23388, A
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851	71	4.5	189	2	US-09-270-767-39457	Sequence 39457, A
852	71	4.5	189	2	US-09-270-767-54674	Sequence 54674, A
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854	71	4.5	230	2	US-09-248-796A-22910	Sequence 22910, A
855	71	4.5	239	2	US-09-248-796A-16743	Sequence 16743, A
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859	71	4.5	316	2	US-09-954-314-10	Sequence 10, Appl
860	71	4.5	316	2	US-10-230-562-10	Sequence 10, Appl
861	71	4.5	385	2	US-09-248-796A-23097	Sequence 23097, A
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865	71	4.5	610	1	US-08-119-262B-6	Sequence 6, Appli
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867	71	4.5	610	1	US-08-234-265A-11	Sequence 11, Appl
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869	71	4.5	633	2	US-09-248-796A-20407	Sequence 20407, A
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871	71	4.5	1011	2	US-09-602-362E-27	Sequence 27, Appl
872	71	4.5	1239	2	US-10-076-622-577	Sequence 577, App
873	71	4.5	1374	2	US-09-771-161A-267	Sequence 267, App
874	71	4.5	1841	2	US-09-477-962-99	Sequence 99, Appl
875	71	4.5	1938	2	US-09-949-016-6609	Sequence 6609, Ap
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877	71	4.5	2035	1	US-08-393-703-5	Sequence 5, Appli
878	71	4.5	2035	4	PCT-US93-11721-5	Sequence 5, Appli
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887	70.5	4.5	213	2	US-09-538-092-1255	Sequence 1255, Ap
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889	70.5	4.5	220	2	US-09-438-185A-442	Sequence 442, App
890	70.5	4.5	232	2	US-09-333-809-214	Sequence 214, App
891	70.5	4.5	232	2	US-09-333-809-215	Sequence 215, App
892	70.5	4.5	232	2	US-09-333-809-216	Sequence 216, App
893	70.5	4.5	232	2	US-09-746-311B-363	Sequence 363, App
894	70.5	4.5	232	2	US-09-746-311B-364	Sequence 364, App
895	70.5	4.5	232	2	US-09-746-311B-365	Sequence 365, App
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901	70.5	4.5	292	2	US-08-852-020-6	Sequence 6, Appli
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905	70.5	4.5	432	2	US-09-134-000C-3498	Sequence 3498, Ap
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910	70.5	4.5	497	2	US-10-104-047-3603	Sequence 3603, Ap
911	70.5	4.5	522	2	US-09-538-092-1096	Sequence 1096, Ap
912	70.5	4.5	526	2	US-09-487-558B-362	Sequence 362, App
913	70.5	4.5	574	2	US-09-248-796A-16162	Sequence 16162, A
914	70.5	4.5	639	2	US-09-252-991A-24474	Sequence 24474, A
915	70.5	4.5	676	2	US-09-003-574-34	Sequence 34, Appl
916	70.5	4.5	676	2	US-09-003-570-34	Sequence 34, Appl
917	70.5	4.5	676	2	US-09-864-541A-34	Sequence 34, Appl
918	70.5	4.5	678	2	US-09-991-181-179	Sequence 179, App
919	70.5	4.5	678	2	US-09-990-444-179	Sequence 179, App
920	70.5	4.5	678	2	US-09-997-333-179	Sequence 179, App
921	70.5	4.5	678	2	US-09-992-598-179	Sequence 179, App
922	70.5	4.5	979	2	US-09-538-092-990	Sequence 990, App
923	70.5	4.5	1014	2	US-09-949-016-8229	Sequence 8229, Ap
924	70.5	4.5	1168	2	US-09-762-311-5	Sequence 5, Appli
925	70.5	4.5	1187	2	US-09-949-016-6513	Sequence 6513, Ap
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928	70.5	4.5	1980	2	US-10-638-333-3	Sequence 3, Appli
929	70.5	4.5	1980	2	US-10-747-133A-3	Sequence 3, Appli
930	70.5	4.5	2169	2	US-09-949-016-6930	Sequence 6930, Ap
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932	70.5	4.5	2442	2	US-09-538-092-1370	Sequence 1370, Ap
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935	70	4.4	135	2	US-09-270-767-50945	Sequence 50945, A
936	70	4.4	222	2	US-09-252-991A-27628	Sequence 27628, A
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938	70	4.4	236	2	US-09-270-767-59225	Sequence 59225, A
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942	70	4.4	353	2	US-09-902-540-9867	Sequence 9867, Ap
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944	70	4.4	360	2	US-09-807-933B-5	Sequence 5, Appli
945	70	4.4	372	2	US-09-489-039A-13193	Sequence 13193, A
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954	70	4.4	692	2	US-09-003-574-31	Sequence 31, Appl
955	70	4.4	692	2	US-09-003-570-31	Sequence 31, Appl
956	70	4.4	692	2	US-09-864-541A-31	Sequence 31, Appl
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958	70	4.4	843	2	US-09-252-991A-32668	Sequence 32668, A
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961	70	4.4	915	2	US-08-988-242-2	Sequence 2, Appli
962	70	4.4	915	2	US-09-138-735-2	Sequence 2, Appli
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973	69.5	4.4	298	2	US-09-852-797-76	Sequence 76, Appl
974	69.5	4.4	298	2	US-09-853-161-76	Sequence 76, Appl
975	69.5	4.4	298	2	US-10-058-993-76	Sequence 76, Appl
976	69.5	4.4	299	2	US-09-712-363-234	Sequence 234, App

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996	69.5	4.4	339	2	US-09-345-294-18	Sequence 18, Appl
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1015	69.5	4.4	2468	2	US-09-976-594-726	Sequence 726, App
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1030	69	4.4	341	2	US-09-902-540-14167	Sequence 14167, A
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1033	69	4.4	423	2	US-09-248-796A-26813	Sequence 26813, A
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1038	69	4.4	509	2	US-09-292-225-38	Sequence 38, Appl
1039	69	4.4	552	2	US-09-540-236-2610	Sequence 2610, Ap
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1073	68.5	4.3	371	2	US-09-533-029-110	Sequence 110, App
1074	68.5	4.3	391	2	US-09-200-090-4	Sequence 4, Appli
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1078	68.5	4.3	498	2	US-09-309-572-4	Sequence 4, Appli
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1088	68.5	4.3	744	2	US-09-202-178A-3	Sequence 3, Appli
1089	68.5	4.3	756	2	US-09-085-199B-9	Sequence 9, Appli
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1094	68.5	4.3	906	2	US-10-307-389-6	Sequence 6, Appli
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1096	68.5	4.3	1167	2	US-10-274-409-2	Sequence 2, Appli
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1126	68	4.3	527	1	US-08-823-516-144	Sequence 144, App
1127	68	4.3	527	2	US-09-320-774-9	Sequence 9, Appli
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1129	68	4.3	527	2	US-09-381-212-144	Sequence 144, App
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1138	68	4.3	654	2	US-09-315-127-12	Sequence 12, Appl
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1160	68	4.3	1155	1	US-08-485-618-46	Sequence 46, Appl
1161	68	4.3	1155	1	US-08-362-652-46	Sequence 46, Appl
1162	68	4.3	1155	1	US-08-605-672-46	Sequence 46, Appl
1163	68	4.3	1155	1	US-08-482-293A-46	Sequence 46, Appl
1164	68	4.3	1155	1	US-08-943-363-46	Sequence 46, Appl
1165	68	4.3	1155	2	US-09-193-043-46	Sequence 46, Appl
1166	68	4.3	1155	2	US-09-688-307A-46	Sequence 46, Appl
1167	68	4.3	1155	2	US-09-350-259-46	Sequence 46, Appl
1168	68	4.3	1161	1	US-08-485-618-53	Sequence 53, Appl
1169	68	4.3	1161	1	US-08-485-618-55	Sequence 55, Appl
1170	68	4.3	1161	1	US-08-362-652-53	Sequence 53, Appl
1171	68	4.3	1161	1	US-08-362-652-55	Sequence 55, Appl
1172	68	4.3	1161	1	US-08-605-672-53	Sequence 53, Appl
1173	68	4.3	1161	1	US-08-605-672-55	Sequence 55, Appl
1174	68	4.3	1161	1	US-08-482-293A-53	Sequence 53, Appl
1175	68	4.3	1161	1	US-08-482-293A-55	Sequence 55, Appl
1176	68	4.3	1161	1	US-08-943-363-53	Sequence 53, Appl
1177	68	4.3	1161	1	US-08-943-363-55	Sequence 55, Appl
1178	68	4.3	1161	2	US-09-193-043-53	Sequence 53, Appl
1179	68	4.3	1161	2	US-09-688-307A-53	Sequence 53, Appl
1180	68	4.3	1161	2	US-09-350-259-53	Sequence 53, Appl
1181	68	4.3	1181	2	US-09-540-236-3804	Sequence 3804, Ap
1182	68	4.3	1309	2	US-09-862-027-82	Sequence 82, Appl
1183	68	4.3	1341	2	US-09-949-016-6890	Sequence 6890, Ap
1184	68	4.3	1344	2	US-09-949-016-10925	Sequence 10925, A
1185	68	4.3	1541	2	US-08-296-791-3	Sequence 3, Appli
1186	68	4.3	1541	2	US-09-839-996-3	Sequence 3, Appli
1187	68	4.3	1541	2	US-10-080-505-3	Sequence 3, Appli
1188	68	4.3	1541	2	US-10-645-655-3	Sequence 3, Appli
1189	68	4.3	1541	4	PCT-US95-10661A-3	Sequence 3, Appli
1190	68	4.3	1545	2	US-08-296-791-4	Sequence 4, Appli
1191	68	4.3	1545	2	US-09-839-996-4	Sequence 4, Appli
1192	68	4.3	1545	2	US-10-080-505-4	Sequence 4, Appli
1193	68	4.3	1545	2	US-10-645-655-4	Sequence 4, Appli
1194	68	4.3	1545	4	PCT-US95-10661A-4	Sequence 4, Appli
1195	68	4.3	1675	2	US-09-540-236-1994	Sequence 1994, Ap
1196	68	4.3	3712	2	US-10-037-417-48	Sequence 48, Appl
1197	68	4.3	3712	2	US-10-037-417-51	Sequence 51, Appl
1198	67.5	4.3	107	2	US-08-961-083-150	Sequence 150, App
1199	67.5	4.3	107	2	US-09-536-784-150	Sequence 150, App
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1201	67.5	4.3	107	2	US-09-765-272A-150	Sequence 150, App
1202	67.5	4.3	137	2	US-09-583-110-4762	Sequence 4762, Ap
1203	67.5	4.3	140	2	US-09-270-767-42846	Sequence 42846, A
1204	67.5	4.3	143	2	US-09-107-433-2613	Sequence 2613, Ap
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1209	67.5	4.3	223	2	US-09-248-796A-17645	Sequence 17645, A
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1211	67.5	4.3	290	2	US-09-270-767-35246	Sequence 35246, A
1212	67.5	4.3	290	2	US-09-270-767-50463	Sequence 50463, A
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1215	67.5	4.3	301	4	PCT-US93-08528-72	Sequence 72, Appl
1216	67.5	4.3	313	2	US-09-270-767-43688	Sequence 43688, A
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1218	67.5	4.3	319	2	US-09-372-498-2	Sequence 2, Appli
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1220	67.5	4.3	365	1	US-08-437-027-20	Sequence 20, Appl
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1223	67.5	4.3	394	2	US-09-949-016-9565	Sequence 9565, Ap
1224	67.5	4.3	401	2	US-09-248-796A-26759	Sequence 26759, A
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1227	67.5	4.3	410	2	US-09-472-880-2	Sequence 2, Appli
1228	67.5	4.3	410	2	US-09-826-509-537	Sequence 537, App
1229	67.5	4.3	424	2	US-09-248-796A-24117	Sequence 24117, A
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1231	67.5	4.3	437	2	US-09-353-332-2	Sequence 2, Appli
1232	67.5	4.3	451	2	US-09-328-352-6012	Sequence 6012, Ap
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1236	67.5	4.3	498	2	US-09-583-110-2949	Sequence 2949, Ap
1237	67.5	4.3	510	2	US-09-107-433-2618	Sequence 2618, Ap
1238	67.5	4.3	522	2	US-09-198-452A-480	Sequence 480, App
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1240	67.5	4.3	549	2	US-08-461-004A-61	Sequence 61, Appl
1241	67.5	4.3	555	2	US-09-107-532A-6422	Sequence 6422, Ap
1242	67.5	4.3	591	2	US-09-949-016-10914	Sequence 10914, A
1243	67.5	4.3	591	2	US-09-949-016-10915	Sequence 10915, A
1244	67.5	4.3	600	2	US-10-104-047-3397	Sequence 3397, Ap
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1250	67.5	4.3	649	2	US-09-499-522-14	Sequence 14, Appl
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1257	67.5	4.3	664	2	US-09-107-532A-7252	Sequence 7252, Ap
1258	67.5	4.3	802	2	US-09-081-345-18	Sequence 18, Appl
1259	67.5	4.3	802	2	US-09-822-295-18	Sequence 18, Appl
1260	67.5	4.3	812	1	US-08-446-794A-4	Sequence 4, Appli
1261	67.5	4.3	877	1	US-08-916-917-2	Sequence 2, Appli
1262	67.5	4.3	877	1	US-08-972-631-2	Sequence 2, Appli
1263	67.5	4.3	877	1	US-08-972-629-2	Sequence 2, Appli
1264	67.5	4.3	877	1	US-08-972-630-2	Sequence 2, Appli
1265	67.5	4.3	877	1	US-08-672-211-2	Sequence 2, Appli
1266	67.5	4.3	877	2	US-09-225-170-2	Sequence 2, Appli
1267	67.5	4.3	973	2	US-09-430-723-2	Sequence 2, Appli
1268	67.5	4.3	999	2	US-09-438-185A-455	Sequence 455, App

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1270	67.5	4.3	1020	2	US-09-538-092-911	Sequence 911, App
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1275	67.5	4.3	1150	2	US-09-870-122A-3	Sequence 3, Appli
1276	67.5	4.3	1301	2	US-09-071-035-234	Sequence 234, App
1277	67.5	4.3	1301	2	US-09-071-035-238	Sequence 238, App
1278	67.5	4.3	1301	2	US-09-071-035-242	Sequence 242, App
1279	67.5	4.3	1301	2	US-10-206-576-234	Sequence 234, App
1280	67.5	4.3	1301	2	US-10-206-576-238	Sequence 238, App
1281	67.5	4.3	1301	2	US-10-206-576-242	Sequence 242, App
1282	67.5	4.3	1574	2	US-09-302-626B-179	Sequence 179, App
1283	67.5	4.3	1978	2	US-09-302-626B-60	Sequence 60, Appl
1284	67.5	4.3	2453	2	US-09-632-033B-4	Sequence 4, Appli
1285	67.5	4.3	3913	2	US-09-949-016-10933	Sequence 10933, A
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1288	67	4.3	137	2	US-10-104-047-2849	Sequence 2849, Ap
1289	67	4.3	149	2	US-09-513-999C-4813	Sequence 4813, Ap
1290	67	4.3	185	2	US-09-902-540-13687	Sequence 13687, A
1291	67	4.3	197	2	US-09-107-532A-7229	Sequence 7229, Ap
1292	67	4.3	206	2	US-09-328-352-6224	Sequence 6224, Ap
1293	67	4.3	208	2	US-10-104-047-2188	Sequence 2188, Ap
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1295	67	4.3	226	2	US-09-107-532A-3715	Sequence 3715, Ap
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1297	67	4.3	246	1	US-08-294-386C-1	Sequence 1, Appli
1298	67	4.3	246	1	US-08-294-386C-3	Sequence 3, Appli
1299	67	4.3	246	1	US-08-299-249A-1	Sequence 1, Appli
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1301	67	4.3	246	1	US-08-590-708-1	Sequence 1, Appli
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1305	67	4.3	246	4	PCT-US95-10224-3	Sequence 3, Appli
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1311	67	4.3	289	2	US-09-765-271-20	Sequence 20, Appl
1312	67	4.3	289	2	US-09-765-272A-20	Sequence 20, Appl
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1314	67	4.3	309	2	US-09-769-787-156	Sequence 156, App
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1318	67	4.3	373	2	US-09-270-767-46313	Sequence 46313, A
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1321	67	4.3	387	2	US-09-570-778A-7	Sequence 7, Appli
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1323	67	4.3	387	2	US-09-570-778A-9	Sequence 9, Appli
1324	67	4.3	387	2	US-09-991-138-2	Sequence 2, Appli
1325	67	4.3	387	2	US-09-991-138-7	Sequence 7, Appli
1326	67	4.3	387	2	US-09-991-138-8	Sequence 8, Appli
1327	67	4.3	387	2	US-09-991-138-9	Sequence 9, Appli
1328	67	4.3	387	2	US-10-037-677A-4	Sequence 4, Appli
1329	67	4.3	387	2	US-10-037-677A-6	Sequence 6, Appli
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1331	67	4.3	389	2	US-10-641-068-23	Sequence 23, Appl
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1333	67	4.3	416	2	US-09-601-478-1	Sequence 1, Appli
1334	67	4.3	416	2	US-09-601-478-4	Sequence 4, Appli
1335	67	4.3	435	2	US-09-949-016-9133	Sequence 9133, Ap
1336	67	4.3	454	2	US-09-949-016-9823	Sequence 9823, Ap
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1338	67	4.3	465	2	US-08-990-571-30	Sequence 30, Appl
1339	67	4.3	465	2	US-08-723-142A-30	Sequence 30, Appl
1340	67	4.3	465	2	US-09-528-784A-30	Sequence 30, Appl
1341	67	4.3	465	2	US-09-569-098A-30	Sequence 30, Appl
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1352	67	4.3	570	2	US-08-925-588-2	Sequence 2, Appli
1353	67	4.3	570	2	US-09-288-292A-7	Sequence 7, Appli
1354	67	4.3	570	2	US-09-372-044-2	Sequence 2, Appli
1355	67	4.3	570	2	US-08-825-486-2	Sequence 2, Appli
1356	67	4.3	570	2	US-08-826-248-2	Sequence 2, Appli
1357	67	4.3	598	2	US-09-538-092-1083	Sequence 1083, Ap
1358	67	4.3	623	2	US-09-485-529-7	Sequence 7, Appli
1359	67	4.3	645	2	US-10-104-047-3227	Sequence 3227, Ap
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1361	67	4.3	661	1	US-08-786-164-12	Sequence 12, Appl
1362	67	4.3	688	2	US-09-477-962-96	Sequence 96, Appl
1363	67	4.3	699	2	US-09-949-016-6158	Sequence 6158, Ap
1364	67	4.3	702	2	US-09-949-016-11476	Sequence 11476, A
1365	67	4.3	702	2	US-09-949-016-11477	Sequence 11477, A
1366	67	4.3	784	2	US-09-538-092-1254	Sequence 1254, Ap
1367	67	4.3	786	2	US-09-949-016-10170	Sequence 10170, A
1368	67	4.3	863	1	US-08-380-182-19	Sequence 19, Appl
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1370	67	4.3	976	1	US-08-702-367A-18	Sequence 18, Appl
1371	67	4.3	976	2	US-09-949-016-6499	Sequence 6499, Ap
1372	67	4.3	976	4	PCT-US95-04681-18	Sequence 18, Appl
1373	67	4.3	1013	2	US-09-949-016-7991	Sequence 7991, Ap
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1376	67	4.3	1132	2	US-09-569-098A-87	Sequence 87, Appl
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1378	67	4.3	1231	2	US-10-206-576-420	Sequence 420, App
1379	67	4.3	1265	2	US-09-071-035-418	Sequence 418, App
1380	67	4.3	1265	2	US-10-206-576-418	Sequence 418, App
1381	67	4.3	1278	2	US-09-134-000C-6043	Sequence 6043, Ap
1382	67	4.3	1279	2	US-09-710-279-3188	Sequence 3188, Ap
1383	67	4.3	1900	2	US-09-538-092-564	Sequence 564, App
1384	67	4.3	1900	2	US-09-487-558B-390	Sequence 390, App
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1386	67	4.3	2005	2	US-09-457-571-7	Sequence 7, Appli
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1388	67	4.3	3696	2	US-09-134-001C-5080	Sequence 5080, Ap
1389	67	4.3	4377	2	US-09-949-016-6978	Sequence 6978, Ap
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1391	66.5	4.2	91	2	US-08-928-361B-19	Sequence 19, Appl
1392	66.5	4.2	91	2	US-09-588-995A-19	Sequence 19, Appl
1393	66.5	4.2	154	2	US-09-252-991A-32034	Sequence 32034, A
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1395	66.5	4.2	176	2	US-09-252-991A-21933	Sequence 21933, A
1396	66.5	4.2	205	2	US-09-134-000C-4540	Sequence 4540, Ap
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1398	66.5	4.2	206	2	US-08-837-058-6	Sequence 6, Appli
1399	66.5	4.2	206	2	US-09-417-264-6	Sequence 6, Appli
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1401	66.5	4.2	235	2	US-09-903-190-126	Sequence 126, App
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1403	66.5	4.2	236	2	US-09-621-011-202	Sequence 202, App
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1406	66.5	4.2	249	2	US-09-188-811-6	Sequence 6, Appli
1407	66.5	4.2	249	2	US-09-514-422-6	Sequence 6, Appli
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1410	66.5	4.2	265	2	US-09-282-357-39	Sequence 39, Appl
1411	66.5	4.2	284	2	US-09-248-796A-20639	Sequence 20639, A
1412	66.5	4.2	305	2	US-09-134-001C-5038	Sequence 5038, Ap
1413	66.5	4.2	319	2	US-09-107-532A-4723	Sequence 4723, Ap
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1416	66.5	4.2	331	2	US-08-808-720-5	Sequence 5, Appli
1417	66.5	4.2	331	2	US-09-467-638-5	Sequence 5, Appli
1418	66.5	4.2	362	2	US-08-899-437-3	Sequence 3, Appli
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1423	66.5	4.2	387	2	US-09-489-847-372	Sequence 372, App
1424	66.5	4.2	407	1	US-08-776-585-3	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
;  APPLICANT: Steve Daniel
;  APPLICANT: James Gilmore
;  APPLICANT: Susan G. Stuart
;  APPLICANT: Laura Stuve
;  TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
;  TITLE OF INVENTION: PROLIFERATION
;  FILE REFERENCE: PA-0003 US
;  CURRENT APPLICATION NUMBER: US/09/232,160
;  CURRENT FILING DATE: 1999-01-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PERL Program
; SEQ ID NO 21
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 3044710
US-09-232-160-21

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RESULT 2
US-09-907-794A-201
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; Sequence 201, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

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; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
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;  PRIOR APPLICATION NUMBER: PCT/US99/20944
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;  PRIOR APPLICATION NUMBER: PCT/US99/28214
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;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
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;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-905-125A-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
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; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
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;  PRIOR FILING DATE: 1999-07-26
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;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
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;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-775A-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
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  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
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Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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Db        317 CLEAEV 322


RESULT 5
US-09-906-700-201
; Sequence 201, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,700
;  CURRENT FILING DATE:  2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-700-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
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Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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Db        317 CLEAEV 322


RESULT 6
US-09-903-603A-201
; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
```

```
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: GNE.1618P2C12
;  CURRENT APPLICATION NUMBER: US/09/903,603A
;  CURRENT FILING DATE:  2001-07-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-903-603A-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
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Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
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Qy        181 KKLICVTEVFMETSTMSTETEPPVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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RESULT 7
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; Patent No. 6806352
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,920A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
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;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-904-920A-201

  Query Match             100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
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Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPPVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Db        197 KKLICVTEVFMETSTMSTETEPPVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 8
US-09-909-064-201
; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,064
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
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;  PRIOR APPLICATION NUMBER: PCT/US99/20944
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;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-909-064-201

  Query Match             100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
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Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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Db        317 CLEAEV 322


RESULT 9
US-09-905-381A-201
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,381A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Artificial sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic protein
US-09-905-381A-201

  Query Match            100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 10
US-09-906-618-201
; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
```

```
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,618
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;    LENGTH: 322
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic protein
US-09-906-618-201

  Query Match             100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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Db        317 CLEAEV 322


RESULT 11
US-09-906-646-201
; Sequence 201, Application US/09906646
; Patent No. 6852848
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,646
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-646-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 12
US-09-904-462-201
; Sequence 201, Application US/09904462
; Patent No. 6878807
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,462
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-462-201

  Query Match           100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
              ||||||
Db        317 CLEAEV 322


RESULT 13
US-09-902-736A-201
; Sequence 201, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,736A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-902-736A-201

  Query Match             100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

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Qy        301 CLEAEV 306
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Db        317 CLEAEV 322


RESULT 14
US-09-906-722A-201
; Sequence 201, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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;  FILE REFERENCE: GNE.1618P2C61
;  CURRENT APPLICATION NUMBER: US/09/906,722A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
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;  PRIOR FILING DATE: 1999-09-13
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;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic protein
US-09-906-722A-201

  Query Match             100.0%;  Score 1575;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db         17 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 76

Qy         61 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDTWT 136

Qy        121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
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Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Db        197 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 256

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        257 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316

Qy        301 CLEAEV 306
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RESULT 15
US-09-949-016-7765
; Sequence 7765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7765
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7765

  Query Match             100.0%;  Score 1575;  DB 2;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-151;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLGLSLAGKDQVET 60
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Db        159 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 218

Qy        181 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 240
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Db        219 KKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGF 278

Qy        241 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300
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Db        279 CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 338

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Db        339 CLEAEV 344


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